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(54) Title: **COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF LUNG CANCER**

(57) Abstract: Compositions and methods for the therapy and diagnosis of cancer, particularly lung cancer, are disclosed. Illustrative compositions comprise one or more lung tumor polypeptides, immunogenic portions thereof, polynucleotides that encode such polypeptides, antigen presenting cell that expresses such polypeptides, and T cells that are specific for cells expressing such polypeptides. The disclosed compositions are useful, for example, in the diagnosis, prevention and/or treatment of diseases, particularly lung cancer.

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COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF LUNG CANCER

TECHNICAL FIELD OF THE INVENTION

The present invention relates generally to therapy and diagnosis of
5 cancer, such as lung cancer. The invention is more specifically related to polypeptides,
comprising at least a portion of a lung tumor protein, and to polynucleotides encoding
such polypeptides. Such polypeptides and polynucleotides are useful in pharmaceutical
compositions, *e.g.*, vaccines, and other compositions for the diagnosis and treatment of
lung cancer.

10 BACKGROUND OF THE INVENTION

Lung cancer is the primary cause of cancer death among both men and
women in the U.S., with an estimated 172,000 new cases being reported in 1994. The
five-year survival rate among all lung cancer patients, regardless of the stage of disease
at diagnosis, is only 13%. This contrasts with a five-year survival rate of 46% among
15 cases detected while the disease is still localized. However, only 16% of lung cancers
are discovered before the disease has spread.

Early detection is difficult since clinical symptoms are often not seen
until the disease has reached an advanced stage. Currently, diagnosis is aided by the
use of chest x-rays, analysis of the type of cells contained in sputum and fiberoptic
20 examination of the bronchial passages. Treatment regimens are determined by the type
and stage of the cancer, and include surgery, radiation therapy and/or chemotherapy. In
spite of considerable research into therapies for the disease, lung cancer remains
difficult to treat.

Accordingly, there remains a need in the art for improved vaccines,
25 treatment methods and diagnostic techniques for lung cancer.

SUMMARY OF THE INVENTION

In one aspect, the present invention provides polynucleotide
compositions comprising a sequence selected from the group consisting of:

(a) sequences provided in SEQ ID NO: 217-390, 392, 394, 396, 398-420 422-424, 428-433 and 440-583;

(b) complements of the sequences provided in SEQ ID NO: 217-390, 392, 394, 396, 398-420 422-424, 428-433 and 440-583;

5 (c) sequences consisting of at least 20 contiguous residues of a sequence provided in SEQ ID NO: 217-390, 392, 394, 396, 398-420 422-424, 428-433 and 440-583;

(d) sequences that hybridize to a sequence provided in SEQ ID NO: 217-390, 392, 394, 396, 398-420 422-424, 428-433 and 440-583, under moderately
10 stringent conditions;

(e) sequences having at least 75% identity to a sequence of SEQ ID NO: 217-390, 392, 394, 396, 398-420 422-424, 428-433 and 440-583;

(f) sequences having at least 90% identity to a sequence of SEQ ID NO: 217-390, 392, 394, 396, 398-420 422-424, 428-433 and 440-583; and

15 (g) degenerate variants of a sequence provided in SEQ ID NO: 217-390, 392, 394, 396, 398-420 422-424, 428-433 and 440-583.

In one preferred embodiment, the polynucleotide compositions of the invention are expressed in at least about 20%, more preferably in at least about 30%, and most preferably in at least about 50% of lung tumors samples tested, at a level that
20 is at least about 2-fold, preferably at least about 5-fold, and most preferably at least about 10-fold higher than that for normal tissues.

The present invention, in another aspect, provides polypeptide compositions comprising an amino acid sequence that is encoded by a polynucleotide sequence described above.

25 In specific embodiments, the present invention provides polypeptide compositions comprising an amino acid sequence selected from the group consisting of sequences recited in SEQ ID NO: 391, 393, 395, 397, 421, 425-427, 434-439 and 584-587.

In certain preferred embodiments, the polypeptides and/or
30 polynucleotides of the present invention are immunogenic, *i.e.*, they are capable of

eliciting an immune response, particularly a humoral and/or cellular immune response, as further described herein.

The present invention further provides fragments, variants and/or derivatives of the disclosed polypeptide and/or polynucleotide sequences, wherein the fragments, variants and/or derivatives preferably have a level of immunogenic activity of at least about 50%, preferably at least about 70% and more preferably at least about 90% of the level of immunogenic activity of a polypeptide sequence set forth in SEQ ID NOs: 391, 393, 395, 397, 421, 425-427, 434-439 and 584-587 or a polypeptide sequence encoded by a polynucleotide sequence set forth in SEQ ID NOs: 217-390, 392, 394, 396, 398-420 422-424, 428-433 and 440-583.

The present invention further provides polynucleotides that encode a polypeptide described above, expression vectors comprising such polynucleotides and host cells transformed or transfected with such expression vectors.

Within other aspects, the present invention provides pharmaceutical compositions comprising a polypeptide or polynucleotide as described above and a physiologically acceptable carrier.

Within a related aspect of the present invention, the pharmaceutical compositions, *e.g.*, vaccine compositions, are provided for prophylactic or therapeutic applications. Such compositions generally comprise an immunogenic polypeptide or polynucleotide of the invention and an immunostimulant, such as an adjuvant.

The present invention further provides pharmaceutical compositions that comprise: (a) an antibody or antigen-binding fragment thereof that specifically binds to a polypeptide of the present invention, or a fragment thereof; and (b) a physiologically acceptable carrier.

Within further aspects, the present invention provides pharmaceutical compositions comprising: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) a pharmaceutically acceptable carrier or excipient. Illustrative antigen presenting cells include dendritic cells, macrophages, monocytes, fibroblasts and B cells.

Within related aspects, pharmaceutical compositions are provided that comprise: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) an immunostimulant.

The present invention further provides, in other aspects, fusion proteins
5 that comprise at least one polypeptide as described above, as well as polynucleotides encoding such fusion proteins, typically in the form of pharmaceutical compositions, *e.g.*, vaccine compositions, comprising a physiologically acceptable carrier and/or an immunostimulant. The fusions proteins may comprise multiple immunogenic polypeptides or portions/variants thereof, as described herein, and may further comprise
10 one or more polypeptide segments for facilitating the expression, purification and/or immunogenicity of the polypeptide(s).

Within further aspects, the present invention provides methods for stimulating an immune response in a patient, preferably a T cell response in a human patient, comprising administering a pharmaceutical composition described herein. The
15 patient may be afflicted with lung cancer, in which case the methods provide treatment for the disease, or patient considered at risk for such a disease may be treated prophylactically.

Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a
20 patient a pharmaceutical composition as recited above. The patient may be afflicted with lung cancer, in which case the methods provide treatment for the disease, or patient considered at risk for such a disease may be treated prophylactically.

The present invention further provides, within other aspects, methods for removing tumor cells from a biological sample, comprising contacting a biological
25 sample with T cells that specifically react with a polypeptide of the present invention, wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the protein from the sample.

Within related aspects, methods are provided for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological
30 sample treated as described above.

Methods are further provided, within other aspects, for stimulating and/or expanding T cells specific for a polypeptide of the present invention, comprising contacting T cells with one or more of: (i) a polypeptide as described above; (ii) a polynucleotide encoding such a polypeptide; and/or (iii) an antigen presenting cell that
5 expresses such a polypeptide; under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells. Isolated T cell populations comprising T cells prepared as described above are also provided.

Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a
10 patient an effective amount of a T cell population as described above.

The present invention further provides methods for inhibiting the development of a cancer in a patient, comprising the steps of: (a) incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with one or more of: (i) a polypeptide comprising at least an immunogenic portion of polypeptide disclosed herein; (ii) a
15 polynucleotide encoding such a polypeptide; and (iii) an antigen-presenting cell that expressed such a polypeptide; and (b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the development of a cancer in the patient. Proliferated cells may, but need not, be cloned prior to administration to the patient.

20 Within further aspects, the present invention provides methods for determining the presence or absence of a cancer, preferably a lung cancer, in a patient comprising: (a) contacting a biological sample obtained from a patient with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; and (c) comparing the amount of
25 polypeptide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within preferred embodiments, the binding agent is an antibody, more preferably a monoclonal antibody.

The present invention also provides, within other aspects, methods for monitoring the progression of a cancer in a patient. Such methods comprise the steps
30 of: (a) contacting a biological sample obtained from a patient at a first point in time

with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polypeptide detected in step (c) with the amount
5 detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

The present invention further provides, within other aspects, methods for determining the presence or absence of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that
10 hybridizes to a polynucleotide that encodes a polypeptide of the present invention; (b) detecting in the sample a level of a polynucleotide, preferably mRNA, that hybridizes to the oligonucleotide; and (c) comparing the level of polynucleotide that hybridizes to the oligonucleotide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within certain embodiments, the amount
15 of mRNA is detected via polymerase chain reaction using, for example, at least one oligonucleotide primer that hybridizes to a polynucleotide encoding a polypeptide as recited above, or a complement of such a polynucleotide. Within other embodiments, the amount of mRNA is detected using a hybridization technique, employing an oligonucleotide probe that hybridizes to a polynucleotide that encodes a polypeptide as
20 recited above, or a complement of such a polynucleotide.

In related aspects, methods are provided for monitoring the progression of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a polypeptide of the present invention; (b) detecting in the sample an amount of
25 a polynucleotide that hybridizes to the oligonucleotide; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polynucleotide detected in step (c) with the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

Within further aspects, the present invention provides antibodies, such as monoclonal antibodies, that bind to a polypeptide as described above, as well as diagnostic kits comprising such antibodies. Diagnostic kits comprising one or more oligonucleotide probes or primers as described above are also provided.

5 These and other aspects of the present invention will become apparent upon reference to the following detailed description. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

SEQUENCE IDENTIFIERS

10 SEQ ID NO: 1 is the determined cDNA sequence for L363C1.cons
 SEQ ID NO: 2 is the determined cDNA sequence for L263C2.cons
 SEQ ID NO: 3 is the determined cDNA sequence for L263C2c
 SEQ ID NO: 4 is the determined cDNA sequence for L263C1.cons
 SEQ ID NO: 5 is the determined cDNA sequence for L263C1b
15 SEQ ID NO: 6 is the determined cDNA sequence for L164C2.cons
 SEQ ID NO: 7 is the determined cDNA sequence for L164C1.cons
 SEQ ID NO: 8 is the determined cDNA sequence for L366C1a
 SEQ ID NO: 9 is the determined cDNA sequence for L260C1.cons
 SEQ ID NO: 10 is the determined cDNA sequence for L163C1c
20 SEQ ID NO: 11 is the determined cDNA sequence for L163C1b
 SEQ ID NO: 12 is the determined cDNA sequence for L255C1.cons
 SEQ ID NO: 13 is the determined cDNA sequence for L255C1b
 SEQ ID NO: 14 is the determined cDNA sequence for L355C1.cons
 SEQ ID NO: 15 is the determined cDNA sequence for L366C1.cons
25 SEQ ID NO: 16 is the determined cDNA sequence for L163C1a
 SEQ ID NO: 17 is the determined cDNA sequence for LT86-1
 SEQ ID NO: 18 is the determined cDNA sequence for LT86-2
 SEQ ID NO: 19 is the determined cDNA sequence for LT86-3
 SEQ ID NO: 20 is the determined cDNA sequence for LT86-4

SEQ ID NO: 21 is the determined cDNA sequence for LT86-5
SEQ ID NO: 22 is the determined cDNA sequence for LT86-6
SEQ ID NO: 23 is the determined cDNA sequence for LT86-7
SEQ ID NO: 24 is the determined cDNA sequence for LT86-8
5 SEQ ID NO: 25 is the determined cDNA sequence for LT86-9
SEQ ID NO: 26 is the determined cDNA sequence for LT86-10
SEQ ID NO: 27 is the determined cDNA sequence for LT86-11
SEQ ID NO: 28 is the determined cDNA sequence for LT86-12
SEQ ID NO: 29 is the determined cDNA sequence for LT86-13
10 SEQ ID NO: 30 is the determined cDNA sequence for LT86-14
SEQ ID NO: 31 is the determined cDNA sequence for LT86-15
SEQ ID NO: 32 is the predicted amino acid sequence for LT86-1
SEQ ID NO: 33 is the predicted amino acid sequence for LT86-2
SEQ ID NO: 34 is the predicted amino acid sequence for LT86-3
15 SEQ ID NO: 35 is the predicted amino acid sequence for LT86-4
SEQ ID NO: 36 is the predicted amino acid sequence for LT86-5
SEQ ID NO: 37 is the predicted amino acid sequence for LT86-6
SEQ ID NO: 38 is the predicted amino acid sequence for LT86-7
SEQ ID NO: 39 is the predicted amino acid sequence for LT86-8
20 SEQ ID NO: 40 is the predicted amino acid sequence for LT86-9
SEQ ID NO: 41 is the predicted amino acid sequence for LT86-10
SEQ ID NO: 42 is the predicted amino acid sequence for LT86-11
SEQ ID NO: 43 is the predicted amino acid sequence for LT86-12
SEQ ID NO: 44 is the predicted amino acid sequence for LT86-13
25 SEQ ID NO: 45 is the predicted amino acid sequence for LT86-14
SEQ ID NO: 46 is the predicted amino acid sequence for LT86-15
SEQ ID NO: 47 is a (dT)₁₂AG primer
SEQ ID NO: 48 is a primer
SEQ ID NO: 49 is the determined 5' cDNA sequence for L86S-3
30 SEQ ID NO: 50 is the determined 5' cDNA sequence for L86S-12

- SEQ ID NO: 51 is the determined 5' cDNA sequence for L86S-16
SEQ ID NO: 52 is the determined 5' cDNA sequence for L86S-25
SEQ ID NO: 53 is the determined 5' cDNA sequence for L86S-36
SEQ ID NO: 54 is the determined 5' cDNA sequence for L86S-40
5 SEQ ID NO: 55 is the determined 5' cDNA sequence for L86S-46
SEQ ID NO: 56 is the predicted amino acid sequence for L86S-3
SEQ ID NO: 57 is the predicted amino acid sequence for L86S-12
SEQ ID NO: 58 is the predicted amino acid sequence for L86S-16
SEQ ID NO: 59 is the predicted amino acid sequence for L86S-25
10 SEQ ID NO: 60 is the predicted amino acid sequence for L86S-36
SEQ ID NO: 61 is the predicted amino acid sequence for L86S-40
SEQ ID NO: 62 is the predicted amino acid sequence for L86S-46
SEQ ID NO: 63 is the determined 5' cDNA sequence for L86S-30
SEQ ID NO: 64 is the determined 5' cDNA sequence for L86S-41
15 SEQ ID NO: 65 is the predicted amino acid sequence from the 5' end of
LT86-9
SEQ ID NO: 66 is the determined extended cDNA sequence for LT86-4
SEQ ID NO: 67 is the predicted extended amino acid sequence for
LT86-4
20 SEQ ID NO: 68 is the determined 5' cDNA sequence for LT86-20
SEQ ID NO: 69 is the determined 3' cDNA sequence for LT86-21
SEQ ID NO: 70 is the determined 5' cDNA sequence for LT86-22
SEQ ID NO: 71 is the determined 5' cDNA sequence for LT86-26
SEQ ID NO: 72 is the determined 5' cDNA sequence for LT86-27
25 SEQ ID NO: 73 is the predicted amino acid sequence for LT86-20
SEQ ID NO: 74 is the predicted amino acid sequence for LT86-21
SEQ ID NO: 75 is the predicted amino acid sequence for LT86-22
SEQ ID NO: 76 is the predicted amino acid sequence for LT86-26
SEQ ID NO: 77 is the predicted amino acid sequence for LT86-27
30 SEQ ID NO: 78 is the determined extended cDNA sequence for L86S-12

SEQ ID NO: 79 is the determined extended cDNA sequence for L86S-36

SEQ ID NO: 80 is the determined extended cDNA sequence for L86S-46

SEQ ID NO: 81 is the predicted extended amino acid sequence for
L86S-12

5 SEQ ID NO: 82 is the predicted extended amino acid sequence for L86S-

36

SEQ ID NO: 83 is the predicted extended amino acid sequence for
L86S-46

SEQ ID NO: 84 is the determined 5' cDNA sequence for L86S-6

10 SEQ ID NO: 85 is the determined 5' cDNA sequence for L86S-11

SEQ ID NO: 86 is the determined 5' cDNA sequence for L86S-14

SEQ ID NO: 87 is the determined 5' cDNA sequence for L86S-29

SEQ ID NO: 88 is the determined 5' cDNA sequence for L86S-34

SEQ ID NO: 89 is the determined 5' cDNA sequence for L86S-39

15 SEQ ID NO: 90 is the determined 5' cDNA sequence for L86S-47

SEQ ID NO: 91 is the determined 5' cDNA sequence for L86S-49

SEQ ID NO: 92 is the determined 5' cDNA sequence for L86S-51

SEQ ID NO: 93 is the predicted amino acid sequence for L86S-6

SEQ ID NO: 94 is the predicted amino acid sequence for L86S-11

20 SEQ ID NO: 95 is the predicted amino acid sequence for L86S-14

SEQ ID NO: 96 is the predicted amino acid sequence for L86S-29

SEQ ID NO: 97 is the predicted amino acid sequence for L86S-34

SEQ ID NO: 98 is the predicted amino acid sequence for L86S-39

SEQ ID NO: 99 is the predicted amino acid sequence for L86S-47

25 SEQ ID NO: 100 is the predicted amino acid sequence for L86S-49

SEQ ID NO: 101 is the predicted amino acid sequence for L86S-51

SEQ ID NO: 102 is the determined DNA sequence for SLT-T1

SEQ ID NO: 103 is the determined 5' cDNA sequence for SLT-T2

SEQ ID NO: 104 is the determined 5' cDNA sequence for SLT-T3

30 SEQ ID NO: 105 is the determined 5' cDNA sequence for SLT-T5

SEQ ID NO: 106 is the determined 5' cDNA sequence for SLT-T7
SEQ ID NO: 107 is the determined 5' cDNA sequence for SLT-T9
SEQ ID NO: 108 is the determined 5' cDNA sequence for SLT-T10
SEQ ID NO: 109 is the determined 5' cDNA sequence for SLT-T11
5 SEQ ID NO: 110 is the determined 5' cDNA sequence for SLT-T12
SEQ ID NO: 111 is the predicted amino acid sequence for SLT-T1
SEQ ID NO: 112 is the predicted amino acid sequence for SLT-T2
SEQ ID NO: 113 is the predicted amino acid sequence for SLT-T3
SEQ ID NO: 114 is the predicted amino acid sequence for SLT-T10
10 SEQ ID NO: 115 is the predicted amino acid sequence for SLT-T12
SEQ ID NO: 116 is the determined 5' cDNA sequence for SALT-T3
SEQ ID NO: 117 is the determined 5' cDNA sequence for SALT-T4
SEQ ID NO: 118 is the determined 5' cDNA sequence for SALT-T7
SEQ ID NO: 119 is the determined 5' cDNA sequence for SALT-T8
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SEQ ID NO: 121 is the predicted amino acid sequence for SALT-T3
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SEQ ID NO: 124 is the predicted amino acid sequence for SALT-T8
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SEQ ID NO: 133 is the determined cDNA sequence for PSLT-40
SEQ ID NO: 134 is the determined cDNA sequence for PSLT-69
30 SEQ ID NO: 135 is the determined cDNA sequence for PSLT-71

SEQ ID NO: 136 is the determined cDNA sequence for PSLT-73
SEQ ID NO: 137 is the determined cDNA sequence for PSLT-79
SEQ ID NO: 138 is the determined cDNA sequence for PSLT-03
SEQ ID NO: 139 is the determined cDNA sequence for PSLT-09
5 SEQ ID NO: 140 is the determined cDNA sequence for PSLT-011
SEQ ID NO: 141 is the determined cDNA sequence for PSLT-041
SEQ ID NO: 142 is the determined cDNA sequence for PSLT-62
SEQ ID NO: 143 is the determined cDNA sequence for PSLT-6
SEQ ID NO: 144 is the determined cDNA sequence for PSLT-37
10 SEQ ID NO: 145 is the determined cDNA sequence for PSLT-74
SEQ ID NO: 146 is the determined cDNA sequence for PSLT-010
SEQ ID NO: 147 is the determined cDNA sequence for PSLT-012
SEQ ID NO: 148 is the determined cDNA sequence for PSLT-037
SEQ ID NO: 149 is the determined 5' cDNA sequence for SAL-3
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SEQ ID NO: 152 is the determined 5' cDNA sequence for SAL-33
SEQ ID NO: 153 is the determined 5' cDNA sequence for SAL-50
SEQ ID NO: 154 is the determined 5' cDNA sequence for SAL-57
20 SEQ ID NO: 155 is the determined 5' cDNA sequence for SAL-66
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SEQ ID NO: 158 is the determined 5' cDNA sequence for SAL-104
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SEQ ID NO: 161 is the determined 5' cDNA sequence for SAL-8
SEQ ID NO: 162 is the determined 5' cDNA sequence for SAL-12
SEQ ID NO: 163 is the determined 5' cDNA sequence for SAL-14
SEQ ID NO: 164 is the determined 5' cDNA sequence for SAL-16
30 SEQ ID NO: 165 is the determined 5' cDNA sequence for SAL-23

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SEQ ID NO: 168 is the determined 5' cDNA sequence for SAL-32
SEQ ID NO: 169 is the determined 5' cDNA sequence for SAL-39
5 SEQ ID NO: 170 is the determined 5' cDNA sequence for SAL-42
SEQ ID NO: 171 is the determined 5' cDNA sequence for SAL-43
SEQ ID NO: 172 is the determined 5' cDNA sequence for SAL-44
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SEQ ID NO: 174 is the determined 5' cDNA sequence for SAL-68
10 SEQ ID NO: 175 is the determined 5' cDNA sequence for SAL-72
SEQ ID NO: 176 is the determined 5' cDNA sequence for SAL-77
SEQ ID NO: 177 is the determined 5' cDNA sequence for SAL-86
SEQ ID NO: 178 is the determined 5' cDNA sequence for SAL-88
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15 SEQ ID NO: 180 is the determined 5' cDNA sequence for SAL-100
SEQ ID NO: 181 is the determined 5' cDNA sequence for SAL-105
SEQ ID NO: 182 is the predicted amino acid sequence for SAL-3
SEQ ID NO: 183 is the predicted amino acid sequence for SAL-24
SEQ ID NO: 184 is a first predicted amino acid sequence for SAL-25
20 SEQ ID NO: 185 is a second predicted amino acid sequence for SAL-25
SEQ ID NO: 186 is the predicted amino acid sequence for SAL-33
SEQ ID NO: 187 is a first predicted amino acid sequence for SAL-50
SEQ ID NO: 188 is the predicted amino acid sequence for SAL-57
SEQ ID NO: 189 is a first predicted amino acid sequence for SAL-66
25 SEQ ID NO: 190 is a second predicted amino acid sequence for SAL-66
SEQ ID NO: 191 is the predicted amino acid sequence for SAL-82
SEQ ID NO: 192 is the predicted amino acid sequence for SAL-99
SEQ ID NO: 193 is the predicted amino acid sequence for SAL-104
SEQ ID NO: 194 is the predicted amino acid sequence for SAL-5
30 SEQ ID NO: 195 is the predicted amino acid sequence for SAL-8

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SEQ ID NO: 197 is the predicted amino acid sequence for SAL-14
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SEQ ID NO: 201 is the predicted amino acid sequence for SAL-29
SEQ ID NO: 202 is the predicted amino acid sequence for SAL-32
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SEQ ID NO: 211 is the predicted amino acid sequence for SAL-86
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SEQ ID NO: 213 is the predicted amino acid sequence for SAL-93
SEQ ID NO: 214 is the predicted amino acid sequence for SAL-100
20 SEQ ID NO: 215 is the predicted amino acid sequence for SAL-105
SEQ ID NO: 216 is a second predicted amino acid sequence for SAL-50
SEQ ID NO: 217 is the determined cDNA sequence for SSLT-4
SEQ ID NO: 218 is the determined cDNA sequence for SSLT-9
SEQ ID NO: 219 is the determined cDNA sequence for SSLT-10
25 SEQ ID NO: 220 is the determined cDNA sequence for SSLT-12
SEQ ID NO: 221 is the determined cDNA sequence for SSLT-19
SEQ ID NO: 222 is the determined cDNA sequence for SSLT-31
SEQ ID NO: 223 is the determined cDNA sequence for SSLT-38
SEQ ID NO: 224 is the determined cDNA sequence for LT4690-2
30 SEQ ID NO: 225 is the determined cDNA sequence for LT4690-3

SEQ ID NO: 226 is the determined cDNA sequence for LT4690-22
SEQ ID NO: 227 is the determined cDNA sequence for LT4690-24
SEQ ID NO: 228 is the determined cDNA sequence for LT4690-37
SEQ ID NO: 229 is the determined cDNA sequence for LT4690-39
5 SEQ ID NO: 230 is the determined cDNA sequence for LT4690-40
SEQ ID NO: 231 is the determined cDNA sequence for LT4690-41
SEQ ID NO: 232 is the determined cDNA sequence for LT4690-49
SEQ ID NO: 233 is the determined 3' cDNA sequence for LT4690-55
SEQ ID NO: 234 is the determined 5' cDNA sequence for LT4690-55
10 SEQ ID NO: 235 is the determined cDNA sequence for LT4690-59
SEQ ID NO: 236 is the determined cDNA sequence for LT4690-63
SEQ ID NO: 237 is the determined cDNA sequence for LT4690-71
SEQ ID NO: 238 is the determined cDNA sequence for 2LT-3
SEQ ID NO: 239 is the determined cDNA sequence for 2LT-6
15 SEQ ID NO: 240 is the determined cDNA sequence for 2LT-22
SEQ ID NO: 241 is the determined cDNA sequence for 2LT-25
SEQ ID NO: 242 is the determined cDNA sequence for 2LT-26
SEQ ID NO: 243 is the determined cDNA sequence for 2LT-31
SEQ ID NO: 244 is the determined cDNA sequence for 2LT-36
20 SEQ ID NO: 245 is the determined cDNA sequence for 2LT-42
SEQ ID NO: 246 is the determined cDNA sequence for 2LT-44
SEQ ID NO: 247 is the determined cDNA sequence for 2LT-54
SEQ ID NO: 248 is the determined cDNA sequence for 2LT-55
SEQ ID NO: 249 is the determined cDNA sequence for 2LT-57
25 SEQ ID NO: 250 is the determined cDNA sequence for 2LT-58
SEQ ID NO: 251 is the determined cDNA sequence for 2LT-59
SEQ ID NO: 252 is the determined cDNA sequence for 2LT-62
SEQ ID NO: 253 is the determined cDNA sequence for 2LT-63
SEQ ID NO: 254 is the determined cDNA sequence for 2LT-65
30 SEQ ID NO: 255 is the determined cDNA sequence for 2LT-66

SEQ ID NO: 256 is the determined cDNA sequence for 2LT-70
SEQ ID NO: 257 is the determined cDNA sequence for 2LT-73
SEQ ID NO: 258 is the determined cDNA sequence for 2LT-74
SEQ ID NO: 259 is the determined cDNA sequence for 2LT-76
5 SEQ ID NO: 260 is the determined cDNA sequence for 2LT-77
SEQ ID NO: 261 is the determined cDNA sequence for 2LT-78
SEQ ID NO: 262 is the determined cDNA sequence for 2LT-80
SEQ ID NO: 263 is the determined cDNA sequence for 2LT-85
SEQ ID NO: 264 is the determined cDNA sequence for 2LT-87
10 SEQ ID NO: 265 is the determined cDNA sequence for 2LT-89
SEQ ID NO: 266 is the determined cDNA sequence for 2LT-94
SEQ ID NO: 267 is the determined cDNA sequence for 2LT-95
SEQ ID NO: 268 is the determined cDNA sequence for 2LT-98
SEQ ID NO: 269 is the determined cDNA sequence for 2LT-100
15 SEQ ID NO: 270 is the determined cDNA sequence for 2LT-103
SEQ ID NO: 271 is the determined cDNA sequence for 2LT-105
SEQ ID NO: 272 is the determined cDNA sequence for 2LT-107
SEQ ID NO: 273 is the determined cDNA sequence for 2LT-108
SEQ ID NO: 274 is the determined cDNA sequence for 2LT-109
20 SEQ ID NO: 275 is the determined cDNA sequence for 2LT-118
SEQ ID NO: 276 is the determined cDNA sequence for 2LT-120
SEQ ID NO: 277 is the determined cDNA sequence for 2LT-121
SEQ ID NO: 278 is the determined cDNA sequence for 2LT-122
SEQ ID NO: 279 is the determined cDNA sequence for 2LT-124
25 SEQ ID NO: 280 is the determined cDNA sequence for 2LT-126
SEQ ID NO: 281 is the determined cDNA sequence for 2LT-127
SEQ ID NO: 282 is the determined cDNA sequence for 2LT-128
SEQ ID NO: 283 is the determined cDNA sequence for 2LT-129
SEQ ID NO: 284 is the determined cDNA sequence for 2LT-133
30 SEQ ID NO: 285 is the determined cDNA sequence for 2LT-137

SEQ ID NO: 286 is the determined cDNA sequence for LT4690-71

SEQ ID NO: 287 is the determined cDNA sequence for LT4690-82

SEQ ID NO: 288 is the determined full-length cDNA sequence for

SSLT-74

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SEQ ID NO: 289 is the determined cDNA sequence for SSLT-78

SEQ ID NO: 290 is the determined cDNA sequence for SCC1-8.

SEQ ID NO: 291 is the determined cDNA sequence for SCC1-12.

SEQ ID NO: 292 is the determined cDNA sequence for SCC1-336

SEQ ID NO: 293 is the determined cDNA sequence for SCC1-344

10

SEQ ID NO: 294 is the determined cDNA sequence for SCC1-345

SEQ ID NO: 295 is the determined cDNA sequence for SCC1-346

SEQ ID NO: 296 is the determined cDNA sequence for SCC1-348

SEQ ID NO: 297 is the determined cDNA sequence for SCC1-350

SEQ ID NO: 298 is the determined cDNA sequence for SCC1-352

15

SEQ ID NO: 299 is the determined cDNA sequence for SCC1-354

SEQ ID NO: 300 is the determined cDNA sequence for SCC1-355

SEQ ID NO: 301 is the determined cDNA sequence for SCC1-356

SEQ ID NO: 302 is the determined cDNA sequence for SCC1-357

SEQ ID NO: 303 is the determined cDNA sequence for SCC1-501

20

SEQ ID NO: 304 is the determined cDNA sequence for SCC1-503

SEQ ID NO: 305 is the determined cDNA sequence for SCC1-513

SEQ ID NO: 306 is the determined cDNA sequence for SCC1-516

SEQ ID NO: 307 is the determined cDNA sequence for SCC1-518

SEQ ID NO: 308 is the determined cDNA sequence for SCC1-519

25

SEQ ID NO: 309 is the determined cDNA sequence for SCC1-522

SEQ ID NO: 310 is the determined cDNA sequence for SCC1-523

SEQ ID NO: 311 is the determined cDNA sequence for SCC1-525

SEQ ID NO: 312 is the determined cDNA sequence for SCC1-527

SEQ ID NO: 313 is the determined cDNA sequence for SCC1-529

30

SEQ ID NO: 314 is the determined cDNA sequence for SCC1-530

SEQ ID NO: 315 is the determined cDNA sequence for SCC1-531
SEQ ID NO: 316 is the determined cDNA sequence for SCC1-532
SEQ ID NO: 317 is the determined cDNA sequence for SCC1-533
SEQ ID NO: 318 is the determined cDNA sequence for SCC1-536
5 SEQ ID NO: 319 is the determined cDNA sequence for SCC1-538
SEQ ID NO: 320 is the determined cDNA sequence for SCC1-539
SEQ ID NO: 321 is the determined cDNA sequence for SCC1-541
SEQ ID NO: 322 is the determined cDNA sequence for SCC1-542
SEQ ID NO: 323 is the determined cDNA sequence for SCC1-546
10 SEQ ID NO: 324 is the determined cDNA sequence for SCC1-549
SEQ ID NO: 325 is the determined cDNA sequence for SCC1-551
SEQ ID NO: 326 is the determined cDNA sequence for SCC1-552
SEQ ID NO: 327 is the determined cDNA sequence for SCC1-554
SEQ ID NO: 328 is the determined cDNA sequence for SCC1-558
15 SEQ ID NO: 329 is the determined cDNA sequence for SCC1-559
SEQ ID NO: 330 is the determined cDNA sequence for SCC1-561
SEQ ID NO: 331 is the determined cDNA sequence for SCC1-562
SEQ ID NO: 332 is the determined cDNA sequence for SCC1-564
SEQ ID NO: 333 is the determined cDNA sequence for SCC1-565
20 SEQ ID NO: 334 is the determined cDNA sequence for SCC1-566
SEQ ID NO: 335 is the determined cDNA sequence for SCC1-567
SEQ ID NO: 336 is the determined cDNA sequence for SCC1-568
SEQ ID NO: 337 is the determined cDNA sequence for SCC1-570
SEQ ID NO: 338 is the determined cDNA sequence for SCC1-572
25 SEQ ID NO: 339 is the determined cDNA sequence for SCC1-575
SEQ ID NO: 340 is the determined cDNA sequence for SCC1-576
SEQ ID NO: 341 is the determined cDNA sequence for SCC1-577
SEQ ID NO: 342 is the determined cDNA sequence for SCC1-578
SEQ ID NO: 343 is the determined cDNA sequence for SCC1-582
30 SEQ ID NO: 344 is the determined cDNA sequence for SCC1-583

SEQ ID NO: 345 is the determined cDNA sequence for SCC1-586
SEQ ID NO: 346 is the determined cDNA sequence for SCC1-588
SEQ ID NO: 347 is the determined cDNA sequence for SCC1-590
SEQ ID NO: 348 is the determined cDNA sequence for SCC1-591
5 SEQ ID NO: 349 is the determined cDNA sequence for SCC1-592
SEQ ID NO: 350 is the determined cDNA sequence for SCC1-593
SEQ ID NO: 351 is the determined cDNA sequence for SCC1-594
SEQ ID NO: 352 is the determined cDNA sequence for SCC1-595
SEQ ID NO: 353 is the determined cDNA sequence for SCC1-596
10 SEQ ID NO: 354 is the determined cDNA sequence for SCC1-598
SEQ ID NO: 355 is the determined cDNA sequence for SCC1-599
SEQ ID NO: 356 is the determined cDNA sequence for SCC1-602
SEQ ID NO: 357 is the determined cDNA sequence for SCC1-604
SEQ ID NO: 358 is the determined cDNA sequence for SCC1-605
15 SEQ ID NO: 359 is the determined cDNA sequence for SCC1-606
SEQ ID NO: 360 is the determined cDNA sequence for SCC1-607
SEQ ID NO: 361 is the determined cDNA sequence for SCC1-608
SEQ ID NO: 362 is the determined cDNA sequence for SCC1-610
SEQ ID NO: 363 is the determined cDNA sequence for clone DMS79T1
20 SEQ ID NO: 364 is the determined cDNA sequence for clone DMS79T2
SEQ ID NO: 365 is the determined cDNA sequence for clone DMS79T3
SEQ ID NO: 366 is the determined cDNA sequence for clone DMS79T5
SEQ ID NO: 367 is the determined cDNA sequence for clone DMS79T6
SEQ ID NO: 368 is the determined cDNA sequence for clone DMS79T7
25 SEQ ID NO: 369 is the determined cDNA sequence for clone DMS79T9
SEQ ID NO: 370 is the determined cDNA sequence for clone
DMS79T10
SEQ ID NO: 371 is the determined cDNA sequence for clone
DMS79T11
30 SEQ ID NO: 372 is the determined cDNA sequence for clone 128T1

SEQ ID NO: 373 is the determined cDNA sequence for clone 128T2
SEQ ID NO: 374 is the determined cDNA sequence for clone 128T3
SEQ ID NO: 375 is the determined cDNA sequence for clone 128T4
SEQ ID NO: 376 is the determined cDNA sequence for clone 128T5
5 SEQ ID NO: 377 is the determined cDNA sequence for clone 128T7
SEQ ID NO: 378 is the determined cDNA sequence for clone 128T9
SEQ ID NO: 379 is the determined cDNA sequence for clone 128T10
SEQ ID NO: 380 is the determined cDNA sequence for clone 128T11
SEQ ID NO: 381 is the determined cDNA sequence for clone 128T12
10 SEQ ID NO: 382 is the determined cDNA sequence for clone
NCIH69T3
SEQ ID NO: 383 is the determined cDNA sequence for clone
NCIH69T5
SEQ ID NO: 384 is the determined cDNA sequence for clone
15 NCIH69T6
SEQ ID NO: 385 is the determined cDNA sequence for clone
NCIH69T7
SEQ ID NO: 386 is the determined cDNA sequence for clone
NCIH69T9
20 SEQ ID NO: 387 is the determined cDNA sequence for clone
NCIH69T10
SEQ ID NO: 388 is the determined cDNA sequence for clone
NCIH69T11
SEQ ID NO: 389 is the determined cDNA sequence for clone
25 NCIH69T12
SEQ ID NO: 390 is the full-length cDNA sequence for 128T1
SEQ ID NO: 391 is the amino acid sequence for 128T1
SEQ ID NO: 392 is the full-length cDNA sequence for 2LT-128
SEQ ID NO: 393 is the amino acid sequence for 2LT-128
30 SEQ ID NO: 394 is an extended cDNA sequence for clone SCC1-542

SEQ ID NO: 395 is the amino acid sequence corresponding to SEQ ID

NO:394

SEQ ID NO: 396 is an extended cDNA sequence for clone SCC1-593

SEQ ID NO: 397 is the amino acid sequence corresponding to SEQ ID

5 NO:396

SEQ ID NO:398 is the determined cDNA sequence for 55508.1

SEQ ID NO:399 is the determined cDNA sequence for 55509.1

SEQ ID NO:400 is the determined cDNA sequence for 54243.1

SEQ ID NO:401 is the determined cDNA sequence for 54251.1

10 SEQ ID NO:402 is the determined cDNA sequence for 54252.1

SEQ ID NO:403 is the determined cDNA sequence for 54253.1

SEQ ID NO:404 is the determined cDNA sequence for 55518.1

SEQ ID NO:405 is the determined cDNA sequence for 54258.1

SEQ ID NO:406 is the determined cDNA sequence for 54575.1

15 SEQ ID NO:407 is the determined cDNA sequence for 54577.1

SEQ ID NO:408 is the determined cDNA sequence for 54584.1

SEQ ID NO:409 is the determined cDNA sequence for 55521.1

SEQ ID NO:410 is the determined cDNA sequence for 54589.1

SEQ ID NO:411 is the determined cDNA sequence for 54592.1

20 SEQ ID NO:412 is the determined cDNA sequence for 55134.1

SEQ ID NO:413 is the determined cDNA sequence for 55137.1

SEQ ID NO:414 is the determined cDNA sequence for 55140.1

SEQ ID NO:415 is the determined cDNA sequence for 55531.1

SEQ ID NO:416 is the determined cDNA sequence for 55532.1

25 SEQ ID NO:417 is the determined cDNA sequence for 54621.1

SEQ ID NO:418 is the determined cDNA sequence for 55548.1

SEQ ID NO:419 is the determined cDNA sequence for 54623.1

SEQ ID NO:420 is the determined cDNA sequence for L39

SEQ ID NO:421 is the predicted amino acid sequence for L39

30 SEQ ID NO:422 is the determined cDNA sequence for SCC2-29

SEQ ID NO:423 is the determined cDNA sequence for SCC2-36

SEQ ID NO:424 is the determined cDNA sequence for SCC2-60

SEQ ID NO:425 is the predicted amino acid sequence for SCC2-29

SEQ ID NO:426 is the predicted amino acid sequence for SCC2-36

5 SEQ ID NO:427 is the predicted amino acid sequence for SCC2-60

SEQ ID NO:428 is an extended cDNA sequence for the clone 20129,
also referred to as 2LT-3, set forth in SEQ ID NO: 238

SEQ ID NO:429 is an extended cDNA sequence for the clone 20347,
also referred to as 2LT-26, set forth in SEQ ID NO: 242

10 SEQ ID NO:430 is an extended cDNA sequence for the clone 21282,
also referred to as 2LT-57, set forth in SEQ ID NO: 249

SEQ ID NO:431 is an extended cDNA sequence for the clone 21283,
also referred to as 2LT-58, set forth in SEQ ID NO: 250

15 SEQ ID NO:432 is an extended cDNA sequence for the clone 21484,
also referred to as 2LT-98, set forth in SEQ ID NO: 268

SEQ ID NO:433 is an extended cDNA sequence for the clone 21871,
also referred to as 2LT-124, set forth in SEQ ID NO: 279

SEQ ID NO:434 is an amino acid sequence encoded by SEQ ID NO: 428

SEQ ID NO:435 is an amino acid sequence encoded by SEQ ID NO: 429

20 SEQ ID NO:436 is an amino acid sequence encoded by SEQ ID NO: 430

SEQ ID NO:437 is an amino acid sequence encoded by SEQ ID NO: 431

SEQ ID NO:438 is an amino acid sequence encoded by SEQ ID NO: 432

SEQ ID NO:439 is an amino acid sequence encoded by SEQ ID NO: 433

SEQ ID NO:440 is the determined cDNA sequence for clone 19A4

25 SEQ ID NO: 441 is the determined full-length cDNA sequence for clone
14F10.

SEQ ID NO: 442 is the determined 5' cDNA sequence for clone 20E10.

SEQ ID NO: 443 is a first determined cDNA sequence for clone 55153.

30 SEQ ID NO: 444 is a second determined cDNA sequence for clone
55153.

SEQ ID NO: 445 is a first determined cDNA sequence for clone 55154.

SEQ ID NO: 446 is a second determined cDNA sequence for clone
55154.

SEQ ID NO: 447 is the determined cDNA sequence for clone 55155.

5 SEQ ID NO: 448 is a first determined cDNA sequence for clone 55156.

SEQ ID NO: 449 is a second determined cDNA sequence for clone
55156.

SEQ ID NO: 450 is a first determined cDNA sequence for clone 55157.

10 SEQ ID NO: 451 is a second determined cDNA sequence for clone
55157.

SEQ ID NO: 452 is the determined cDNA sequence for clone 55158.

SEQ ID NO: 453 is the determined cDNA sequence for clone 55159.

SEQ ID NO: 454 is a first determined cDNA sequence for clone 55161.

15 SEQ ID NO: 455 is a second determined cDNA sequence for clone
55161.

SEQ ID NO: 456 is a first determined cDNA sequence for clone 55162.

SEQ ID NO: 457 is a second determined cDNA sequence for clone
55162.

SEQ ID NO: 458 is a first determined cDNA sequence for clone 55163.

20 SEQ ID NO: 459 is a second determined cDNA sequence for clone
55163.

SEQ ID NO: 460 is a first determined cDNA sequence for clone 55164.

SEQ ID NO: 461 is a second determined cDNA sequence for clone
55164.

25 SEQ ID NO: 462 is a first determined cDNA sequence for clone 55165.

SEQ ID NO: 463 is a second determined cDNA sequence for clone
55165.

SEQ ID NO: 464 is a first determined cDNA sequence for clone 55166.

30 SEQ ID NO: 465 is a second determined cDNA sequence for clone
55166.

SEQ ID NO: 466 is a first determined cDNA sequence for clone 55167.

SEQ ID NO: 467 is a second determined cDNA sequence for clone
55167.

SEQ ID NO: 468 is a first determined cDNA sequence for clone 55168.

5 SEQ ID NO: 469 is a second determined cDNA sequence for clone
55168.

SEQ ID NO: 470 is a first determined cDNA sequence for clone 55169.

SEQ ID NO: 471 is a second determined cDNA sequence for clone
55169.

10 SEQ ID NO: 472 is a first determined cDNA sequence for clone 55170.

SEQ ID NO: 473 is a second determined cDNA sequence for clone
55170.

SEQ ID NO: 474 is the determined cDNA sequence for clone 55171.

SEQ ID NO: 475 is the determined cDNA sequence for clone 55172.

15 SEQ ID NO: 476 is the determined cDNA sequence for clone 55173.

SEQ ID NO: 477 is a first determined cDNA sequence for clone 55174.

SEQ ID NO: 478 is a second determined cDNA sequence for clone
55174.

SEQ ID NO: 479 is the determined cDNA sequence for clone 55175.

20 SEQ ID NO: 480 is the determined cDNA sequence for clone 55176.

SEQ ID NO: 481 is the determined cDNA sequence for contig 525.

SEQ ID NO: 482 is the determined cDNA sequence for contig 526.

SEQ ID NO: 483 is the determined cDNA sequence for contig 527.

SEQ ID NO: 484 is the determined cDNA sequence for contig 528.

25 SEQ ID NO: 485 is the determined cDNA sequence for contig 529.

SEQ ID NO: 486 is the determined cDNA sequence for contig 530.

SEQ ID NO: 487 is the determined cDNA sequence for contig 531.

SEQ ID NO: 488 is the determined cDNA sequence for contig 532.

SEQ ID NO: 489 is the determined cDNA sequence for contig 533.

30 SEQ ID NO: 490 is the determined cDNA sequence for contig 534.

SEQ ID NO: 491 is the determined cDNA sequence for contig 535.
SEQ ID NO: 492 is the determined cDNA sequence for contig 536.
SEQ ID NO: 493 is the determined cDNA sequence for contig 537.
SEQ ID NO: 494 is the determined cDNA sequence for contig 538.
5 SEQ ID NO: 495 is the determined cDNA sequence for contig 539.
SEQ ID NO: 496 is the determined cDNA sequence for contig 540.
SEQ ID NO: 497 is the determined cDNA sequence for contig 541.
SEQ ID NO: 498 is the determined cDNA sequence for contig 542.
SEQ ID NO: 499 is the determined cDNA sequence for contig 543.
10 SEQ ID NO: 500 is the determined cDNA sequence for contig 544.
SEQ ID NO: 501 is the determined cDNA sequence for contig 545.
SEQ ID NO: 502 is the determined cDNA sequence for contig 546.
SEQ ID NO: 503 is the determined cDNA sequence for contig 547.
SEQ ID NO: 504 is the determined cDNA sequence for contig 548.
15 SEQ ID NO: 505 is the determined cDNA sequence for contig 549.
SEQ ID NO: 506 is the determined cDNA sequence for contig 550.
SEQ ID NO: 507 is the determined cDNA sequence for contig 551.
SEQ ID NO: 508 is the determined cDNA sequence for contig 552.
SEQ ID NO: 509 is the determined cDNA sequence for contig 553.
20 SEQ ID NO: 510 is the determined cDNA sequence for contig 554.
SEQ ID NO: 511 is the determined cDNA sequence for contig 555.
SEQ ID NO: 512 is the determined cDNA sequence for clone 57207.
SEQ ID NO: 513 is the determined cDNA sequence for clone 57209.
SEQ ID NO: 514 is the determined cDNA sequence for clone 57210.
25 SEQ ID NO: 515 is the determined cDNA sequence for clone 57211.
SEQ ID NO: 516 is the determined cDNA sequence for clone 57212.
SEQ ID NO: 517 is the determined cDNA sequence for clone 57213.
SEQ ID NO: 518 is the determined cDNA sequence for clone 57215.
SEQ ID NO: 519 is the determined cDNA sequence for clone 57219.
30 SEQ ID NO: 520 is the determined cDNA sequence for clone 57221.

SEQ ID NO: 521 is the determined cDNA sequence for clone 57222.
SEQ ID NO: 522 is the determined cDNA sequence for clone 57223.
SEQ ID NO: 523 is the determined cDNA sequence for clone 57225.
SEQ ID NO: 524 is the determined cDNA sequence for clone 57227.
5 SEQ ID NO: 525 is the determined cDNA sequence for clone 57228.
SEQ ID NO: 526 is the determined cDNA sequence for clone 57229.
SEQ ID NO: 527 is the determined cDNA sequence for clone 57230.
SEQ ID NO: 528 is the determined cDNA sequence for clone 57231.
SEQ ID NO: 529 is the determined cDNA sequence for clone 57232.
10 SEQ ID NO: 530 is the determined cDNA sequence for clone 57233.
SEQ ID NO: 531 is the determined cDNA sequence for clone 57234.
SEQ ID NO: 532 is the determined cDNA sequence for clone 57235.
SEQ ID NO: 533 is the determined cDNA sequence for clone 57236.
SEQ ID NO: 534 is the determined cDNA sequence for clone 57237.
15 SEQ ID NO: 535 is the determined cDNA sequence for clone 57238.
SEQ ID NO: 536 is the determined cDNA sequence for clone 57239.
SEQ ID NO: 537 is the determined cDNA sequence for clone 57240.
SEQ ID NO: 538 is the determined cDNA sequence for clone 57242.
SEQ ID NO: 539 is the determined cDNA sequence for clone 57243.
20 SEQ ID NO: 540 is the determined cDNA sequence for clone 57245.
SEQ ID NO: 541 is the determined cDNA sequence for clone 57248.
SEQ ID NO: 542 is the determined cDNA sequence for clone 57249.
SEQ ID NO: 543 is the determined cDNA sequence for clone 57250.
SEQ ID NO: 544 is the determined cDNA sequence for clone 57251.
25 SEQ ID NO: 545 is the determined cDNA sequence for clone 57253.
SEQ ID NO: 546 is the determined cDNA sequence for clone 57254.
SEQ ID NO: 547 is the determined cDNA sequence for clone 57255.
SEQ ID NO: 548 is the determined cDNA sequence for clone 57257.
SEQ ID NO: 549 is the determined cDNA sequence for clone 57258.
30 SEQ ID NO: 550 is the determined cDNA sequence for clone 57259.

SEQ ID NO: 551 is the determined cDNA sequence for clone 57261.
SEQ ID NO: 552 is the determined cDNA sequence for clone 57262.
SEQ ID NO: 553 is the determined cDNA sequence for clone 57263.
SEQ ID NO: 554 is the determined cDNA sequence for clone 57264.
5 SEQ ID NO: 555 is the determined cDNA sequence for clone 57265.
SEQ ID NO: 556 is the determined cDNA sequence for clone 57266.
SEQ ID NO: 557 is the determined cDNA sequence for clone 57267.
SEQ ID NO: 558 is the determined cDNA sequence for clone 57268.
SEQ ID NO: 559 is the determined cDNA sequence for clone 57269.
10 SEQ ID NO: 560 is the determined cDNA sequence for clone 57270.
SEQ ID NO: 561 is the determined cDNA sequence for clone 57271.
SEQ ID NO: 562 is the determined cDNA sequence for clone 57272.
SEQ ID NO: 563 is the determined cDNA sequence for clone 57274.
SEQ ID NO: 564 is the determined cDNA sequence for clone 57275.
15 SEQ ID NO: 565 is the determined cDNA sequence for clone 57277.
SEQ ID NO: 566 is the determined cDNA sequence for clone 57280.
SEQ ID NO: 567 is the determined cDNA sequence for clone 57281.
SEQ ID NO: 568 is the determined cDNA sequence for clone 57282.
SEQ ID NO: 569 is the determined cDNA sequence for clone 57283.
20 SEQ ID NO: 570 is the determined cDNA sequence for clone 57285.
SEQ ID NO: 571 is the determined cDNA sequence for clone 57287.
SEQ ID NO: 572 is the determined cDNA sequence for clone 57288.
SEQ ID NO: 573 is the determined cDNA sequence for clone 57289.
SEQ ID NO: 574 is the determined cDNA sequence for clone 57290.
25 SEQ ID NO: 575 is the determined cDNA sequence for clone 57292.
SEQ ID NO: 576 is the determined cDNA sequence for clone 57295.
SEQ ID NO: 577 is the determined cDNA sequence for clone 57296.
SEQ ID NO: 578 is the determined cDNA sequence for clone 57297.
SEQ ID NO: 579 is the determined cDNA sequence for clone 57299.
30 SEQ ID NO: 580 is the determined cDNA sequence for clone 57301.

SEQ ID NO: 581 is the determined cDNA sequence for clone 57302.

SEQ ID NO: 582 is the determined cDNA sequence for the beta chain of a lung tumor specific T cell receptor.

5 SEQ ID NO: 583 is the determined cDNA sequence for the alpha chain of a lung tumor specific T cell receptor.

SEQ ID NO: 584 is the amino acid sequence encoded by SEQ ID NO: 583.

SEQ ID NO: 585 is the amino acid sequence encoded by SEQ ID NO: 582.

10 SEQ ID NO: 586 is the amino acid sequence encoded by the 5' terminus of 14F10.

SEQ ID NO: 587 is the amino acid sequence of a T cell epitope contained within SEQ ID NO: 586.

DETAILED DESCRIPTION OF THE INVENTION

15 The present invention is directed generally to compositions and their use in the therapy and diagnosis of cancer, particularly lung cancer. As described further below, illustrative compositions of the present invention include, but are not restricted to, polypeptides, particularly immunogenic polypeptides, polynucleotides encoding such polypeptides, antibodies and other binding agents, antigen presenting cells (APCs)
20 and immune system cells (e.g., T cells).

The practice of the present invention will employ, unless indicated specifically to the contrary, conventional methods of virology, immunology, microbiology, molecular biology and recombinant DNA techniques within the skill of the art, many of which are described below for the purpose of illustration. Such
25 techniques are explained fully in the literature. See, e.g., Sambrook, et al. Molecular Cloning: A Laboratory Manual (2nd Edition, 1989); Maniatis et al. Molecular Cloning: A Laboratory Manual (1982); DNA Cloning: A Practical Approach, vol. I & II (D. Glover, ed.); Oligonucleotide Synthesis (N. Gait, ed., 1984); Nucleic Acid Hybridization (B. Hames & S. Higgins, eds., 1985); Transcription and Translation (B.

Hames & S. Higgins, eds., 1984); Animal Cell Culture (R. Freshney, ed., 1986); Perbal, A Practical Guide to Molecular Cloning (1984).

All publications, patents and patent applications cited herein, whether *supra* or *infra*, are hereby incorporated by reference in their entirety.

5 As used in this specification and the appended claims, the singular forms "a," "an" and "the" include plural references unless the content clearly dictates otherwise.

Polypeptide Compositions

As used herein, the term "polypeptide" is used in its conventional
10 meaning, *i.e.*, as a sequence of amino acids. The polypeptides are not limited to a specific length of the product; thus, peptides, oligopeptides, and proteins are included within the definition of polypeptide, and such terms may be used interchangeably herein unless specifically indicated otherwise. This term also does not refer to or exclude post-expression modifications of the polypeptide, for example, glycosylations, acetylations,
15 phosphorylations and the like, as well as other modifications known in the art, both naturally occurring and non-naturally occurring. A polypeptide may be an entire protein, or a subsequence thereof. Particular polypeptides of interest in the context of this invention are amino acid subsequences comprising epitopes, *i.e.*, antigenic determinants substantially responsible for the immunogenic properties of a polypeptide
20 and being capable of evoking an immune response.

Particularly illustrative polypeptides of the present invention comprise those encoded by a polynucleotide sequence set forth in any one of SEQ ID NOs: 217-390, 392, 394, 396, 398-420 422-424, 428-433 and 440-583, or a sequence that hybridizes under moderately stringent conditions, or, alternatively, under highly
25 stringent conditions, to a polynucleotide sequence set forth in any one of SEQ ID NOs: 217-390, 392, 394, 396, 398-420 422-424, 428-433 and 440-583. Certain other illustrative polypeptides of the invention comprise amino acid sequences as set forth in any one of SEQ ID NOs: 391, 393, 395, 397, 421, 425-427, 434-439 and 584-587.

The polypeptides of the present invention are sometimes herein referred to as lung tumor proteins or lung tumor polypeptides, as an indication that their identification has been based at least in part upon their increased levels of expression in lung tumor samples. Thus, a "lung tumor polypeptide" or "lung tumor protein," refers generally to a polypeptide sequence of the present invention, or a polynucleotide sequence encoding such a polypeptide, that is expressed in a substantial proportion of lung tumor samples, for example preferably greater than about 20%, more preferably greater than about 30%, and most preferably greater than about 50% or more of lung tumor samples tested, at a level that is at least two fold, and preferably at least five fold, greater than the level of expression in normal tissues, as determined using a representative assay provided herein. A lung tumor polypeptide sequence of the invention, based upon its increased level of expression in tumor cells, has particular utility both as a diagnostic marker as well as a therapeutic target, as further described below.

In certain preferred embodiments, the polypeptides of the invention are immunogenic, *i.e.*, they react detectably within an immunoassay (such as an ELISA or T-cell stimulation assay) with antisera and/or T-cells from a patient with lung cancer. Screening for immunogenic activity can be performed using techniques well known to the skilled artisan. For example, such screens can be performed using methods such as those described in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In one illustrative example, a polypeptide may be immobilized on a solid support and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, ¹²⁵I-labeled Protein A.

As would be recognized by the skilled artisan, immunogenic portions of the polypeptides disclosed herein are also encompassed by the present invention. An "immunogenic portion," as used herein, is a fragment of an immunogenic polypeptide of the invention that itself is immunologically reactive (*i.e.*, specifically binds) with the B-cells and/or T-cell surface antigen receptors that recognize the polypeptide. Immunogenic portions may generally be identified using well known techniques, such

as those summarized in Paul, *Fundamental Immunology*, 3rd ed., 243-247 (Raven Press, 1993) and references cited therein. Such techniques include screening polypeptides for the ability to react with antigen-specific antibodies, antisera and/or T-cell lines or clones. As used herein, antisera and antibodies are "antigen-specific" if they
5 specifically bind to an antigen (*i.e.*, they react with the protein in an ELISA or other immunoassay, and do not react detectably with unrelated proteins). Such antisera and antibodies may be prepared as described herein, and using well-known techniques.

In one preferred embodiment, an immunogenic portion of a polypeptide of the present invention is a portion that reacts with antisera and/or T-cells at a level that
10 is not substantially less than the reactivity of the full-length polypeptide (*e.g.*, in an ELISA and/or T-cell reactivity assay). Preferably, the level of immunogenic activity of the immunogenic portion is at least about 50%, preferably at least about 70% and most preferably greater than about 90% of the immunogenicity for the full-length polypeptide. In some instances, preferred immunogenic portions will be identified that
15 have a level of immunogenic activity greater than that of the corresponding full-length polypeptide, *e.g.*, having greater than about 100% or 150% or more immunogenic activity.

In certain other embodiments, illustrative immunogenic portions may include peptides in which an N-terminal leader sequence and/or transmembrane domain
20 have been deleted. Other illustrative immunogenic portions will contain a small N- and/or C-terminal deletion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids), relative to the mature protein.

In another embodiment, a polypeptide composition of the invention may also comprise one or more polypeptides that are immunologically reactive with T cells
25 and/or antibodies generated against a polypeptide of the invention, particularly a polypeptide having an amino acid sequence disclosed herein, or to an immunogenic fragment or variant thereof.

In another embodiment of the invention, polypeptides are provided that comprise one or more polypeptides that are capable of eliciting T cells and/or antibodies
30 that are immunologically reactive with one or more polypeptides described herein, or

one or more polypeptides encoded by contiguous nucleic acid sequences contained in the polynucleotide sequences disclosed herein, or immunogenic fragments or variants thereof, or to one or more nucleic acid sequences which hybridize to one or more of these sequences under conditions of moderate to high stringency.

5 The present invention, in another aspect, provides polypeptide fragments comprising at least about 5, 10, 15, 20, 25, 50, or 100 contiguous amino acids, or more, including all intermediate lengths, of a polypeptide compositions set forth herein, such as those set forth in SEQ ID NOs: 391, 393, 395, 397, 421, 425-427, 434-439 and 584-587, or those encoded by a polynucleotide sequence set forth in a sequence of SEQ ID
10 NOs: 217-390, 392, 394, 396, 398-420 422-424, 428-433 and 440-583.

 In another aspect, the present invention provides variants of the polypeptide compositions described herein. Polypeptide variants generally encompassed by the present invention will typically exhibit at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or more identity
15 (determined as described below), along its length, to a polypeptide sequences set forth herein.

 In one preferred embodiment, the polypeptide fragments and variants provide by the present invention are immunologically reactive with an antibody and/or T-cell that reacts with a full-length polypeptide specifically set for the herein.

20 In another preferred embodiment, the polypeptide fragments and variants provided by the present invention exhibit a level of immunogenic activity of at least about 50%, preferably at least about 70%, and most preferably at least about 90% or more of that exhibited by a full-length polypeptide sequence specifically set forth herein.

25 A polypeptide "variant," as the term is used herein, is a polypeptide that typically differs from a polypeptide specifically disclosed herein in one or more substitutions, deletions, additions and/or insertions. Such variants may be naturally occurring or may be synthetically generated, for example, by modifying one or more of the above polypeptide sequences of the invention and evaluating their immunogenic

activity as described herein and/or using any of a number of techniques well known in the art.

For example, certain illustrative variants of the polypeptides of the invention include those in which one or more portions, such as an N-terminal leader
5 sequence or transmembrane domain, have been removed. Other illustrative variants include variants in which a small portion (e.g., 1-30 amino acids, preferably 5-15 amino acids) has been removed from the N- and/or C-terminal of the mature protein.

In many instances, a variant will contain conservative substitutions. A
"conservative substitution" is one in which an amino acid is substituted for another
10 amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydrophobic nature of the polypeptide to be substantially unchanged. As described above, modifications may be made in the structure of the polynucleotides and polypeptides of the present invention and still obtain a functional molecule that encodes a variant or derivative polypeptide
15 with desirable characteristics, e.g., with immunogenic characteristics. When it is desired to alter the amino acid sequence of a polypeptide to create an equivalent, or even an improved, immunogenic variant or portion of a polypeptide of the invention, one skilled in the art will typically change one or more of the codons of the encoding DNA sequence according to Table 1.

20 For example, certain amino acids may be substituted for other amino acids in a protein structure without appreciable loss of interactive binding capacity with structures such as, for example, antigen-binding regions of antibodies or binding sites on substrate molecules. Since it is the interactive capacity and nature of a protein that defines that protein's biological functional activity, certain amino acid sequence
25 substitutions can be made in a protein sequence, and, of course, its underlying DNA coding sequence, and nevertheless obtain a protein with like properties. It is thus contemplated that various changes may be made in the peptide sequences of the disclosed compositions, or corresponding DNA sequences which encode said peptides without appreciable loss of their biological utility or activity.

TABLE 1

Amino Acids			Codons						
Alanine	Ala	A	GCA	GCC	GCG	GCU			
Cysteine	Cys	C	UGC	UGU					
Aspartic acid	Asp	D	GAC	GAU					
Glutamic acid	Glu	E	GAA	GAG					
Phenylalanine	Phe	F	UUC	UUU					
Glycine	Gly	G	GGA	GGC	GGG	GGU			
Histidine	His	H	CAC	CAU					
Isoleucine	Ile	I	AUA	AUC	AUU				
Lysine	Lys	K	AAA	AAG					
Leucine	Leu	L	UUA	UUG	CUA	CUC	CUG	CUU	
Methionine	Met	M	AUG						
Asparagine	Asn	N	AAC	AAU					
Proline	Pro	P	CCA	CCC	CCG	CCU			
Glutamine	Gln	Q	CAA	CAG					
Arginine	Arg	R	AGA	AGG	CGA	CGC	CGG	CGU	
Serine	Ser	S	AGC	AGU	UCA	UCC	UCG	UCU	
Threonine	Thr	T	ACA	ACC	ACG	ACU			
Valine	Val	V	GUA	GUC	GUG	GUU			
Tryptophan	Trp	W	UGG						
Tyrosine	Tyr	Y	UAC	UAU					

In making such changes, the hydrophobic index of amino acids may be considered. The importance of the hydrophobic amino acid index in conferring

5 interactive biologic function on a protein is generally understood in the art (Kyte and Doolittle, 1982, incorporated herein by reference). It is accepted that the relative hydrophobic character of the amino acid contributes to the secondary structure of the resultant protein, which in turn defines the interaction of the protein with other molecules, for example, enzymes, substrates, receptors, DNA, antibodies, antigens, and

10 the like. Each amino acid has been assigned a hydrophobic index on the basis of its

hydrophobicity and charge characteristics (Kyte and Doolittle, 1982). These values are: isoleucine (+4.5); valine (+4.2); leucine (+3.8); phenylalanine (+2.8); cysteine/cystine (+2.5); methionine (+1.9); alanine (+1.8); glycine (-0.4); threonine (-0.7); serine (-0.8); tryptophan (-0.9); tyrosine (-1.3); proline (-1.6); histidine (-3.2); glutamate (-3.5);
5 glutamine (-3.5); aspartate (-3.5); asparagine (-3.5); lysine (-3.9); and arginine (-4.5).

It is known in the art that certain amino acids may be substituted by other amino acids having a similar hydropathic index or score and still result in a protein with similar biological activity, *i.e.* still obtain a biological functionally equivalent protein. In making such changes, the substitution of amino acids whose
10 hydropathic indices are within ± 2 is preferred, those within ± 1 are particularly preferred, and those within ± 0.5 are even more particularly preferred. It is also understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity. U. S. Patent 4,554,101 (specifically incorporated herein by reference in its entirety), states that the greatest local average hydrophilicity of a
15 protein, as governed by the hydrophilicity of its adjacent amino acids, correlates with a biological property of the protein.

As detailed in U. S. Patent 4,554,101, the following hydrophilicity values have been assigned to amino acid residues: arginine (+3.0); lysine (+3.0); aspartate (+3.0 \pm 1); glutamate (+3.0 \pm 1); serine (+0.3); asparagine (+0.2); glutamine
20 (+0.2); glycine (0); threonine (-0.4); proline (-0.5 \pm 1); alanine (-0.5); histidine (-0.5); cysteine (-1.0); methionine (-1.3); valine (-1.5); leucine (-1.8); isoleucine (-1.8); tyrosine (-2.3); phenylalanine (-2.5); tryptophan (-3.4). It is understood that an amino acid can be substituted for another having a similar hydrophilicity value and still obtain a biologically equivalent, and in particular, an immunologically equivalent protein. In
25 such changes, the substitution of amino acids whose hydrophilicity values are within ± 2 is preferred, those within ± 1 are particularly preferred, and those within ± 0.5 are even more particularly preferred.

As outlined above, amino acid substitutions are generally therefore based on the relative similarity of the amino acid side-chain substituents, for example, their
30 hydrophobicity, hydrophilicity, charge, size, and the like. Exemplary substitutions that

take various of the foregoing characteristics into consideration are well known to those of skill in the art and include: arginine and lysine; glutamate and aspartate; serine and threonine; glutamine and asparagine; and valine, leucine and isoleucine.

In addition, any polynucleotide may be further modified to increase
5 stability *in vivo*. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends; the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages in the backbone; and/or the inclusion of nontraditional bases such as inosine, queosine and wybutosine, as well as acetyl-methyl-, thio- and other modified forms of adenine, cytidine, guanine, thymine and
10 uridine.

Amino acid substitutions may further be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the residues. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and
15 amino acids with uncharged polar head groups having similar hydrophilicity values include leucine, isoleucine and valine; glycine and alanine; asparagine and glutamine; and serine, threonine, phenylalanine and tyrosine. Other groups of amino acids that may represent conservative changes include: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp,
20 his. A variant may also, or alternatively, contain nonconservative changes. In a preferred embodiment, variant polypeptides differ from a native sequence by substitution, deletion or addition of five amino acids or fewer. Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino acids that have minimal influence on the immunogenicity, secondary structure and hydrophobic
25 nature of the polypeptide.

As noted above, polypeptides may comprise a signal (or leader) sequence at the N-terminal end of the protein, which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the

polypeptide (e.g., poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

When comparing polypeptide sequences, two sequences are said to be "identical" if the sequence of amino acids in the two sequences is the same when
5 aligned for maximum correspondence, as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, 40 to about 50, in which a sequence may be compared to a
10 reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several
15 alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins – Matrices for detecting distant relationships. In Dayhoff, M.O. (ed.) Atlas of Protein Sequence and Structure, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenies pp. 626-645 *Methods in Enzymology*
20 vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) *CABIOS* 5:151-153; Myers, E.W. and Muller W. (1988) *CABIOS* 4:11-17; Robinson, E.D. (1971) *Comb. Theor* 11:105; Santou, N. Nes, M. (1987) *Mol. Biol. Evol.* 4:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and
25 Lipman, D.J. (1983) *Proc. Natl. Acad. Sci. USA* 80:726-730.

Alternatively, optimal alignment of sequences for comparison may be conducted by the local identity algorithm of Smith and Waterman (1981) *Add. APL Math* 2:482, by the identity alignment algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443, by the search for similarity methods of Pearson and Lipman (1988)
30 *Proc. Natl. Acad. Sci. USA* 85: 2444, by computerized implementations of these

algorithms (GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, WI), or by inspection.

One preferred example of algorithms that are suitable for determining
5 percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al. (1977) *Nucl. Acids Res.* 25:3389-3402 and Altschul et al. (1990) *J. Mol. Biol.* 215:403-410, respectively. BLAST and BLAST 2.0 can be used, for example with the parameters described herein, to determine percent sequence identity for the polynucleotides and polypeptides of the invention. Software
10 for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. For amino acid sequences, a scoring matrix can be used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of
15 one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T and X determine the sensitivity and speed of the alignment.

In one preferred approach, the "percentage of sequence identity" is determined by comparing two optimally aligned sequences over a window of
20 comparison of at least 20 positions, wherein the portion of the polypeptide sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at
25 which the identical amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (*i.e.*, the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

Within other illustrative embodiments, a polypeptide may be a fusion
30 polypeptide that comprises multiple polypeptides as described herein, or that comprises

at least one polypeptide as described herein and an unrelated sequence, such as a known tumor protein. A fusion partner may, for example, assist in providing T helper epitopes (an immunological fusion partner), preferably T helper epitopes recognized by humans, or may assist in expressing the protein (an expression enhancer) at higher yields than the native recombinant protein. Certain preferred fusion partners are both immunological and expression enhancing fusion partners. Other fusion partners may be selected so as to increase the solubility of the polypeptide or to enable the polypeptide to be targeted to desired intracellular compartments. Still further fusion partners include affinity tags, which facilitate purification of the polypeptide.

Fusion polypeptides may generally be prepared using standard techniques, including chemical conjugation. Preferably, a fusion polypeptide is expressed as a recombinant polypeptide, allowing the production of increased levels, relative to a non-fused polypeptide, in an expression system. Briefly, DNA sequences encoding the polypeptide components may be assembled separately, and ligated into an appropriate expression vector. The 3' end of the DNA sequence encoding one polypeptide component is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide component so that the reading frames of the sequences are in phase. This permits translation into a single fusion polypeptide that retains the biological activity of both component polypeptides.

A peptide linker sequence may be employed to separate the first and second polypeptide components by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion polypeptide using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as

linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may generally be from 1 to about 50 amino acids in length. Linker sequences are not required when the first and second
5 polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding
10 the first polypeptides. Similarly, stop codons required to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

The fusion polypeptide can comprise a polypeptide as described herein together with an unrelated immunogenic protein, such as an immunogenic protein
15 capable of eliciting a recall response. Examples of such proteins include tetanus, tuberculosis and hepatitis proteins (see, for example, Stoute et al. *New Engl. J. Med.*, 336:86-91, 1997).

In one preferred embodiment, the immunological fusion partner is derived from a *Mycobacterium* sp., such as a *Mycobacterium tuberculosis*-derived Ra12
20 fragment. Ra12 compositions and methods for their use in enhancing the expression and/or immunogenicity of heterologous polynucleotide/polypeptide sequences is described in U.S. Patent Application 60/158,585, the disclosure of which is incorporated herein by reference in its entirety. Briefly, Ra12 refers to a polynucleotide region that is a subsequence of a *Mycobacterium tuberculosis* MTB32A nucleic acid.
25 MTB32A is a serine protease of 32 KD molecular weight encoded by a gene in virulent and avirulent strains of *M. tuberculosis*. The nucleotide sequence and amino acid sequence of MTB32A have been described (for example, U.S. Patent Application 60/158,585; see also, Skeiky et al., *Infection and Immun.* (1999) 67:3998-4007, incorporated herein by reference). C-terminal fragments of the MTB32A coding
30 sequence express at high levels and remain as a soluble polypeptides throughout the

purification process. Moreover, Ra12 may enhance the immunogenicity of heterologous immunogenic polypeptides with which it is fused. One preferred Ra12 fusion polypeptide comprises a 14 KD C-terminal fragment corresponding to amino acid residues 192 to 323 of MTB32A. Other preferred Ra12 polynucleotides generally
5 comprise at least about 15 consecutive nucleotides, at least about 30 nucleotides, at least about 60 nucleotides, at least about 100 nucleotides, at least about 200 nucleotides, or at least about 300 nucleotides that encode a portion of a Ra12 polypeptide. Ra12 polynucleotides may comprise a native sequence (*i.e.*, an endogenous sequence that encodes a Ra12 polypeptide or a portion thereof) or may comprise a variant of such a
10 sequence. Ra12 polynucleotide variants may contain one or more substitutions, additions, deletions and/or insertions such that the biological activity of the encoded fusion polypeptide is not substantially diminished, relative to a fusion polypeptide comprising a native Ra12 polypeptide. Variants preferably exhibit at least about 70% identity, more preferably at least about 80% identity and most preferably at least about
15 90% identity to a polynucleotide sequence that encodes a native Ra12 polypeptide or a portion thereof.

Within other preferred embodiments, an immunological fusion partner is derived from protein D, a surface protein of the gram-negative bacterium *Haemophilus influenza B* (WO 91/18926). Preferably, a protein D derivative comprises
20 approximately the first third of the protein (*e.g.*, the first N-terminal 100-110 amino acids), and a protein D derivative may be lipidated. Within certain preferred embodiments, the first 109 residues of a Lipoprotein D fusion partner is included on the N-terminus to provide the polypeptide with additional exogenous T-cell epitopes and to increase the expression level in *E. coli* (thus functioning as an expression enhancer).
25 The lipid tail ensures optimal presentation of the antigen to antigen presenting cells. Other fusion partners include the non-structural protein from influenzae virus, NS1 (hemagglutinin). Typically, the N-terminal 81 amino acids are used, although different fragments that include T-helper epitopes may be used.

In another embodiment, the immunological fusion partner is the protein
30 known as LYTA, or a portion thereof (preferably a C-terminal portion). LYTA is

derived from *Streptococcus pneumoniae*, which synthesizes an N-acetyl-L-alanine amidase known as amidase LYTA (encoded by the *LytA* gene; *Gene* 43:265-292, 1986). LYTA is an autolysin that specifically degrades certain bonds in the peptidoglycan backbone. The C-terminal domain of the LYTA protein is responsible
5 for the affinity to the choline or to some choline analogues such as DEAE. This property has been exploited for the development of *E. coli* C-LYTA expressing plasmids useful for expression of fusion proteins. Purification of hybrid proteins containing the C-LYTA fragment at the amino terminus has been described (see *Biotechnology* 10:795-798, 1992). Within a preferred embodiment, a repeat portion of
10 LYTA may be incorporated into a fusion polypeptide. A repeat portion is found in the C-terminal region starting at residue 178. A particularly preferred repeat portion incorporates residues 188-305.

Yet another illustrative embodiment involves fusion polypeptides, and the polynucleotides encoding them, wherein the fusion partner comprises a targeting
15 signal capable of directing a polypeptide to the endosomal/lysosomal compartment, as described in U.S. Patent No. 5,633,234. An immunogenic polypeptide of the invention, when fused with this targeting signal, will associate more efficiently with MHC class II molecules and thereby provide enhanced in vivo stimulation of CD4⁺ T-cells specific for the polypeptide.

20 Polypeptides of the invention are prepared using any of a variety of well known synthetic and/or recombinant techniques, the latter of which are further described below. Polypeptides, portions and other variants generally less than about 150 amino acids can be generated by synthetic means, using techniques well known to those of ordinary skill in the art. In one illustrative example, such polypeptides are
25 synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and
30 may be operated according to the manufacturer's instructions.

In general, polypeptide compositions (including fusion polypeptides) of the invention are isolated. An "isolated" polypeptide is one that is removed from its original environment. For example, a naturally-occurring protein or polypeptide is isolated if it is separated from some or all of the coexisting materials in the natural system. Preferably, such polypeptides are also purified, *e.g.*, are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure.

Polynucleotide Compositions

The present invention, in other aspects, provides polynucleotide compositions. The terms "DNA" and "polynucleotide" are used essentially interchangeably herein to refer to a DNA molecule that has been isolated free of total genomic DNA of a particular species. "Isolated," as used herein, means that a polynucleotide is substantially away from other coding sequences, and that the DNA molecule does not contain large portions of unrelated coding DNA, such as large chromosomal fragments or other functional genes or polypeptide coding regions. Of course, this refers to the DNA molecule as originally isolated, and does not exclude genes or coding regions later added to the segment by the hand of man.

As will be understood by those skilled in the art, the polynucleotide compositions of this invention can include genomic sequences, extra-genomic and plasmid-encoded sequences and smaller engineered gene segments that express, or may be adapted to express, proteins, polypeptides, peptides and the like. Such segments may be naturally isolated, or modified synthetically by the hand of man.

As will be also recognized by the skilled artisan, polynucleotides of the invention may be single-stranded (coding or antisense) or double-stranded, and may be DNA (genomic, cDNA or synthetic) or RNA molecules. RNA molecules may include HnRNA molecules, which contain introns and correspond to a DNA molecule in a one-to-one manner, and mRNA molecules, which do not contain introns. Additional coding or non-coding sequences may, but need not, be present within a polynucleotide of the

present invention, and a polynucleotide may, but need not, be linked to other molecules and/or support materials.

Polynucleotides may comprise a native sequence (*i.e.*, an endogenous sequence that encodes a polypeptide/protein of the invention or a portion thereof) or
5 may comprise a sequence that encodes a variant or derivative, preferably and immunogenic variant or derivative, of such a sequence.

Therefore, according to another aspect of the present invention, polynucleotide compositions are provided that comprise some or all of a polynucleotide sequence set forth in any one of SEQ ID NOs: 217-390, 392, 394, 396, 398-420 422-
10 424, 428-433 and 440-583, complements of a polynucleotide sequence set forth in any one of SEQ ID NOs: 217-390, 392, 394, 396, 398-420 422-424, 428-433 and 440-583, and degenerate variants of a polynucleotide sequence set forth in any one of SEQ ID NOs: 217-390, 392, 394, 396, 398-420 422-424, 428-433 and 440-583. In certain preferred embodiments, the polynucleotide sequences set forth herein encode
15 immunogenic polypeptides, as described above.

In other related embodiments, the present invention provides polynucleotide variants having substantial identity to the sequences disclosed herein in SEQ ID NOs: 217-390, 392, 394, 396, 398-420 422-424, 428-433 and 440-583, for example those comprising at least 70% sequence identity, preferably at least 75%, 80%,
20 85%, 90%, 95%, 96%, 97%, 98%, or 99% or higher, sequence identity compared to a polynucleotide sequence of this invention using the methods described herein, (*e.g.*, BLAST analysis using standard parameters, as described below). One skilled in this art will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into
25 account codon degeneracy, amino acid similarity, reading frame positioning and the like.

Typically, polynucleotide variants will contain one or more substitutions, additions, deletions and/or insertions, preferably such that the immunogenicity of the polypeptide encoded by the variant polynucleotide is not substantially diminished
30 relative to a polypeptide encoded by a polynucleotide sequence specifically set forth

herein). The term "variants" should also be understood to encompass homologous genes of xenogenic origin.

In additional embodiments, the present invention provides polynucleotide fragments comprising various lengths of contiguous stretches of sequence identical to or complementary to one or more of the sequences disclosed herein. For example, polynucleotides are provided by this invention that comprise at least about 10, 15, 20, 30, 40, 50, 75, 100, 150, 200, 300, 400, 500 or 1000 or more contiguous nucleotides of one or more of the sequences disclosed herein as well as all intermediate lengths there between. It will be readily understood that "intermediate lengths", in this context, means any length between the quoted values, such as 16, 17, 18, 19, *etc.*; 21, 22, 23, *etc.*; 30, 31, 32, *etc.*; 50, 51, 52, 53, *etc.*; 100, 101, 102, 103, *etc.*; 150, 151, 152, 153, *etc.*; including all integers through 200-500; 500-1,000, and the like.

In another embodiment of the invention, polynucleotide compositions are provided that are capable of hybridizing under moderate to high stringency conditions to a polynucleotide sequence provided herein, or a fragment thereof, or a complementary sequence thereof. Hybridization techniques are well known in the art of molecular biology. For purposes of illustration, suitable moderately stringent conditions for testing the hybridization of a polynucleotide of this invention with other polynucleotides include prewashing in a solution of 5 X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50°C-60°C, 5 X SSC, overnight; followed by washing twice at 65°C for 20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1% SDS. One skilled in the art will understand that the stringency of hybridization can be readily manipulated, such as by altering the salt content of the hybridization solution and/or the temperature at which the hybridization is performed. For example, in another embodiment, suitable highly stringent hybridization conditions include those described above, with the exception that the temperature of hybridization is increased, *e.g.*, to 60-65°C or 65-70°C.

In certain preferred embodiments, the polynucleotides described above, *e.g.*, polynucleotide variants, fragments and hybridizing sequences, encode polypeptides

that are immunologically cross-reactive with a polypeptide sequence specifically set forth herein. In other preferred embodiments, such polynucleotides encode polypeptides that have a level of immunogenic activity of at least about 50%, preferably at least about 70%, and more preferably at least about 90% of that for a polypeptide sequence specifically set forth herein.

The polynucleotides of the present invention, or fragments thereof, regardless of the length of the coding sequence itself, may be combined with other DNA sequences, such as promoters, polyadenylation signals, additional restriction enzyme sites, multiple cloning sites, other coding segments, and the like, such that their overall length may vary considerably. It is therefore contemplated that a nucleic acid fragment of almost any length may be employed, with the total length preferably being limited by the ease of preparation and use in the intended recombinant DNA protocol. For example, illustrative polynucleotide segments with total lengths of about 10,000, about 5000, about 3000, about 2,000, about 1,000, about 500, about 200, about 100, about 50 base pairs in length, and the like, (including all intermediate lengths) are contemplated to be useful in many implementations of this invention.

When comparing polynucleotide sequences, two sequences are said to be "identical" if the sequence of nucleotides in the two sequences is the same when aligned for maximum correspondence, as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins – Matrices for detecting distant relationships.

- In Dayhoff, M.O. (ed.) Atlas of Protein Sequence and Structure, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenies pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) *CABIOS* 5:151-153; Myers, E.W. and Muller W. (1988) *CABIOS* 4:11-17; Robinson, E.D. (1971) *Comb. Theor* 11:105; Santou, N. Nes, M. (1987) *Mol. Biol. Evol.* 4:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) *Proc. Natl. Acad., Sci. USA* 80:726-730.
- 10 Alternatively, optimal alignment of sequences for comparison may be conducted by the local identity algorithm of Smith and Waterman (1981) *Add. APL. Math.* 2:482, by the identity alignment algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443, by the search for similarity methods of Pearson and Lipman (1988) *Proc. Natl. Acad. Sci. USA* 85: 2444, by computerized implementations of these
- 15 algorithms (GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, WI), or by inspection.
- One preferred example of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0
- 20 algorithms, which are described in Altschul et al. (1977) *Nucl. Acids Res.* 25:3389-3402 and Altschul et al. (1990) *J. Mol. Biol.* 215:403-410, respectively. BLAST and BLAST 2.0 can be used, for example with the parameters described herein, to determine percent sequence identity for the polynucleotides of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology
- 25 Information. In one illustrative example, cumulative scores can be calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0) and N (penalty score for mismatching residues; always <0). Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero
- 30 or below, due to the accumulation of one or more negative-scoring residue alignments;

or the end of either sequence is reached. The BLAST algorithm parameters W, T and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) *Proc. Natl. Acad. Sci. USA* 89:10915) alignments, (B) of 50, expectation (E) of 10, M=5, N=4 and a comparison of both strands.

Preferably, the "percentage of sequence identity" is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid bases occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (*i.e.*, the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

It will be appreciated by those of ordinary skill in the art that, as a result of the degeneracy of the genetic code, there are many nucleotide sequences that encode a polypeptide as described herein. Some of these polynucleotides bear minimal homology to the nucleotide sequence of any native gene. Nonetheless, polynucleotides that vary due to differences in codon usage are specifically contemplated by the present invention. Further, alleles of the genes comprising the polynucleotide sequences provided herein are within the scope of the present invention. Alleles are endogenous genes that are altered as a result of one or more mutations, such as deletions, additions and/or substitutions of nucleotides. The resulting mRNA and protein may, but need not, have an altered structure or function. Alleles may be identified using standard techniques (such as hybridization, amplification and/or database sequence comparison).

Therefore, in another embodiment of the invention, a mutagenesis approach, such as site-specific mutagenesis, is employed for the preparation of

immunogenic variants and/or derivatives of the polypeptides described herein. By this approach, specific modifications in a polypeptide sequence can be made through mutagenesis of the underlying polynucleotides that encode them. These techniques provides a straightforward approach to prepare and test sequence variants, for example, incorporating one or more of the foregoing considerations, by introducing one or more nucleotide sequence changes into the polynucleotide.

Site-specific mutagenesis allows the production of mutants through the use of specific oligonucleotide sequences which encode the DNA sequence of the desired mutation, as well as a sufficient number of adjacent nucleotides, to provide a primer sequence of sufficient size and sequence complexity to form a stable duplex on both sides of the deletion junction being traversed. Mutations may be employed in a selected polynucleotide sequence to improve, alter, decrease, modify, or otherwise change the properties of the polynucleotide itself, and/or alter the properties, activity, composition, stability, or primary sequence of the encoded polypeptide.

In certain embodiments of the present invention, the inventors contemplate the mutagenesis of the disclosed polynucleotide sequences to alter one or more properties of the encoded polypeptide, such as the immunogenicity of a polypeptide vaccine. The techniques of site-specific mutagenesis are well-known in the art, and are widely used to create variants of both polypeptides and polynucleotides. For example, site-specific mutagenesis is often used to alter a specific portion of a DNA molecule. In such embodiments, a primer comprising typically about 14 to about 25 nucleotides or so in length is employed, with about 5 to about 10 residues on both sides of the junction of the sequence being altered.

As will be appreciated by those of skill in the art, site-specific mutagenesis techniques have often employed a phage vector that exists in both a single stranded and double stranded form. Typical vectors useful in site-directed mutagenesis include vectors such as the M13 phage. These phage are readily commercially-available and their use is generally well-known to those skilled in the art. Double-stranded plasmids are also routinely employed in site directed mutagenesis that eliminates the step of transferring the gene of interest from a plasmid to a phage.

In general, site-directed mutagenesis in accordance herewith is performed by first obtaining a single-stranded vector or melting apart of two strands of a double-stranded vector that includes within its sequence a DNA sequence that encodes the desired peptide. An oligonucleotide primer bearing the desired mutated sequence is prepared, generally synthetically. This primer is then annealed with the single-stranded vector, and subjected to DNA polymerizing enzymes such as *E. coli* polymerase I Klenow fragment, in order to complete the synthesis of the mutation-bearing strand. Thus, a heteroduplex is formed wherein one strand encodes the original non-mutated sequence and the second strand bears the desired mutation. This heteroduplex vector is then used to transform appropriate cells, such as *E. coli* cells, and clones are selected which include recombinant vectors bearing the mutated sequence arrangement.

The preparation of sequence variants of the selected peptide-encoding DNA segments using site-directed mutagenesis provides a means of producing potentially useful species and is not meant to be limiting as there are other ways in which sequence variants of peptides and the DNA sequences encoding them may be obtained. For example, recombinant vectors encoding the desired peptide sequence may be treated with mutagenic agents, such as hydroxylamine, to obtain sequence variants. Specific details regarding these methods and protocols are found in the teachings of Maloy *et al.*, 1994; Segal, 1976; Prokop and Bajpai, 1991; Kuby, 1994; and Maniatis *et al.*, 1982, each incorporated herein by reference, for that purpose.

As used herein, the term "oligonucleotide directed mutagenesis procedure" refers to template-dependent processes and vector-mediated propagation which result in an increase in the concentration of a specific nucleic acid molecule relative to its initial concentration, or in an increase in the concentration of a detectable signal, such as amplification. As used herein, the term "oligonucleotide directed mutagenesis procedure" is intended to refer to a process that involves the template-dependent extension of a primer molecule. The term template dependent process refers to nucleic acid synthesis of an RNA or a DNA molecule wherein the sequence of the newly synthesized strand of nucleic acid is dictated by the well-known rules of complementary base pairing (see, for example, Watson, 1987). Typically,

vector mediated methodologies involve the introduction of the nucleic acid fragment into a DNA or RNA vector, the clonal amplification of the vector, and the recovery of the amplified nucleic acid fragment. Examples of such methodologies are provided by U. S. Patent No. 4,237,224, specifically incorporated herein by reference in its entirety.

5 In another approach for the production of polypeptide variants of the present invention, recursive sequence recombination, as described in U.S. Patent No. 5,837,458, may be employed. In this approach, iterative cycles of recombination and screening or selection are performed to "evolve" individual polynucleotide variants of the invention having, for example, enhanced immunogenic activity.

10 In other embodiments of the present invention, the polynucleotide sequences provided herein can be advantageously used as probes or primers for nucleic acid hybridization. As such, it is contemplated that nucleic acid segments that comprise a sequence region of at least about 15 nucleotide long contiguous sequence that has the same sequence as, or is complementary to, a 15 nucleotide long contiguous sequence
15 disclosed herein will find particular utility. Longer contiguous identical or complementary sequences, *e.g.*, those of about 20, 30, 40, 50, 100, 200, 500, 1000 (including all intermediate lengths) and even up to full length sequences will also be of use in certain embodiments.

The ability of such nucleic acid probes to specifically hybridize to a
20 sequence of interest will enable them to be of use in detecting the presence of complementary sequences in a given sample. However, other uses are also envisioned, such as the use of the sequence information for the preparation of mutant species primers, or primers for use in preparing other genetic constructions.

Polynucleotide molecules having sequence regions consisting of
25 contiguous nucleotide stretches of 10-14, 15-20, 30, 50, or even of 100-200 nucleotides or so (including intermediate lengths as well), identical or complementary to a polynucleotide sequence disclosed herein, are particularly contemplated as hybridization probes for use in, *e.g.*, Southern and Northern blotting. This would allow a gene product, or fragment thereof, to be analyzed, both in diverse cell types and also
30 in various bacterial cells. The total size of fragment, as well as the size of the

complementary stretch(es), will ultimately depend on the intended use or application of the particular nucleic acid segment. Smaller fragments will generally find use in hybridization embodiments, wherein the length of the contiguous complementary region may be varied, such as between about 15 and about 100 nucleotides, but larger
5 contiguous complementarity stretches may be used, according to the length complementary sequences one wishes to detect.

The use of a hybridization probe of about 15-25 nucleotides in length allows the formation of a duplex molecule that is both stable and selective. Molecules having contiguous complementary sequences over stretches greater than 15 bases in
10 length are generally preferred, though, in order to increase stability and selectivity of the hybrid, and thereby improve the quality and degree of specific hybrid molecules obtained. One will generally prefer to design nucleic acid molecules having gene-complementary stretches of 15 to 25 contiguous nucleotides, or even longer where desired.

15 Hybridization probes may be selected from any portion of any of the sequences disclosed herein. All that is required is to review the sequences set forth herein, or to any continuous portion of the sequences, from about 15-25 nucleotides in length up to and including the full length sequence, that one wishes to utilize as a probe or primer. The choice of probe and primer sequences may be governed by various
20 factors. For example, one may wish to employ primers from towards the termini of the total sequence.

Small polynucleotide segments or fragments may be readily prepared by, for example, directly synthesizing the fragment by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer. Also, fragments may be
25 obtained by application of nucleic acid reproduction technology, such as the PCR™ technology of U. S. Patent 4,683,202 (incorporated herein by reference), by introducing selected sequences into recombinant vectors for recombinant production, and by other recombinant DNA techniques generally known to those of skill in the art of molecular biology.

The nucleotide sequences of the invention may be used for their ability to selectively form duplex molecules with complementary stretches of the entire gene or gene fragments of interest. Depending on the application envisioned, one will typically desire to employ varying conditions of hybridization to achieve varying degrees of selectivity of probe towards target sequence. For applications requiring high selectivity, one will typically desire to employ relatively stringent conditions to form the hybrids, e.g., one will select relatively low salt and/or high temperature conditions, such as provided by a salt concentration of from about 0.02 M to about 0.15 M salt at temperatures of from about 50°C to about 70°C. Such selective conditions tolerate little, if any, mismatch between the probe and the template or target strand, and would be particularly suitable for isolating related sequences.

Of course, for some applications, for example, where one desires to prepare mutants employing a mutant primer strand hybridized to an underlying template, less stringent (reduced stringency) hybridization conditions will typically be needed in order to allow formation of the heteroduplex. In these circumstances, one may desire to employ salt conditions such as those of from about 0.15 M to about 0.9 M salt, at temperatures ranging from about 20°C to about 55°C. Cross-hybridizing species can thereby be readily identified as positively hybridizing signals with respect to control hybridizations. In any case, it is generally appreciated that conditions can be rendered more stringent by the addition of increasing amounts of formamide, which serves to destabilize the hybrid duplex in the same manner as increased temperature. Thus, hybridization conditions can be readily manipulated, and thus will generally be a method of choice depending on the desired results.

According to another embodiment of the present invention, polynucleotide compositions comprising antisense oligonucleotides are provided. Antisense oligonucleotides have been demonstrated to be effective and targeted inhibitors of protein synthesis, and, consequently, provide a therapeutic approach by which a disease can be treated by inhibiting the synthesis of proteins that contribute to the disease. The efficacy of antisense oligonucleotides for inhibiting protein synthesis is well established. For example, the synthesis of polygalacturonase and the muscarine

type 2 acetylcholine receptor are inhibited by antisense oligonucleotides directed to their respective mRNA sequences (U. S. Patent 5,739,119 and U. S. Patent 5,759,829). Further, examples of antisense inhibition have been demonstrated with the nuclear protein cyclin, the multiple drug resistance gene (MDG1), ICAM-1, E-selectin, STK-1, 5 striatal GABA_A receptor and human EGF (Jaskulski *et al.*, Science. 1988 Jun 10;240(4858):1544-6; Vasanthakumar and Ahmed, Cancer Commun. 1989;1(4):225-32; Peris *et al.*, Brain Res Mol Brain Res. 1998 Jun 15;57(2):310-20; U. S. Patent 5,801,154; U.S. Patent 5,789,573; U. S. Patent 5,718,709 and U.S. Patent 5,610,288). Antisense constructs have also been described that inhibit and can be used to treat a 10 variety of abnormal cellular proliferations, *e.g.* cancer (U. S. Patent 5,747,470; U. S. Patent 5,591,317 and U. S. Patent 5,783,683).

Therefore, in certain embodiments, the present invention provides oligonucleotide sequences that comprise all, or a portion of, any sequence that is capable of specifically binding to polynucleotide sequence described herein, or a 15 complement thereof. In one embodiment, the antisense oligonucleotides comprise DNA or derivatives thereof. In another embodiment, the oligonucleotides comprise RNA or derivatives thereof. In a third embodiment, the oligonucleotides are modified DNAs comprising a phosphorothioated modified backbone. In a fourth embodiment, the oligonucleotide sequences comprise peptide nucleic acids or derivatives thereof. In 20 each case, preferred compositions comprise a sequence region that is complementary, and more preferably substantially-complementary, and even more preferably, completely complementary to one or more portions of polynucleotides disclosed herein. Selection of antisense compositions specific for a given gene sequence is based upon analysis of the chosen target sequence and determination of secondary structure, T_m , 25 binding energy, and relative stability. Antisense compositions may be selected based upon their relative inability to form dimers, hairpins, or other secondary structures that would reduce or prohibit specific binding to the target mRNA in a host cell. Highly preferred target regions of the mRNA, are those which are at or near the AUG translation initiation codon, and those sequences which are substantially complementary 30 to 5' regions of the mRNA. These secondary structure analyses and target site selection

considerations can be performed, for example, using v.4 of the OLIGO primer analysis software and/or the BLASTN 2.0.5 algorithm software (Altschul *et al.*, Nucleic Acids Res. 1997, 25(17):3389-402).

The use of an antisense delivery method employing a short peptide
5 vector, termed MPG (27 residues), is also contemplated. The MPG peptide contains a hydrophobic domain derived from the fusion sequence of HIV gp41 and a hydrophilic domain from the nuclear localization sequence of SV40 T-antigen (Morris *et al.*, Nucleic Acids Res. 1997 Jul 15;25(14):2730-6). It has been demonstrated that several molecules of the MPG peptide coat the antisense oligonucleotides and can be delivered
10 into cultured mammalian cells in less than 1 hour with relatively high efficiency (90%). Further, the interaction with MPG strongly increases both the stability of the oligonucleotide to nuclease and the ability to cross the plasma membrane.

According to another embodiment of the invention, the polynucleotide compositions described herein are used in the design and preparation of ribozyme
15 molecules for inhibiting expression of the tumor polypeptides and proteins of the present invention in tumor cells. Ribozymes are RNA-protein complexes that cleave nucleic acids in a site-specific fashion. Ribozymes have specific catalytic domains that possess endonuclease activity (Kim and Cech, Proc Natl Acad Sci U S A. 1987 Dec;84(24):8788-92; Forster and Symons, Cell. 1987 Apr 24;49(2):211-20). For
20 example, a large number of ribozymes accelerate phosphoester transfer reactions with a high degree of specificity, often cleaving only one of several phosphoesters in an oligonucleotide substrate (Cech *et al.*, Cell. 1981 Dec;27(3 Pt 2):487-96; Michel and Westhof, J Mol Biol. 1990 Dec 5;216(3):585-610; Reinhold-Hurek and Shub, Nature. 1992 May 14;357(6374):173-6). This specificity has been attributed to the requirement
25 that the substrate bind via specific base-pairing interactions to the internal guide sequence ("IGS") of the ribozyme prior to chemical reaction.

Six basic varieties of naturally-occurring enzymatic RNAs are known presently. Each can catalyze the hydrolysis of RNA phosphodiester bonds *in trans* (and thus can cleave other RNA molecules) under physiological conditions. In general,
30 enzymatic nucleic acids act by first binding to a target RNA. Such binding occurs

through the target binding portion of an enzymatic nucleic acid which is held in close proximity to an enzymatic portion of the molecule that acts to cleave the target RNA. Thus, the enzymatic nucleic acid first recognizes and then binds a target RNA through complementary base-pairing, and once bound to the correct site, acts enzymatically to cut the target RNA. Strategic cleavage of such a target RNA will destroy its ability to direct synthesis of an encoded protein. After an enzymatic nucleic acid has bound and cleaved its RNA target, it is released from that RNA to search for another target and can repeatedly bind and cleave new targets.

The enzymatic nature of a ribozyme is advantageous over many technologies, such as antisense technology (where a nucleic acid molecule simply binds to a nucleic acid target to block its translation) since the concentration of ribozyme necessary to affect a therapeutic treatment is lower than that of an antisense oligonucleotide. This advantage reflects the ability of the ribozyme to act enzymatically. Thus, a single ribozyme molecule is able to cleave many molecules of target RNA. In addition, the ribozyme is a highly specific inhibitor, with the specificity of inhibition depending not only on the base pairing mechanism of binding to the target RNA, but also on the mechanism of target RNA cleavage. Single mismatches, or base-substitutions, near the site of cleavage can completely eliminate catalytic activity of a ribozyme. Similar mismatches in antisense molecules do not prevent their action (Woolf *et al.*, Proc Natl Acad Sci U S A. 1992 Aug 15;89(16):7305-9). Thus, the specificity of action of a ribozyme is greater than that of an antisense oligonucleotide binding the same RNA site.

The enzymatic nucleic acid molecule may be formed in a hammerhead

1;31(47):11843-52; an example of the RNaseP motif is described by Guerrier-Takada *et al.*, Cell. 1983 Dec;35(3 Pt 2):849-57; Neurospora VS RNA ribozyme motif is described by Collins (Saville and Collins, Cell. 1990 May 18;61(4):685-96; Saville and Collins, Proc Natl Acad Sci U S A. 1991 Oct 1;88(19):8826-30; Collins and Olive, 5 Biochemistry. 1993 Mar 23;32(11):2795-9); and an example of the Group I intron is described in (U. S. Patent 4,987,071). All that is important in an enzymatic nucleic acid molecule of this invention is that it has a specific substrate binding site which is complementary to one or more of the target gene RNA regions, and that it have nucleotide sequences within or surrounding that substrate binding site which impart an 10 RNA cleaving activity to the molecule. Thus the ribozyme constructs need not be limited to specific motifs mentioned herein.

Ribozymes may be designed as described in Int. Pat. Appl. Publ. No. WO 93/23569 and Int. Pat. Appl. Publ. No. WO 94/02595, each specifically incorporated herein by reference) and synthesized to be tested *in vitro* and *in vivo*, as 15 described. Such ribozymes can also be optimized for delivery. While specific examples are provided, those in the art will recognize that equivalent RNA targets in other species can be utilized when necessary.

Ribozyme activity can be optimized by altering the length of the ribozyme binding arms, or chemically synthesizing ribozymes with modifications that 20 prevent their degradation by serum ribonucleases (see *e.g.*, Int. Pat. Appl. Publ. No. WO 92/07065; Int. Pat. Appl. Publ. No. WO 93/15187; Int. Pat. Appl. Publ. No. WO 91/03162; Eur. Pat. Appl. Publ. No. 92110298.4; U. S. Patent 5,334,711; and Int. Pat. Appl. Publ. No. WO 94/13688, which describe various chemical modifications that can be made to the sugar moieties of enzymatic RNA molecules), modifications which 25 enhance their efficacy in cells, and removal of stem II bases to shorten RNA synthesis times and reduce chemical requirements.

Sullivan *et al.* (Int. Pat. Appl. Publ. No. WO 94/02595) describes the general methods for delivery of enzymatic RNA molecules. Ribozymes may be administered to cells by a variety of methods known to those familiar to the art, 30 including, but not restricted to, encapsulation in liposomes, by iontophoresis, or by

incorporation into other vehicles, such as hydrogels, cyclodextrins, biodegradable nanocapsules, and bioadhesive microspheres. For some indications, ribozymes may be directly delivered *ex vivo* to cells or tissues with or without the aforementioned vehicles. Alternatively, the RNA/vehicle combination may be locally delivered by direct
5 inhalation, by direct injection or by use of a catheter, infusion pump or stent. Other routes of delivery include, but are not limited to, intravascular, intramuscular, subcutaneous or joint injection, aerosol inhalation, oral (tablet or pill form), topical, systemic, ocular, intraperitoneal and/or intrathecal delivery. More detailed descriptions of ribozyme delivery and administration are provided in Int. Pat. Appl. Publ. No. WO
10 94/02595 and Int. Pat. Appl. Publ. No. WO 93/23569, each specifically incorporated herein by reference.

Another means of accumulating high concentrations of a ribozyme(s) within cells is to incorporate the ribozyme-encoding sequences into a DNA expression vector. Transcription of the ribozyme sequences are driven from a promoter for
15 eukaryotic RNA polymerase I (pol I), RNA polymerase II (pol II), or RNA polymerase III (pol III). Transcripts from pol II or pol III promoters will be expressed at high levels in all cells; the levels of a given pol II promoter in a given cell type will depend on the nature of the gene regulatory sequences (enhancers, silencers, *etc.*) present nearby. Prokaryotic RNA polymerase promoters may also be used, providing that the
20 prokaryotic RNA polymerase enzyme is expressed in the appropriate cells. Ribozymes expressed from such promoters have been shown to function in mammalian cells. Such transcription units can be incorporated into a variety of vectors for introduction into mammalian cells, including but not restricted to, plasmid DNA vectors, viral DNA vectors (such as adenovirus or adeno-associated vectors), or viral RNA vectors (such as
25 retroviral, semliki forest virus, sindbis virus vectors).

In another embodiment of the invention, peptide nucleic acids (PNAs) compositions are provided. PNA is a DNA mimic in which the nucleobases are attached to a pseudopeptide backbone (Good and Nielsen, Antisense Nucleic Acid Drug Dev. 1997 7(4) 431-37). PNA is able to be utilized in a number methods that
30 traditionally have used RNA or DNA. Often PNA sequences perform better in

techniques than the corresponding RNA or DNA sequences and have utilities that are not inherent to RNA or DNA. A review of PNA including methods of making, characteristics of, and methods of using, is provided by Corey (*Trends Biotechnol* 1997 Jun;15(6):224-9). As such, in certain embodiments, one may prepare PNA sequences
5 that are complementary to one or more portions of the ACE mRNA sequence, and such PNA compositions may be used to regulate, alter, decrease, or reduce the translation of ACE-specific mRNA, and thereby alter the level of ACE activity in a host cell to which such PNA compositions have been administered.

PNAs have 2-aminoethyl-glycine linkages replacing the normal
10 phosphodiester backbone of DNA (Nielsen *et al.*, *Science* 1991 Dec 6;254(5037):1497-500; Hanvey *et al.*, *Science*. 1992 Nov 27;258(5087):1481-5; Hyrup and Nielsen, *Bioorg Med Chem*. 1996 Jan;4(1):5-23). This chemistry has three important consequences: firstly, in contrast to DNA or phosphorothioate oligonucleotides, PNAs are neutral molecules; secondly, PNAs are achiral, which avoids the need to develop a
15 stereoselective synthesis; and thirdly, PNA synthesis uses standard Boc or Fmoc protocols for solid-phase peptide synthesis, although other methods, including a modified Merrifield method, have been used.

PNA monomers or ready-made oligomers are commercially available from PerSeptive Biosystems (Framingham, MA). PNA syntheses by either Boc or
20 Fmoc protocols are straightforward using manual or automated protocols (Norton *et al.*, *Bioorg Med Chem*. 1995 Apr;3(4):437-45). The manual protocol lends itself to the production of chemically modified PNAs or the simultaneous synthesis of families of closely related PNAs.

As with peptide synthesis, the success of a particular PNA synthesis will
25 depend on the properties of the chosen sequence. For example, while in theory PNAs can incorporate any combination of nucleotide bases, the presence of adjacent purines can lead to deletions of one or more residues in the product. In expectation of this difficulty, it is suggested that, in producing PNAs with adjacent purines, one should repeat the coupling of residues likely to be added inefficiently. This should be followed
30 by the purification of PNAs by reverse-phase high-pressure liquid chromatography,

providing yields and purity of product similar to those observed during the synthesis of peptides.

Modifications of PNAs for a given application may be accomplished by coupling amino acids during solid-phase synthesis or by attaching compounds that contain a carboxylic acid group to the exposed N-terminal amine. Alternatively, PNAs can be modified after synthesis by coupling to an introduced lysine or cysteine. The ease with which PNAs can be modified facilitates optimization for better solubility or for specific functional requirements. Once synthesized, the identity of PNAs and their derivatives can be confirmed by mass spectrometry. Several studies have made and utilized modifications of PNAs (for example, Norton *et al.*, *Bioorg Med Chem.* 1995 Apr;3(4):437-45; Petersen *et al.*, *J Pept Sci.* 1995 May-Jun;1(3):175-83; Orum *et al.*, *Biotechniques.* 1995 Sep;19(3):472-80; Footer *et al.*, *Biochemistry.* 1996 Aug 20;35(33):10673-9; Griffith *et al.*, *Nucleic Acids Res.* 1995 Aug 11;23(15):3003-8; Pardridge *et al.*, *Proc Natl Acad Sci U S A.* 1995 Jun 6;92(12):5592-6; Boffa *et al.*, *Proc Natl Acad Sci U S A.* 1995 Mar 14;92(6):1901-5; Gambacorti-Passerini *et al.*, *Blood.* 1996 Aug 15;88(4):1411-7; Armitage *et al.*, *Proc Natl Acad Sci U S A.* 1997 Nov 11;94(23):12320-5; Seeger *et al.*, *Biotechniques.* 1997 Sep;23(3):512-7). U.S. Patent No. 5,700,922 discusses PNA-DNA-PNA chimeric molecules and their uses in diagnostics, modulating protein in organisms, and treatment of conditions susceptible to therapeutics.

Methods of characterizing the antisense binding properties of PNAs are discussed in Rose (*Anal Chem.* 1993 Dec 15;65(24):3545-9) and Jensen *et al.* (*Biochemistry.* 1997 Apr 22;36(16):5072-7). Rose uses capillary gel electrophoresis to determine binding of PNAs to their complementary oligonucleotide, measuring the relative binding kinetics and stoichiometry. Similar types of measurements were made by Jensen *et al.* using BIAcore™ technology.

Other applications of PNAs that have been described and will be apparent to the skilled artisan include use in DNA strand invasion, antisense inhibition, mutational analysis, enhancers of transcription, nucleic acid purification, isolation of

transcriptionally active genes, blocking of transcription factor binding, genome cleavage, biosensors, *in situ* hybridization, and the like.

Polynucleotide Identification, Characterization and Expression

Polynucleotides compositions of the present invention may be identified, prepared and/or manipulated using any of a variety of well established techniques (see generally, Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989, and other like references). For example, a polynucleotide may be identified, as described in more detail below, by screening a microarray of cDNAs for tumor-associated expression (*i.e.*, expression that is at least two fold greater in a tumor than in normal tissue, as determined using a representative assay provided herein). Such screens may be performed, for example, using the microarray technology of Affymetrix, Inc. (Santa Clara, CA) according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997). Alternatively, polynucleotides may be amplified from cDNA prepared from cells expressing the proteins described herein, such as tumor cells.

Many template dependent processes are available to amplify a target sequences of interest present in a sample. One of the best known amplification methods is the polymerase chain reaction (PCRTM) which is described in detail in U.S. Patent Nos. 4,683,195, 4,683,202 and 4,800,159, each of which is incorporated herein by reference in its entirety. Briefly, in PCRTM, two primer sequences are prepared which are complementary to regions on opposite complementary strands of the target sequence. An excess of deoxynucleoside triphosphates is added to a reaction mixture along with a DNA polymerase (*e.g.*, *Taq* polymerase). If the target sequence is present in a sample, the primers will bind to the target and the polymerase will cause the primers to be extended along the target sequence by adding on nucleotides. By raising and lowering the temperature of the reaction mixture, the extended primers will dissociate from the target to form reaction products, excess primers will bind to the target and to the reaction product and the process is repeated. Preferably reverse

transcription and PCRTM amplification procedure may be performed in order to quantify the amount of mRNA amplified. Polymerase chain reaction methodologies are well known in the art.

Any of a number of other template dependent processes, many of which
5 are variations of the PCRTM amplification technique, are readily known and available in the art. Illustratively, some such methods include the ligase chain reaction (referred to as LCR), described, for example, in Eur. Pat. Appl. Publ. No. 320,308 and U.S. Patent No. 4,883,750; Qbeta Replicase, described in PCT Intl. Pat. Appl. Publ. No. PCT/US87/00880; Strand Displacement Amplification (SDA) and Repair Chain
10 Reaction (RCR). Still other amplification methods are described in Great Britain Pat. Appl. No. 2 202 328, and in PCT Intl. Pat. Appl. Publ. No. PCT/US89/01025. Other nucleic acid amplification procedures include transcription-based amplification systems (TAS) (PCT Intl. Pat. Appl. Publ. No. WO 88/10315), including nucleic acid sequence based amplification (NASBA) and 3SR. Eur. Pat. Appl. Publ. No. 329,822 describes a
15 nucleic acid amplification process involving cyclically synthesizing single-stranded RNA ("ssRNA"), ssDNA, and double-stranded DNA (dsDNA). PCT Intl. Pat. Appl. Publ. No. WO 89/06700 describes a nucleic acid sequence amplification scheme based on the hybridization of a promoter/primer sequence to a target single-stranded DNA ("ssDNA") followed by transcription of many RNA copies of the sequence. Other
20 amplification methods such as "RACE" (Frohman, 1990), and "one-sided PCR" (Ohara, 1989) are also well-known to those of skill in the art.

An amplified portion of a polynucleotide of the present invention may be used to isolate a full length gene from a suitable library (e.g., a tumor cDNA library) using well known techniques. Within such techniques, a library (cDNA or genomic) is
25 screened using one or more polynucleotide probes or primers suitable for amplification. Preferably, a library is size-selected to include larger molecules. Random primed libraries may also be preferred for identifying 5' and upstream regions of genes. Genomic libraries are preferred for obtaining introns and extending 5' sequences.

For hybridization techniques, a partial sequence may be labeled (e.g., by
30 nick-translation or end-labeling with ³²P) using well known techniques. A bacterial or

bacteriophage library is then generally screened by hybridizing filters containing denatured bacterial colonies (or lawns containing phage plaques) with the labeled probe (see Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989). Hybridizing colonies or plaques are
5 selected and expanded, and the DNA is isolated for further analysis. cDNA clones may be analyzed to determine the amount of additional sequence by, for example, PCR using a primer from the partial sequence and a primer from the vector. Restriction maps and partial sequences may be generated to identify one or more overlapping clones. The complete sequence may then be determined using standard techniques, which may
10 involve generating a series of deletion clones. The resulting overlapping sequences can then be assembled into a single contiguous sequence. A full length cDNA molecule can be generated by ligating suitable fragments, using well known techniques.

Alternatively, amplification techniques, such as those described above, can be useful for obtaining a full length coding sequence from a partial cDNA sequence.
15 One such amplification technique is inverse PCR (see Triglia et al., *Nucl. Acids Res.* 16:8186, 1988), which uses restriction enzymes to generate a fragment in the known region of the gene. The fragment is then circularized by intramolecular ligation and used as a template for PCR with divergent primers derived from the known region. Within an alternative approach, sequences adjacent to a partial sequence may be
20 retrieved by amplification with a primer to a linker sequence and a primer specific to a known region. The amplified sequences are typically subjected to a second round of amplification with the same linker primer and a second primer specific to the known region. A variation on this procedure, which employs two primers that initiate extension in opposite directions from the known sequence, is described in WO
25 96/38591. Another such technique is known as "rapid amplification of cDNA ends" or RACE. This technique involves the use of an internal primer and an external primer, which hybridizes to a polyA region or vector sequence, to identify sequences that are 5' and 3' of a known sequence. Additional techniques include capture PCR (Lagerstrom et al., *PCR Methods Applic.* 1:111-19, 1991) and walking PCR (Parker et al., *Nucl.*

Acids. Res. 19:3055-60, 1991). Other methods employing amplification may also be employed to obtain a full length cDNA sequence.

In certain instances, it is possible to obtain a full length cDNA sequence by analysis of sequences provided in an expressed sequence tag (EST) database, such as that available from GenBank. Searches for overlapping ESTs may generally be performed using well known programs (*e.g.*, NCBI BLAST searches), and such ESTs may be used to generate a contiguous full length sequence. Full length DNA sequences may also be obtained by analysis of genomic fragments.

In other embodiments of the invention, polynucleotide sequences or fragments thereof which encode polypeptides of the invention, or fusion proteins or functional equivalents thereof, may be used in recombinant DNA molecules to direct expression of a polypeptide in appropriate host cells. Due to the inherent degeneracy of the genetic code, other DNA sequences that encode substantially the same or a functionally equivalent amino acid sequence may be produced and these sequences may be used to clone and express a given polypeptide.

As will be understood by those of skill in the art, it may be advantageous in some instances to produce polypeptide-encoding nucleotide sequences possessing non-naturally occurring codons. For example, codons preferred by a particular prokaryotic or eukaryotic host can be selected to increase the rate of protein expression or to produce a recombinant RNA transcript having desirable properties, such as a half-life which is longer than that of a transcript generated from the naturally occurring sequence.

Moreover, the polynucleotide sequences of the present invention can be engineered using methods generally known in the art in order to alter polypeptide encoding sequences for a variety of reasons, including but not limited to, alterations which modify the cloning, processing, and/or expression of the gene product. For example, DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides may be used to engineer the nucleotide sequences. In addition, site-directed mutagenesis may be used to insert new restriction

sites, alter glycosylation patterns, change codon preference, produce splice variants, or introduce mutations, and so forth.

In another embodiment of the invention, natural, modified, or recombinant nucleic acid sequences may be ligated to a heterologous sequence to encode a fusion protein. For example, to screen peptide libraries for inhibitors of polypeptide activity, it may be useful to encode a chimeric protein that can be recognized by a commercially available antibody. A fusion protein may also be engineered to contain a cleavage site located between the polypeptide-encoding sequence and the heterologous protein sequence, so that the polypeptide may be cleaved and purified away from the heterologous moiety.

Sequences encoding a desired polypeptide may be synthesized, in whole or in part, using chemical methods well known in the art (see Caruthers, M. H. et al. (1980) *Nucl. Acids Res. Symp. Ser.* 215-223, Horn, T. et al. (1980) *Nucl. Acids Res. Symp. Ser.* 225-232). Alternatively, the protein itself may be produced using chemical methods to synthesize the amino acid sequence of a polypeptide, or a portion thereof. For example, peptide synthesis can be performed using various solid-phase techniques (Roberge, J. Y. et al. (1995) *Science* 269:202-204) and automated synthesis may be achieved, for example, using the ABI 431A Peptide Synthesizer (Perkin Elmer, Palo Alto, CA).

A newly synthesized peptide may be substantially purified by preparative high performance liquid chromatography (e.g., Creighton, T. (1983) *Proteins, Structures and Molecular Principles*, WH Freeman and Co., New York, N.Y.) or other comparable techniques available in the art. The composition of the synthetic peptides may be confirmed by amino acid analysis or sequencing (e.g., the Edman degradation procedure). Additionally, the amino acid sequence of a polypeptide, or any part thereof, may be altered during direct synthesis and/or combined using chemical methods with sequences from other proteins, or any part thereof, to produce a variant polypeptide.

In order to express a desired polypeptide, the nucleotide sequences encoding the polypeptide, or functional equivalents, may be inserted into appropriate

expression vector, *i.e.*, a vector which contains the necessary elements for the transcription and translation of the inserted coding sequence. Methods which are well known to those skilled in the art may be used to construct expression vectors containing sequences encoding a polypeptide of interest and appropriate transcriptional and translational control elements. These methods include *in vitro* recombinant DNA techniques, synthetic techniques, and *in vivo* genetic recombination. Such techniques are described, for example, in Sambrook, J. et al. (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Plainview, N.Y., and Ausubel, F. M. et al. (1989) Current Protocols in Molecular Biology, John Wiley & Sons, New York.

A variety of expression vector/host systems may be utilized to contain and express polynucleotide sequences. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with virus expression vectors (*e.g.*, baculovirus); plant cell systems transformed with virus expression vectors (*e.g.*, cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or with bacterial expression vectors (*e.g.*, Ti or pBR322 plasmids); or animal cell systems.

The "control elements" or "regulatory sequences" present in an expression vector are those non-translated regions of the vector--enhancers, promoters, 5' and 3' untranslated regions--which interact with host cellular proteins to carry out transcription and translation. Such elements may vary in their strength and specificity. Depending on the vector system and host utilized, any number of suitable transcription and translation elements, including constitutive and inducible promoters, may be used. For example, when cloning in bacterial systems, inducible promoters such as the hybrid lacZ promoter of the PBLUESCRIPT phagemid (Stratagene, La Jolla, Calif.) or PSPORT1 plasmid (Gibco BRL, Gaithersburg, MD) and the like may be used. In mammalian cell systems, promoters from mammalian genes or from mammalian viruses are generally preferred. If it is necessary to generate a cell line that contains

multiple copies of the sequence encoding a polypeptide, vectors based on SV40 or EBV may be advantageously used with an appropriate selectable marker.

In bacterial systems, any of a number of expression vectors may be selected depending upon the use intended for the expressed polypeptide. For example, when large quantities are needed, for example for the induction of antibodies, vectors which direct high level expression of fusion proteins that are readily purified may be used. Such vectors include, but are not limited to, the multifunctional *E. coli* cloning and expression vectors such as BLUESCRIPT (Stratagene), in which the sequence encoding the polypeptide of interest may be ligated into the vector in frame with sequences for the amino-terminal Met and the subsequent 7 residues of β -galactosidase so that a hybrid protein is produced; pIN vectors (Van Heeke, G. and S. M. Schuster (1989) *J. Biol. Chem.* 264:5503-5509); and the like. pGEX Vectors (Promega, Madison, Wis.) may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption to glutathione-agarose beads followed by elution in the presence of free glutathione. Proteins made in such systems may be designed to include heparin, thrombin, or factor XA protease cleavage sites so that the cloned polypeptide of interest can be released from the GST moiety at will.

In the yeast, *Saccharomyces cerevisiae*, a number of vectors containing constitutive or inducible promoters such as alpha factor, alcohol oxidase, and PGH may be used. For reviews, see Ausubel et al. (supra) and Grant et al. (1987) *Methods Enzymol.* 153:516-544.

In cases where plant expression vectors are used, the expression of sequences encoding polypeptides may be driven by any of a number of promoters. For example, viral promoters such as the 35S and 19S promoters of CaMV may be used alone or in combination with the omega leader sequence from TMV (Takamatsu, N. (1987) *EMBO J.* 6:307-311. Alternatively, plant promoters such as the small subunit of RUBISCO or heat shock promoters may be used (Coruzzi, G. et al. (1984) *EMBO J.* 3:1671-1680; Broglie, R. et al. (1984) *Science* 224:838-843; and Winter, J. et al. (1991)

Results Probl. Cell Differ. 17:85-105). These constructs can be introduced into plant cells by direct DNA transformation or pathogen-mediated transfection. Such techniques are described in a number of generally available reviews (see, for example, Hobbs, S. or Murry, L. E. in McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York, N.Y.; pp. 191-196).

An insect system may also be used to express a polypeptide of interest. For example, in one such system, Autographa californica nuclear polyhedrosis virus (AcNPV) is used as a vector to express foreign genes in *Spodoptera frugiperda* cells or in *Trichoplusia* larvae. The sequences encoding the polypeptide may be cloned into a non-essential region of the virus, such as the polyhedrin gene, and placed under control of the polyhedrin promoter. Successful insertion of the polypeptide-encoding sequence will render the polyhedrin gene inactive and produce recombinant virus lacking coat protein. The recombinant viruses may then be used to infect, for example, *S. frugiperda* cells or *Trichoplusia* larvae in which the polypeptide of interest may be expressed (Engelhard, E. K. et al. (1994) *Proc. Natl. Acad. Sci.* 91 :3224-3227).

In mammalian host cells, a number of viral-based expression systems are generally available. For example, in cases where an adenovirus is used as an expression vector, sequences encoding a polypeptide of interest may be ligated into an adenovirus transcription/translation complex consisting of the late promoter and tripartite leader sequence. Insertion in a non-essential E1 or E3 region of the viral genome may be used to obtain a viable virus which is capable of expressing the polypeptide in infected host cells (Logan, J. and Shenk, T. (1984) *Proc. Natl. Acad. Sci.* 81:3655-3659). In addition, transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used to increase expression in mammalian host cells.

Specific initiation signals may also be used to achieve more efficient translation of sequences encoding a polypeptide of interest. Such signals include the ATG initiation codon and adjacent sequences. In cases where sequences encoding the polypeptide, its initiation codon, and upstream sequences are inserted into the appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a portion

thereof, is inserted, exogenous translational control signals including the ATG initiation codon should be provided. Furthermore, the initiation codon should be in the correct reading frame to ensure translation of the entire insert. Exogenous translational elements and initiation codons may be of various origins, both natural and synthetic.

- 5 The efficiency of expression may be enhanced by the inclusion of enhancers which are appropriate for the particular cell system which is used, such as those described in the literature (Scharf, D. et al. (1994) *Results Probl. Cell Differ.* 20:125-162).

In addition, a host cell strain may be chosen for its ability to modulate the expression of the inserted sequences or to process the expressed protein in the
10 desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" form of the protein may also be used to facilitate correct insertion, folding and/or function. Different host cells such as CHO, COS, HeLa, MDCK, HEK293, and WI38, which have specific cellular
15 machinery and characteristic mechanisms for such post-translational activities, may be chosen to ensure the correct modification and processing of the foreign protein.

For long-term, high-yield production of recombinant proteins, stable expression is generally preferred. For example, cell lines which stably express a polynucleotide of interest may be transformed using expression vectors which may
20 contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Following the introduction of the vector, cells may be allowed to grow for 1-2 days in an enriched media before they are switched to selective media. The purpose of the selectable marker is to confer resistance to selection, and its presence allows growth and recovery of cells which
25 successfully express the introduced sequences. Resistant clones of stably transformed cells may be proliferated using tissue culture techniques appropriate to the cell type.

Any number of selection systems may be used to recover transformed cell lines. These include, but are not limited to, the herpes simplex virus thymidine kinase (Wigler, M. et al. (1977) *Cell* 11:223-32) and adenine phosphoribosyltransferase
30 (Lowy, I. et al. (1990) *Cell* 22:817-23) genes which can be employed in tk.sup.- or

aprt.sup. cells, respectively. Also, antimetabolite, antibiotic or herbicide resistance can be used as the basis for selection; for example, dhfr which confers resistance to methotrexate (Wigler, M. et al. (1980) *Proc. Natl. Acad. Sci.* 77:3567-70); npt, which confers resistance to the aminoglycosides, neomycin and G-418 (Colbere-Garapin, F. et al (1981) *J. Mol. Biol.* 150:1-14); and als or pat, which confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively (Murry, *supra*). Additional selectable genes have been described, for example, trpB, which allows cells to utilize indole in place of tryptophan, or hisD, which allows cells to utilize histinol in place of histidine (Hartman, S. C. and R. C. Mulligan (1988) *Proc. Natl. Acad. Sci.* 85:8047-51). The use of visible markers has gained popularity with such markers as anthocyanins, beta-glucuronidase and its substrate GUS, and luciferase and its substrate luciferin, being widely used not only to identify transformants, but also to quantify the amount of transient or stable protein expression attributable to a specific vector system (Rhodes, C. A. et al. (1995) *Methods Mol. Biol.* 55:121-131).

Although the presence/absence of marker gene expression suggests that the gene of interest is also present, its presence and expression may need to be confirmed. For example, if the sequence encoding a polypeptide is inserted within a marker gene sequence, recombinant cells containing sequences can be identified by the absence of marker gene function. Alternatively, a marker gene can be placed in tandem with a polypeptide-encoding sequence under the control of a single promoter. Expression of the marker gene in response to induction or selection usually indicates expression of the tandem gene as well.

Alternatively, host cells that contain and express a desired polynucleotide sequence may be identified by a variety of procedures known to those of skill in the art. These procedures include, but are not limited to, DNA-DNA or DNA-RNA hybridizations and protein bioassay or immunoassay techniques which include, for example, membrane, solution, or chip based technologies for the detection and/or quantification of nucleic acid or protein.

A variety of protocols for detecting and measuring the expression of polynucleotide-encoded products, using either polyclonal or monoclonal antibodies

specific for the product are known in the art. Examples include enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA), and fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering epitopes on a given polypeptide may be preferred for some applications, but a competitive binding assay may also be employed. These and other assays are described, among other places, in Hampton, R. et al. (1990; Serological Methods, a Laboratory Manual, APS Press, St Paul, Minn.) and Maddox, D. E. et al. (1983; *J. Exp. Med.* 158:1211-1216).

A wide variety of labels and conjugation techniques are known by those skilled in the art and may be used in various nucleic acid and amino acid assays. Means for producing labeled hybridization or PCR probes for detecting sequences related to polynucleotides include oligolabeling, nick translation, end-labeling or PCR amplification using a labeled nucleotide. Alternatively, the sequences, or any portions thereof may be cloned into a vector for the production of an mRNA probe. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by addition of an appropriate RNA polymerase such as T7, T3, or SP6 and labeled nucleotides. These procedures may be conducted using a variety of commercially available kits. Suitable reporter molecules or labels, which may be used include radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

Host cells transformed with a polynucleotide sequence of interest may be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The protein produced by a recombinant cell may be secreted or contained intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides of the invention may be designed to contain signal sequences which direct secretion of the encoded polypeptide through a prokaryotic or eukaryotic cell membrane. Other recombinant constructions may be used to join sequences encoding a polypeptide of interest to nucleotide sequence encoding a polypeptide domain which will facilitate purification of soluble proteins. Such purification facilitating domains include, but are

not limited to, metal chelating peptides such as histidine-tryptophan modules that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp., Seattle, Wash.). The inclusion of cleavable linker sequences such as those specific for Factor XA or enterokinase (Invitrogen, San Diego, Calif.) between the purification domain and the encoded polypeptide may be used to facilitate purification. One such expression vector provides for expression of a fusion protein containing a polypeptide of interest and a nucleic acid encoding 6 histidine residues preceding a thioredoxin or an enterokinase cleavage site. The histidine residues facilitate purification on IMIAC (immobilized metal ion affinity chromatography) as described in Porath, J. et al. (1992, *Prot. Exp. Purif.* 3:263-281) while the enterokinase cleavage site provides a means for purifying the desired polypeptide from the fusion protein. A discussion of vectors which contain fusion proteins is provided in Kroll, D. J. et al. (1993; *DNA Cell Biol.* 12:441-453).

In addition to recombinant production methods, polypeptides of the invention, and fragments thereof, may be produced by direct peptide synthesis using solid-phase techniques (Merrifield J. (1963) *J. Am. Chem. Soc.* 85:2149-2154). Protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be achieved, for example, using Applied Biosystems 431A Peptide Synthesizer (Perkin Elmer). Alternatively, various fragments may be chemically synthesized separately and combined using chemical methods to produce the full length molecule.

Antibody Compositions, Fragments Thereof and Other Binding Agents

According to another aspect, the present invention further provides binding agents, such as antibodies and antigen-binding fragments thereof, that exhibit immunological binding to a tumor polypeptide disclosed herein, or to a portion, variant or derivative thereof. An antibody, or antigen-binding fragment thereof, is said to "specifically bind," "immunologically bind," and/or is "immunologically reactive" to a polypeptide of the invention if it reacts at a detectable level (within, for example, an

ELISA assay) with the polypeptide, and does not react detectably with unrelated polypeptides under similar conditions.

Immunological binding, as used in this context, generally refers to the non-covalent interactions of the type which occur between an immunoglobulin molecule and an antigen for which the immunoglobulin is specific. The strength, or affinity of immunological binding interactions can be expressed in terms of the dissociation constant (K_d) of the interaction, wherein a smaller K_d represents a greater affinity. Immunological binding properties of selected polypeptides can be quantified using methods well known in the art. One such method entails measuring the rates of antigen-binding site/antigen complex formation and dissociation, wherein those rates depend on the concentrations of the complex partners, the affinity of the interaction, and on geometric parameters that equally influence the rate in both directions. Thus, both the "on rate constant" (K_{on}) and the "off rate constant" (K_{off}) can be determined by calculation of the concentrations and the actual rates of association and dissociation. The ratio of K_{off}/K_{on} enables cancellation of all parameters not related to affinity, and is thus equal to the dissociation constant K_d . See, generally, Davies et.al. (1990) Annual Rev. Biochem. 59:439-473.

An "antigen-binding site," or "binding portion" of an antibody refers to the part of the immunoglobulin molecule that participates in antigen binding. The antigen binding site is formed by amino acid residues of the N-terminal variable ("V") regions of the heavy ("H") and light ("L") chains. Three highly divergent stretches within the V regions of the heavy and light chains are referred to as "hypervariable regions" which are interposed between more conserved flanking stretches known as "framework regions," or "FRs". Thus the term "FR" refers to amino acid sequences which are naturally found between and adjacent to hypervariable regions in immunoglobulins. In an antibody molecule, the three hypervariable regions of a light chain and the three hypervariable regions of a heavy chain are disposed relative to each other in three dimensional space to form an antigen-binding surface. The antigen-binding surface is complementary to the three-dimensional surface of a bound antigen,

and the three hypervariable regions of each of the heavy and light chains are referred to as "complementarity-determining regions," or "CDRs."

Binding agents may be further capable of differentiating between patients with and without a cancer, such as lung cancer, using the representative assays provided herein. For example, antibodies or other binding agents that bind to a tumor protein will preferably generate a signal indicating the presence of a cancer in at least about 20% of patients with the disease, more preferably at least about 30% of patients. Alternatively, or in addition, the antibody will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without the cancer. To determine whether a binding agent satisfies this requirement, biological samples (e.g., blood, sera, sputum, urine and/or tumor biopsies) from patients with and without a cancer (as determined using standard clinical tests) may be assayed as described herein for the presence of polypeptides that bind to the binding agent. Preferably, a statistically significant number of samples with and without the disease will be assayed. Each binding agent should satisfy the above criteria; however, those of ordinary skill in the art will recognize that binding agents may be used in combination to improve sensitivity.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome, with or without a peptide component, an RNA molecule or a polypeptide. In a preferred embodiment, a binding agent is an antibody or an antigen-binding fragment thereof. Antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, antibodies can be produced by cell culture techniques, including the generation of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies. In one technique, an immunogen comprising the polypeptide is initially injected into any of a wide variety of mammals (e.g., mice, rats, rabbits, sheep or goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a

superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically.

- 5 Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

- Monoclonal antibodies specific for an antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (*i.e.*, reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and their culture supernatants tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.
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- Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and
- 25

extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

A number of therapeutically useful molecules are known in the art which comprise antigen-binding sites that are capable of exhibiting immunological binding properties of an antibody molecule. The proteolytic enzyme papain preferentially cleaves IgG molecules to yield several fragments, two of which (the "F(ab)" fragments) each comprise a covalent heterodimer that includes an intact antigen-binding site. The enzyme pepsin is able to cleave IgG molecules to provide several fragments, including the "F(ab)₂" fragment which comprises both antigen-binding sites. An "Fv" fragment can be produced by preferential proteolytic cleavage of an IgM, and on rare occasions IgG or IgA immunoglobulin molecule. Fv fragments are, however, more commonly derived using recombinant techniques known in the art. The Fv fragment includes a non-covalent V_H::V_L heterodimer including an antigen-binding site which retains much of the antigen recognition and binding capabilities of the native antibody molecule.

15 Inbar et al. (1972) Proc. Nat. Acad. Sci. USA 69:2659-2662; Hochman et al. (1976) Biochem 15:2706-2710; and Ehrlich et al. (1980) Biochem 19:4091-4096.

A single chain Fv ("sFv") polypeptide is a covalently linked V_H::V_L heterodimer which is expressed from a gene fusion including V_H- and V_L-encoding genes linked by a peptide-encoding linker. Huston et al. (1988) Proc. Nat. Acad. Sci. USA 85(16):5879-5883. A number of methods have been described to discern chemical structures for converting the naturally aggregated--but chemically separated--light and heavy polypeptide chains from an antibody V region into an sFv molecule which will fold into a three dimensional structure substantially similar to the structure of an antigen-binding site. See, e.g., U.S. Pat. Nos. 5,091,513 and 5,132,405, to Huston et al.;

20 and U.S. Pat. No. 4,946,778, to Ladner et al.

Each of the above-described molecules includes a heavy chain and a light chain CDR set, respectively interposed between a heavy chain and a light chain FR set which provide support to the CDRs and define the spatial relationship of the CDRs relative to each other. As used herein, the term "CDR set" refers to the three hypervariable regions of a heavy or light chain V region. Proceeding from the N-

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terminus of a heavy or light chain, these regions are denoted as "CDR1," "CDR2," and "CDR3" respectively. An antigen-binding site, therefore, includes six CDRs, comprising the CDR set from each of a heavy and a light chain V region. A polypeptide comprising a single CDR, (e.g., a CDR1, CDR2 or CDR3) is referred to herein as a
5 "molecular recognition unit." Crystallographic analysis of a number of antigen-antibody complexes has demonstrated that the amino acid residues of CDRs form extensive contact with bound antigen, wherein the most extensive antigen contact is with the heavy chain CDR3. Thus, the molecular recognition units are primarily responsible for the specificity of an antigen-binding site.

10 As used herein, the term "FR set" refers to the four flanking amino acid sequences which frame the CDRs of a CDR set of a heavy or light chain V region. Some FR residues may contact bound antigen; however, FRs are primarily responsible for folding the V region into the antigen-binding site, particularly the FR residues directly adjacent to the CDRs. Within FRs, certain amino residues and certain structural
15 features are very highly conserved. In this regard, all V region sequences contain an internal disulfide loop of around 90 amino acid residues. When the V regions fold into a binding-site, the CDRs are displayed as projecting loop motifs which form an antigen-binding surface. It is generally recognized that there are conserved structural regions of FRs which influence the folded shape of the CDR loops into certain "canonical"
20 structures--regardless of the precise CDR amino acid sequence. Further, certain FR residues are known to participate in non-covalent interdomain contacts which stabilize the interaction of the antibody heavy and light chains.

A number of "humanized" antibody molecules comprising an antigen-binding site derived from a non-human immunoglobulin have been described, including
25 chimeric antibodies having rodent V regions and their associated CDRs fused to human constant domains (Winter et al. (1991) Nature 349:293-299; Lobuglio et al. (1989) Proc. Nat. Acad. Sci. USA 86:4220-4224; Shaw et al. (1987) J Immunol. 138:4534-4538; and Brown et al. (1987) Cancer Res. 47:3577-3583), rodent CDRs grafted into a human supporting FR prior to fusion with an appropriate human antibody constant
30 domain (Riechmann et al. (1988) Nature 332:323-327; Verhoeyen et al. (1988) Science

239:1534-1536; and Jones et al. (1986) Nature 321:522-525), and rodent CDRs supported by recombinantly veneered rodent FRs (European Patent Publication No. 519,596, published Dec. 23, 1992). These "humanized" molecules are designed to minimize unwanted immunological response toward rodent antihuman antibody
5 molecules which limits the duration and effectiveness of therapeutic applications of those moieties in human recipients.

As used herein, the terms "veneered FRs" and "recombinantly veneered FRs" refer to the selective replacement of FR residues from, *e.g.*, a rodent heavy or light chain V region, with human FR residues in order to provide a xenogeneic molecule
10 comprising an antigen-binding site which retains substantially all of the native FR polypeptide folding structure. Veneering techniques are based on the understanding that the ligand binding characteristics of an antigen-binding site are determined primarily by the structure and relative disposition of the heavy and light chain CDR sets within the antigen-binding surface. Davies et al. (1990) Ann. Rev. Biochem. 59:439-473. Thus,
15 antigen binding specificity can be preserved in a humanized antibody only wherein the CDR structures, their interaction with each other, and their interaction with the rest of the V region domains are carefully maintained. By using veneering techniques, exterior (*e.g.*, solvent-accessible) FR residues which are readily encountered by the immune system are selectively replaced with human residues to provide a hybrid molecule that
20 comprises either a weakly immunogenic, or substantially non-immunogenic veneered surface.

The process of veneering makes use of the available sequence data for human antibody variable domains compiled by Kabat et al., in Sequences of Proteins of Immunological Interest, 4th ed., (U.S. Dept. of Health and Human Services, U.S.
25 Government Printing Office, 1987), updates to the Kabat database, and other accessible U.S. and foreign databases (both nucleic acid and protein). Solvent accessibilities of V region amino acids can be deduced from the known three-dimensional structure for human and murine antibody fragments. There are two general steps in veneering a murine antigen-binding site. Initially, the FRs of the variable domains of an antibody
30 molecule of interest are compared with corresponding FR sequences of human variable

domains obtained from the above-identified sources. The most homologous human V regions are then compared residue by residue to corresponding murine amino acids. The residues in the murine FR which differ from the human counterpart are replaced by the residues present in the human moiety using recombinant techniques well known in the art. Residue switching is only carried out with moieties which are at least partially exposed (solvent accessible), and care is exercised in the replacement of amino acid residues which may have a significant effect on the tertiary structure of V region domains, such as proline, glycine and charged amino acids.

In this manner, the resultant "veneered" murine antigen-binding sites are thus designed to retain the murine CDR residues, the residues substantially adjacent to the CDRs, the residues identified as buried or mostly buried (solvent inaccessible), the residues believed to participate in non-covalent (*e.g.*, electrostatic and hydrophobic) contacts between heavy and light chain domains, and the residues from conserved structural regions of the FRs which are believed to influence the "canonical" tertiary structures of the CDR loops. These design criteria are then used to prepare recombinant nucleotide sequences which combine the CDRs of both the heavy and light chain of a murine antigen-binding site into human-appearing FRs that can be used to transfect mammalian cells for the expression of recombinant human antibodies which exhibit the antigen specificity of the murine antibody molecule.

In another embodiment of the invention, monoclonal antibodies of the present invention may be coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include ^{90}Y , ^{123}I , ^{125}I , ^{131}I , ^{186}Re , ^{188}Re , ^{211}At , and ^{212}Bi . Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, *Shigella* toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a

substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (e.g., a halide) on the other.

5 Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in
10 chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

 It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker
15 group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, e.g., U.S. Patent No. 4,671,958, to Rodwell et al.

 Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a
20 linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (e.g., U.S. Patent No. 4,489,710, to Spitler), by irradiation of a photolabile bond (e.g., U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of
25 derivatized amino acid side chains (e.g., U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (e.g., U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (e.g., U.S. Patent No. 4,569,789, to Blattler et al.).

 It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In
30 another embodiment, more than one type of agent may be coupled to one antibody.

Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers that provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

5 A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (e.g., U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (e.g., U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a
10 liposome vesicle (e.g., U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing nitrogen and sulfur
15 atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

T Cell Compositions

 The present invention, in another aspect, provides T cells specific for a
20 tumor polypeptide disclosed herein, or for a variant or derivative thereof. Such cells may generally be prepared *in vitro* or *ex vivo*, using standard procedures. For example, T cells may be isolated from bone marrow, peripheral blood, or a fraction of bone marrow or peripheral blood of a patient, using a commercially available cell separation system, such as the Isolex™ System, available from Nexell Therapeutics, Inc. (Irvine,
25 CA; see also U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). Alternatively, T cells may be derived from related or unrelated humans, non-human mammals, cell lines or cultures.

 T cells may be stimulated with a polypeptide, polynucleotide encoding a polypeptide and/or an antigen presenting cell (APC) that expresses such a polypeptide.

Such stimulation is performed under conditions and for a time sufficient to permit the generation of T cells that are specific for the polypeptide of interest. Preferably, a tumor polypeptide or polynucleotide of the invention is present within a delivery vehicle, such as a microsphere, to facilitate the generation of specific T cells.

5 T cells are considered to be specific for a polypeptide of the present invention if the T cells specifically proliferate, secrete cytokines or kill target cells coated with the polypeptide or expressing a gene encoding the polypeptide. T cell specificity may be evaluated using any of a variety of standard techniques. For example, within a chromium release assay or proliferation assay, a stimulation index of
10 more than two fold increase in lysis and/or proliferation, compared to negative controls, indicates T cell specificity. Such assays may be performed, for example, as described in Chen et al., *Cancer Res.* 54:1065-1070, 1994. Alternatively, detection of the proliferation of T cells may be accomplished by a variety of known techniques. For example, T cell proliferation can be detected by measuring an increased rate of DNA
15 synthesis (e.g., by pulse-labeling cultures of T cells with tritiated thymidine and measuring the amount of tritiated thymidine incorporated into DNA). Contact with a tumor polypeptide (100 ng/ml - 100 µg/ml, preferably 200 ng/ml - 25 µg/ml) for 3 - 7 days will typically result in at least a two fold increase in proliferation of the T cells. Contact as described above for 2-3 hours should result in activation of the T cells, as
20 measured using standard cytokine assays in which a two fold increase in the level of cytokine release (e.g., TNF or IFN-γ) is indicative of T cell activation (see Coligan et al., *Current Protocols in Immunology*, vol. 1, Wiley Interscience (Greene 1998)). T cells that have been activated in response to a tumor polypeptide, polynucleotide or polypeptide-expressing APC may be CD4⁺ and/or CD8⁺. Tumor polypeptide-specific T
25 cells may be expanded using standard techniques. Within preferred embodiments, the T cells are derived from a patient, a related donor or an unrelated donor, and are administered to the patient following stimulation and expansion.

For therapeutic purposes, CD4⁺ or CD8⁺ T cells that proliferate in response to a tumor polypeptide, polynucleotide or APC can be expanded in number
30 either *in vitro* or *in vivo*. Proliferation of such T cells *in vitro* may be accomplished in a

variety of ways. For example, the T cells can be re-exposed to a tumor polypeptide, or a short peptide corresponding to an immunogenic portion of such a polypeptide, with or without the addition of T cell growth factors, such as interleukin-2, and/or stimulator cells that synthesize a tumor polypeptide. Alternatively, one or more T cells that proliferate in the presence of the tumor polypeptide can be expanded in number by cloning. Methods for cloning cells are well known in the art, and include limiting dilution.

Pharmaceutical Compositions

In additional embodiments, the present invention concerns formulation of one or more of the polynucleotide, polypeptide, T-cell and/or antibody compositions disclosed herein in pharmaceutically-acceptable carriers for administration to a cell or an animal, either alone, or in combination with one or more other modalities of therapy.

It will be understood that, if desired, a composition as disclosed herein may be administered in combination with other agents as well, such as, *e.g.*, other proteins or polypeptides or various pharmaceutically-active agents. In fact, there is virtually no limit to other components that may also be included, given that the additional agents do not cause a significant adverse effect upon contact with the target cells or host tissues. The compositions may thus be delivered along with various other agents as required in the particular instance. Such compositions may be purified from host cells or other biological sources, or alternatively may be chemically synthesized as described herein. Likewise, such compositions may further comprise substituted or derivatized RNA or DNA compositions.

Therefore, in another aspect of the present invention, pharmaceutical compositions are provided comprising one or more of the polynucleotide, polypeptide, antibody, and/or T-cell compositions described herein in combination with a physiologically acceptable carrier. In certain preferred embodiments, the pharmaceutical compositions of the invention comprise immunogenic polynucleotide and/or polypeptide compositions of the invention for use in prophylactic and therapeutic vaccine applications. Vaccine preparation is generally described in, for example, M.F.

Powell and M.J. Newman, eds., "Vaccine Design (the subunit and adjuvant approach)," Plenum Press (NY, 1995). Generally, such compositions will comprise one or more polynucleotide and/or polypeptide compositions of the present invention in combination with one or more immunostimulants.

5 It will be apparent that any of the pharmaceutical compositions described herein can contain pharmaceutically acceptable salts of the polynucleotides and polypeptides of the invention. Such salts can be prepared, for example, from pharmaceutically acceptable non-toxic bases, including organic bases (e.g., salts of primary, secondary and tertiary amines and basic amino acids) and inorganic bases
10 (e.g., sodium, potassium, lithium, ammonium, calcium and magnesium salts).

In another embodiment, illustrative immunogenic compositions, e.g., vaccine compositions, of the present invention comprise DNA encoding one or more of the polypeptides as described above, such that the polypeptide is generated *in situ*. As noted above, the polynucleotide may be administered within any of a variety of delivery
15 systems known to those of ordinary skill in the art. Indeed, numerous gene delivery techniques are well known in the art, such as those described by Rolland, *Crit. Rev. Therap. Drug Carrier Systems* 15:143-198, 1998, and references cited therein. Appropriate polynucleotide expression systems will, of course, contain the necessary regulatory DNA regulatory sequences for expression in a patient (such as a suitable
20 promoter and terminating signal). Alternatively, bacterial delivery systems may involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface or secretes such an epitope.

Therefore, in certain embodiments, polynucleotides encoding immunogenic polypeptides described herein are introduced into suitable mammalian
25 host cells for expression using any of a number of known viral-based systems. In one illustrative embodiment, retroviruses provide a convenient and effective platform for gene delivery systems. A selected nucleotide sequence encoding a polypeptide of the present invention can be inserted into a vector and packaged in retroviral particles using techniques known in the art. The recombinant virus can then be isolated and delivered
30 to a subject. A number of illustrative retroviral systems have been described (e.g., U.S.

Pat. No. 5,219,740; Miller and Rosman (1989) *BioTechniques* 7:980-990; Miller, A. D. (1990) *Human Gene Therapy* 1:5-14; Scarpa et al. (1991) *Virology* 180:849-852; Burns et al. (1993) *Proc. Natl. Acad. Sci. USA* 90:8033-8037; and Boris-Lawrie and Temin (1993) *Cur. Opin. Genet. Develop.* 3:102-109.

5 In addition, a number of illustrative adenovirus-based systems have also been described. Unlike retroviruses which integrate into the host genome, adenoviruses persist extrachromosomally thus minimizing the risks associated with insertional mutagenesis (Haj-Ahmad and Graham (1986) *J. Virol.* 57:267-274; Bett et al. (1993) *J. Virol.* 67:5911-5921; Mittereder et al. (1994) *Human Gene Therapy* 5:717-729; Seth et al. (1994) *J. Virol.* 68:933-940; Barr et al. (1994) *Gene Therapy* 1:51-58; Berkner, K. L. 10 (1988) *BioTechniques* 6:616-629; and Rich et al. (1993) *Human Gene Therapy* 4:461-476).

 Various adeno-associated virus (AAV) vector systems have also been developed for polynucleotide delivery. AAV vectors can be readily constructed using 15 techniques well known in the art. See, e.g., U.S. Pat. Nos. 5,173,414 and 5,139,941; International Publication Nos. WO 92/01070 and WO 93/03769; Lebkowski et al. (1988) *Molec. Cell. Biol.* 8:3988-3996; Vincent et al. (1990) *Vaccines 90* (Cold Spring Harbor Laboratory Press); Carter, B. J. (1992) *Current Opinion in Biotechnology* 3:533-539; Muzyczka, N. (1992) *Current Topics in Microbiol. and Immunol.* 158:97-129; 20 Kotin, R. M. (1994) *Human Gene Therapy* 5:793-801; Shelling and Smith (1994) *Gene Therapy* 1:165-169; and Zhou et al. (1994) *J. Exp. Med.* 179:1867-1875.

 Additional viral vectors useful for delivering the polynucleotides encoding polypeptides of the present invention by gene transfer include those derived from the pox family of viruses, such as vaccinia virus and avian poxvirus. By way of 25 example, vaccinia virus recombinants expressing the novel molecules can be constructed as follows. The DNA encoding a polypeptide is first inserted into an appropriate vector so that it is adjacent to a vaccinia promoter and flanking vaccinia DNA sequences, such as the sequence encoding thymidine kinase (TK). This vector is then used to transfect cells which are simultaneously infected with vaccinia. 30 Homologous recombination serves to insert the vaccinia promoter plus the gene

encoding the polypeptide of interest into the viral genome. The resulting TK.sup.(-) recombinant can be selected by culturing the cells in the presence of 5-bromodeoxyuridine and picking viral plaques resistant thereto.

A vaccinia-based infection/transfection system can be conveniently used to provide for inducible, transient expression or coexpression of one or more polypeptides described herein in host cells of an organism. In this particular system, cells are first infected in vitro with a vaccinia virus recombinant that encodes the bacteriophage T7 RNA polymerase. This polymerase displays exquisite specificity in that it only transcribes templates bearing T7 promoters. Following infection, cells are transfected with the polynucleotide or polynucleotides of interest, driven by a T7 promoter. The polymerase expressed in the cytoplasm from the vaccinia virus recombinant transcribes the transfected DNA into RNA which is then translated into polypeptide by the host translational machinery. The method provides for high level, transient, cytoplasmic production of large quantities of RNA and its translation products. See, *e.g.*, Elroy-Stein and Moss, *Proc. Natl. Acad. Sci. USA* (1990) 87:6743-6747; Fuerst et al. *Proc. Natl. Acad. Sci. USA* (1986) 83:8122-8126.

Alternatively, avipoxviruses, such as the fowlpox and canarypox viruses, can also be used to deliver the coding sequences of interest. Recombinant avipox viruses, expressing immunogens from mammalian pathogens, are known to confer protective immunity when administered to non-avian species. The use of an Avipox vector is particularly desirable in human and other mammalian species since members of the Avipox genus can only productively replicate in susceptible avian species and therefore are not infective in mammalian cells. Methods for producing recombinant Avipoxviruses are known in the art and employ genetic recombination, as described above with respect to the production of vaccinia viruses. See, *e.g.*, WO 91/12882; WO 89/03429; and WO 92/03545.

Any of a number of alphavirus vectors can also be used for delivery of polynucleotide compositions of the present invention, such as those vectors described in U.S. Patent Nos. 5,843,723; 6,015,686; 6,008,035 and 6,015,694. Certain vectors based

on Venezuelan Equine Encephalitis (VEE) can also be used, illustrative examples of which can be found in U.S. Patent Nos. 5,505,947 and 5,643,576.

Moreover, molecular conjugate vectors, such as the adenovirus chimeric vectors described in Michael et al. *J. Biol. Chem.* (1993) 268:6866-6869 and Wagner et al. *Proc. Natl. Acad. Sci. USA* (1992) 89:6099-6103, can also be used for gene delivery under the invention.

Additional illustrative information on these and other known viral-based delivery systems can be found, for example, in Fisher-Hoch et al., *Proc. Natl. Acad. Sci. USA* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *Proc. Natl. Acad. Sci. USA* 91:215-219, 1994; Kass-Eisler et al., *Proc. Natl. Acad. Sci. USA* 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993.

In certain embodiments, a polynucleotide may be integrated into the genome of a target cell. This integration may be in the specific location and orientation via homologous recombination (gene replacement) or it may be integrated in a random, non-specific location (gene augmentation). In yet further embodiments, the polynucleotide may be stably maintained in the cell as a separate, episomal segment of DNA. Such polynucleotide segments or "episomes" encode sequences sufficient to permit maintenance and replication independent of or in synchronization with the host cell cycle. The manner in which the expression construct is delivered to a cell and where in the cell the polynucleotide remains is dependent on the type of expression construct employed.

In another embodiment of the invention, a polynucleotide is administered/delivered as "naked" DNA, for example as described in Ulmer et al., *Science* 259:1745-1749, 1993 and reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

In still another embodiment, a composition of the present invention can be delivered via a particle bombardment approach, many of which have been described. In one illustrative example, gas-driven particle acceleration can be achieved with devices such as those manufactured by Powderject Pharmaceuticals PLC (Oxford, UK) and Powderject Vaccines Inc. (Madison, WI), some examples of which are described in U.S. Patent Nos. 5,846,796; 6,010,478; 5,865,796; 5,584,807; and EP Patent No. 0500 799. This approach offers a needle-free delivery approach wherein a dry powder formulation of microscopic particles, such as polynucleotide or polypeptide particles, are accelerated to high speed within a helium gas jet generated by a hand held device, propelling the particles into a target tissue of interest.

In a related embodiment, other devices and methods that may be useful for gas-driven needle-less injection of compositions of the present invention include those provided by Bioject, Inc. (Portland, OR), some examples of which are described in U.S. Patent Nos. 4,790,824; 5,064,413; 5,312,335; 5,383,851; 5,399,163; 5,520,639 and 5,993,412.

According to another embodiment, the pharmaceutical compositions described herein will comprise one or more immunostimulants in addition to the immunogenic polynucleotide, polypeptide, antibody, T-cell and/or APC compositions of this invention. An immunostimulant refers to essentially any substance that enhances or potentiates an immune response (antibody and/or cell-mediated) to an exogenous antigen. One preferred type of immunostimulant comprises an adjuvant. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Certain adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes;

biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Within certain embodiments of the invention, the adjuvant composition
5 is preferably one that induces an immune response predominantly of the Th1 type. High levels of Th1-type cytokines (e.g., IFN- γ , TNF α , IL-2 and IL-12) tend to favor the induction of cell mediated immune responses to an administered antigen. In contrast, high levels of Th2-type cytokines (e.g., IL-4, IL-5, IL-6 and IL-10) tend to favor the induction of humoral immune responses. Following application of a vaccine as
10 provided herein, a patient will support an immune response that includes Th1- and Th2-type responses. Within a preferred embodiment, in which a response is predominantly Th1-type, the level of Th1-type cytokines will increase to a greater extent than the level of Th2-type cytokines. The levels of these cytokines may be readily assessed using standard assays. For a review of the families of cytokines, see Mosmann and Coffman,
15 *Ann. Rev. Immunol.* 7:145-173, 1989.

Certain preferred adjuvants for eliciting a predominantly Th1-type response include, for example, a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A, together with an aluminum salt. MPL[®] adjuvants are available from Corixa Corporation (Seattle, WA; see, for example, US
20 Patent Nos. 4,436,727; 4,877,611; 4,866,034 and 4,912,094). CpG-containing oligonucleotides (in which the CpG dinucleotide is unmethylated) also induce a predominantly Th1 response. Such oligonucleotides are well known and are described, for example, in WO 96/02555, WO 99/33488 and U.S. Patent Nos. 6,008,200 and 5,856,462. Immunostimulatory DNA sequences are also described, for example, by
25 Sato et al., *Science* 273:352, 1996. Another preferred adjuvant comprises a saponin, such as Quil A, or derivatives thereof, including QS21 and QS7 (Aquila Biopharmaceuticals Inc., Framingham, MA); Escin; Digitonin; or *Gypsophila* or *Chenopodium quinoa* saponins. Other preferred formulations include more than one saponin in the adjuvant combinations of the present invention, for example

combinations of at least two of the following group comprising QS21, QS7, Quil A, β -escin, or digitonin.

Alternatively the saponin formulations may be combined with vaccine vehicles composed of chitosan or other polycationic polymers, polylactide and
5 polylactide-co-glycolide particles, poly-N-acetyl glucosamine-based polymer matrix, particles composed of polysaccharides or chemically modified polysaccharides, liposomes and lipid-based particles, particles composed of glycerol monoesters, etc. The saponins may also be formulated in the presence of cholesterol to form particulate structures such as liposomes or ISCOMs. Furthermore, the saponins may be formulated
10 together with a polyoxyethylene ether or ester, in either a non-particulate solution or suspension, or in a particulate structure such as a paucilamellar liposome or ISCOM. The saponins may also be formulated with excipients such as Carbopol^R to increase viscosity, or may be formulated in a dry powder form with a powder excipient such as lactose.

15 In one preferred embodiment, the adjuvant system includes the combination of a monophosphoryl lipid A and a saponin derivative, such as the combination of QS21 and 3D-MPL[®] adjuvant, as described in WO 94/00153, or a less reactogenic composition where the QS21 is quenched with cholesterol, as described in WO 96/33739. Other preferred formulations comprise an oil-in-water emulsion and
20 tocopherol. Another particularly preferred adjuvant formulation employing QS21, 3D-MPL[®] adjuvant and tocopherol in an oil-in-water emulsion is described in WO 95/17210.

Another enhanced adjuvant system involves the combination of a CpG-containing oligonucleotide and a saponin derivative particularly the combination of
25 CpG and QS21 is disclosed in WO 00/09159. Preferably the formulation additionally comprises an oil in water emulsion and tocopherol.

Additional illustrative adjuvants for use in the pharmaceutical compositions of the invention include Montanide ISA 720 (Seppic, France), SAF (Chiron, California, United States), ISCOMS (CSL), MF-59 (Chiron), the SBAS series
30 of adjuvants (e.g., SBAS-2 or SBAS-4, available from SmithKline Beecham, Rixensart,

Belgium), Detox (Enhanzyn®) (Corixa, Hamilton, MT), RC-529 (Corixa, Hamilton, MT) and other aminoalkyl glucosaminide 4-phosphates (AGPs), such as those described in pending U.S. Patent Application Serial Nos. 08/853,826 and 09/074,720, the disclosures of which are incorporated herein by reference in their entireties, and
5 polyoxyethylene ether adjuvants such as those described in WO 99/52549A1.

Other preferred adjuvants include adjuvant molecules of the general formula



wherein, n is 1-50, A is a bond or $-\text{C}(\text{O})-$, R is C_{1-50} alkyl or Phenyl C_{1-50} alkyl.

10 One embodiment of the present invention consists of a vaccine formulation comprising a polyoxyethylene ether of general formula (I); wherein n is between 1 and 50, preferably 4-24, most preferably 9; the R component is C_{1-50} , preferably $\text{C}_4\text{-C}_{20}$ alkyl and most preferably C_{12} alkyl, and A is a bond. The concentration of the polyoxyethylene ethers should be in the range 0.1-20%, preferably
15 from 0.1-10%, and most preferably in the range 0.1-1%. Preferred polyoxyethylene ethers are selected from the following group: polyoxyethylene-9-lauryl ether, polyoxyethylene-9-stearyl ether, polyoxyethylene-8-stearyl ether, polyoxyethylene-4-lauryl ether, polyoxyethylene-35-lauryl ether, and polyoxyethylene-23-lauryl ether. Polyoxyethylene ethers such as polyoxyethylene lauryl ether are described in the Merck
20 index (12th edition: entry 7717). These adjuvant molecules are described in WO 99/52549.

The polyoxyethylene ether according to the general formula (I) above may, if desired, be combined with another adjuvant. For example, a preferred adjuvant combination is preferably with CpG as described in the pending UK patent application
25 GB 9820956.2.

According to another embodiment of this invention, an immunogenic composition described herein is delivered to a host via antigen presenting cells (APCs), such as dendritic cells, macrophages, B cells, monocytes and other cells that may be engineered to be efficient APCs. Such cells may, but need not, be genetically modified
30 to increase the capacity for presenting the antigen, to improve activation and/or

maintenance of the T cell response, to have anti-tumor effects *per se* and/or to be immunologically compatible with the receiver (*i.e.*, matched HLA haplotype). APCs may generally be isolated from any of a variety of biological fluids and organs, including tumor and peritumoral tissues, and may be autologous, allogeneic, syngeneic or xenogeneic cells.

Certain preferred embodiments of the present invention use dendritic cells or progenitors thereof as antigen-presenting cells. Dendritic cells are highly potent APCs (Banchereau and Steinman, *Nature* 392:245-251, 1998) and have been shown to be effective as a physiological adjuvant for eliciting prophylactic or therapeutic antitumor immunity (*see* Timmerman and Levy, *Ann. Rev. Med.* 50:507-529, 1999). In general, dendritic cells may be identified based on their typical shape (stellate *in situ*, with marked cytoplasmic processes (dendrites) visible *in vitro*), their ability to take up, process and present antigens with high efficiency and their ability to activate naïve T cell responses. Dendritic cells may, of course, be engineered to express specific cell-surface receptors or ligands that are not commonly found on dendritic cells *in vivo* or *ex vivo*, and such modified dendritic cells are contemplated by the present invention. As an alternative to dendritic cells, secreted vesicles antigen-loaded dendritic cells (called exosomes) may be used within a vaccine (*see* Zitvogel et al., *Nature Med.* 4:594-600, 1998).

Dendritic cells and progenitors may be obtained from peripheral blood, bone marrow, tumor-infiltrating cells, peritumoral tissues-infiltrating cells, lymph nodes, spleen, skin, umbilical cord blood or any other suitable tissue or fluid. For example, dendritic cells may be differentiated *ex vivo* by adding a combination of cytokines such as GM-CSF, IL-4, IL-13 and/or TNF α to cultures of monocytes harvested from peripheral blood. Alternatively, CD34 positive cells harvested from peripheral blood, umbilical cord blood or bone marrow may be differentiated into dendritic cells by adding to the culture medium combinations of GM-CSF, IL-3, TNF α , CD40 ligand, LPS, flt3 ligand and/or other compound(s) that induce differentiation, maturation and proliferation of dendritic cells.

Dendritic cells are conveniently categorized as "immature" and "mature" cells, which allows a simple way to discriminate between two well characterized phenotypes. However, this nomenclature should not be construed to exclude all possible intermediate stages of differentiation. Immature dendritic cells are
5 characterized as APC with a high capacity for antigen uptake and processing, which correlates with the high expression of Fcγ receptor and mannose receptor. The mature phenotype is typically characterized by a lower expression of these markers, but a high expression of cell surface molecules responsible for T cell activation such as class I and class II MHC, adhesion molecules (*e.g.*, CD54 and CD11) and costimulatory molecules
10 (*e.g.*, CD40, CD80, CD86 and 4-1BB).

APCs may generally be transfected with a polynucleotide of the invention (or portion or other variant thereof) such that the encoded polypeptide, or an immunogenic portion thereof, is expressed on the cell surface. Such transfection may take place *ex vivo*, and a pharmaceutical composition comprising such transfected cells
15 may then be used for therapeutic purposes, as described herein. Alternatively, a gene delivery vehicle that targets a dendritic or other antigen presenting cell may be administered to a patient, resulting in transfection that occurs *in vivo*. *In vivo* and *ex vivo* transfection of dendritic cells, for example, may generally be performed using any methods known in the art, such as those described in WO 97/24447, or the gene gun
20 approach described by Mahvi et al., *Immunology and cell Biology* 75:456-460, 1997. Antigen loading of dendritic cells may be achieved by incubating dendritic cells or progenitor cells with the tumor polypeptide, DNA (naked or within a plasmid vector) or RNA; or with antigen-expressing recombinant bacterium or viruses (*e.g.*, vaccinia, fowlpox, adenovirus or lentivirus vectors). Prior to loading, the polypeptide may be
25 covalently conjugated to an immunological partner that provides T cell help (*e.g.*, a carrier molecule). Alternatively, a dendritic cell may be pulsed with a non-conjugated immunological partner, separately or in the presence of the polypeptide.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier
30 will typically vary depending on the mode of administration. Compositions of the

present invention may be formulated for any appropriate manner of administration, including for example, topical, oral, nasal, mucosal, intravenous, intracranial, intraperitoneal, subcutaneous and intramuscular administration.

Carriers for use within such pharmaceutical compositions are
5 biocompatible, and may also be biodegradable. In certain embodiments, the formulation preferably provides a relatively constant level of active component release. In other embodiments, however, a more rapid rate of release immediately upon administration may be desired. The formulation of such compositions is well within the level of ordinary skill in the art using known techniques. Illustrative carriers useful in
10 this regard include microparticles of poly(lactide-co-glycolide), polyacrylate, latex, starch, cellulose, dextran and the like. Other illustrative delayed-release carriers include supramolecular biovectors, which comprise a non-liquid hydrophilic core (e.g., a cross-linked polysaccharide or oligosaccharide) and, optionally, an external layer comprising an amphiphilic compound, such as a phospholipid (*see e.g.*, U.S. Patent No.
15 5,151,254 and PCT applications WO 94/20078, WO/94/23701 and WO 96/06638). The amount of active compound contained within a sustained release formulation depends upon the site of implantation, the rate and expected duration of release and the nature of the condition to be treated or prevented.

In another illustrative embodiment, biodegradable microspheres (e.g.,
20 polylactate polyglycolate) are employed as carriers for the compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268; 5,075,109; 5,928,647; 5,811,128; 5,820,883; 5,853,763; 5,814,344, 5,407,609 and 5,942,252. Modified hepatitis B core protein carrier systems, such as described in WO/99 40934, and references cited therein, will also be useful for
25 many applications. Another illustrative carrier/delivery system employs a carrier comprising particulate-protein complexes, such as those described in U.S. Patent No. 5,928,647, which are capable of inducing a class I-restricted cytotoxic T lymphocyte responses in a host.

The pharmaceutical compositions of the invention will often further
30 comprise one or more buffers (e.g., neutral buffered saline or phosphate buffered

saline), carbohydrates (e.g., glucose, mannose, sucrose or dextrans), mannitol, proteins, polypeptides or amino acids such as glycine, antioxidants, bacteriostats, chelating agents such as EDTA or glutathione, adjuvants (e.g., aluminum hydroxide), solutes that render the formulation isotonic, hypotonic or weakly hypertonic with the blood of a recipient, suspending agents, thickening agents and/or preservatives. Alternatively, compositions of the present invention may be formulated as a lyophilizate.

The pharmaceutical compositions described herein may be presented in unit-dose or multi-dose containers, such as sealed ampoules or vials. Such containers are typically sealed in such a way to preserve the sterility and stability of the formulation until use. In general, formulations may be stored as suspensions, solutions or emulsions in oily or aqueous vehicles. Alternatively, a pharmaceutical composition may be stored in a freeze-dried condition requiring only the addition of a sterile liquid carrier immediately prior to use.

The development of suitable dosing and treatment regimens for using the particular compositions described herein in a variety of treatment regimens, including e.g., oral, parenteral, intravenous, intranasal, and intramuscular administration and formulation, is well known in the art, some of which are briefly discussed below for general purposes of illustration.

In certain applications, the pharmaceutical compositions disclosed herein may be delivered *via* oral administration to an animal. As such, these compositions may be formulated with an inert diluent or with an assimilable edible carrier, or they may be enclosed in hard- or soft-shell gelatin capsule, or they may be compressed into tablets, or they may be incorporated directly with the food of the diet.

The active compounds may even be incorporated with excipients and used in the form of ingestible tablets, buccal tables, troches, capsules, elixirs, suspensions, syrups, wafers, and the like (see, for example, Mathiowitz *et al.*, Nature 1997 Mar 27;386(6623):410-4; Hwang *et al.*, Crit Rev Ther Drug Carrier Syst 1998;15(3):243-84; U. S. Patent 5,641,515; U. S. Patent 5,580,579 and U. S. Patent 5,792,451). Tablets, troches, pills, capsules and the like may also contain any of a variety of additional components, for example, a binder, such as gum tragacanth, acacia,

cornstarch, or gelatin; excipients, such as dicalcium phosphate; a disintegrating agent, such as corn starch, potato starch, alginic acid and the like; a lubricant, such as magnesium stearate; and a sweetening agent, such as sucrose, lactose or saccharin may be added or a flavoring agent, such as peppermint, oil of wintergreen, or cherry
5 flavoring. When the dosage unit form is a capsule, it may contain, in addition to materials of the above type, a liquid carrier. Various other materials may be present as coatings or to otherwise modify the physical form of the dosage unit. For instance, tablets, pills, or capsules may be coated with shellac, sugar, or both. Of course, any material used in preparing any dosage unit form should be pharmaceutically pure and
10 substantially non-toxic in the amounts employed. In addition, the active compounds may be incorporated into sustained-release preparation and formulations.

Typically, these formulations will contain at least about 0.1% of the active compound or more, although the percentage of the active ingredient(s) may, of course, be varied and may conveniently be between about 1 or 2% and about 60% or
15 70% or more of the weight or volume of the total formulation. Naturally, the amount of active compound(s) in each therapeutically useful composition may be prepared in such a way that a suitable dosage will be obtained in any given unit dose of the compound. Factors such as solubility, bioavailability, biological half-life, route of administration, product shelf life, as well as other pharmacological considerations will be contemplated
20 by one skilled in the art of preparing such pharmaceutical formulations, and as such, a variety of dosages and treatment regimens may be desirable.

For oral administration the compositions of the present invention may alternatively be incorporated with one or more excipients in the form of a mouthwash, dentifrice, buccal tablet, oral spray, or sublingual orally-administered formulation.
25 Alternatively, the active ingredient may be incorporated into an oral solution such as one containing sodium borate, glycerin and potassium bicarbonate, or dispersed in a dentifrice, or added in a therapeutically-effective amount to a composition that may include water, binders, abrasives, flavoring agents, foaming agents, and humectants. Alternatively the compositions may be fashioned into a tablet or solution form that may
30 be placed under the tongue or otherwise dissolved in the mouth.

In certain circumstances it will be desirable to deliver the pharmaceutical compositions disclosed herein parenterally, intravenously, intramuscularly, or even intraperitoneally. Such approaches are well known to the skilled artisan, some of which are further described, for example, in U. S. Patent 5,543,158; U. S. Patent 5,641,515 and
5 U. S. Patent 5,399,363. In certain embodiments, solutions of the active compounds as free base or pharmacologically acceptable salts may be prepared in water suitably mixed with a surfactant, such as hydroxypropylcellulose. Dispersions may also be prepared in glycerol, liquid polyethylene glycols, and mixtures thereof and in oils. Under ordinary conditions of storage and use, these preparations generally will contain
10 a preservative to prevent the growth of microorganisms.

Illustrative pharmaceutical forms suitable for injectable use include sterile aqueous solutions or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersions (for example, see U. S. Patent 5,466,468). In all cases the form must be sterile and must be fluid to the extent that
15 easy syringability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms, such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (e.g., glycerol, propylene glycol, and liquid polyethylene glycol, and the like), suitable mixtures thereof, and/or vegetable
20 oils. Proper fluidity may be maintained, for example, by the use of a coating, such as lecithin, by the maintenance of the required particle size in the case of dispersion and/or by the use of surfactants. The prevention of the action of microorganisms can be facilitated by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, sorbic acid, thimerosal, and the like. In many cases, it will be
25 preferable to include isotonic agents, for example, sugars or sodium chloride. Prolonged absorption of the injectable compositions can be brought about by the use in the compositions of agents delaying absorption, for example, aluminum monostearate and gelatin.

In one embodiment, for parenteral administration in an aqueous solution,
30 the solution should be suitably buffered if necessary and the liquid diluent first rendered

isotonic with sufficient saline or glucose. These particular aqueous solutions are especially suitable for intravenous, intramuscular, subcutaneous and intraperitoneal administration. In this connection, a sterile aqueous medium that can be employed will be known to those of skill in the art in light of the present disclosure. For example, one dosage may be dissolved in 1 ml of isotonic NaCl solution and either added to 1000 ml of hypodermoclysis fluid or injected at the proposed site of infusion, (see for example, "Remington's Pharmaceutical Sciences" 15th Edition, pages 1035-1038 and 1570-1580). Some variation in dosage will necessarily occur depending on the condition of the subject being treated. Moreover, for human administration, preparations will of course preferably meet sterility, pyrogenicity, and the general safety and purity standards as required by FDA Office of Biologics standards.

In another embodiment of the invention, the compositions disclosed herein may be formulated in a neutral or salt form. Illustrative pharmaceutically-acceptable salts include the acid addition salts (formed with the free amino groups of the protein) and which are formed with inorganic acids such as, for example, hydrochloric or phosphoric acids, or such organic acids as acetic, oxalic, tartaric, mandelic, and the like. Salts formed with the free carboxyl groups can also be derived from inorganic bases such as, for example, sodium, potassium, ammonium, calcium, or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, histidine, procaine and the like. Upon formulation, solutions will be administered in a manner compatible with the dosage formulation and in such amount as is therapeutically effective.

The carriers can further comprise any and all solvents, dispersion media, vehicles, coatings, diluents, antibacterial and antifungal agents, isotonic and absorption delaying agents, buffers, carrier solutions, suspensions, colloids, and the like. The use of such media and agents for pharmaceutical active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active ingredient, its use in the therapeutic compositions is contemplated. Supplementary active ingredients can also be incorporated into the compositions. The phrase

"pharmaceutically-acceptable" refers to molecular entities and compositions that do not produce an allergic or similar untoward reaction when administered to a human.

In certain embodiments, the pharmaceutical compositions may be delivered by intranasal sprays, inhalation, and/or other aerosol delivery vehicles.

5 Methods for delivering genes, nucleic acids, and peptide compositions directly to the lungs *via* nasal aerosol sprays has been described, *e.g.*, in U. S. Patent 5,756,353 and U. S. Patent 5,804,212. Likewise, the delivery of drugs using intranasal microparticle resins (Takenaga *et al.*, J Controlled Release 1998 Mar 2;52(1-2):81-7) and lysophosphatidyl-glycerol compounds (U. S. Patent 5,725,871) are also well-known in

10 the pharmaceutical arts. Likewise, illustrative transmucosal drug delivery in the form of a polytetrafluoroethylene support matrix is described in U. S. Patent 5,780,045.

In certain embodiments, liposomes, nanocapsules, microparticles, lipid particles, vesicles, and the like, are used for the introduction of the compositions of the present invention into suitable host cells/organisms. In particular, the compositions of

15 the present invention may be formulated for delivery either encapsulated in a lipid particle, a liposome, a vesicle, a nanosphere, or a nanoparticle or the like. Alternatively, compositions of the present invention can be bound, either covalently or non-covalently, to the surface of such carrier vehicles.

The formation and use of liposome and liposome-like preparations as

20 potential drug carriers is generally known to those of skill in the art (see for example, Lasic, Trends Biotechnol 1998 Jul;16(7):307-21; Takakura, Nippon Rinsho 1998 Mar;56(3):691-5; Chandran *et al.*, Indian J Exp Biol. 1997 Aug;35(8):801-9; Margalit, Crit Rev Ther Drug Carrier Syst. 1995;12(2-3):233-61; U.S. Patent 5,567,434; U.S. Patent 5,552,157; U.S. Patent 5,565,213; U.S. Patent 5,738,868 and U.S. Patent

25 5,795,587, each specifically incorporated herein by reference in its entirety).

Liposomes have been used successfully with a number of cell types that are normally difficult to transfect by other procedures, including T cell suspensions, primary hepatocyte cultures and PC 12 cells (Renneisen *et al.*, J Biol Chem. 1990 Sep 25;265(27):16337-42; Muller *et al.*, DNA Cell Biol. 1990 Apr;9(3):221-9). In addition,

30 liposomes are free of the DNA length constraints that are typical of viral-based delivery

systems. Liposomes have been used effectively to introduce genes, various drugs, radiotherapeutic agents, enzymes, viruses, transcription factors, allosteric effectors and the like, into a variety of cultured cell lines and animals. Furthermore, the use of liposomes does not appear to be associated with autoimmune responses or unacceptable toxicity after systemic delivery.

In certain embodiments, liposomes are formed from phospholipids that are dispersed in an aqueous medium and spontaneously form multilamellar concentric bilayer vesicles (also termed multilamellar vesicles (MLVs)).

Alternatively, in other embodiments, the invention provides for pharmaceutically-acceptable nanocapsule formulations of the compositions of the present invention. Nanocapsules can generally entrap compounds in a stable and reproducible way (see, for example, Quintanar-Guerrero *et al.*, Drug Dev Ind Pharm. 1998 Dec;24(12):1113-28). To avoid side effects due to intracellular polymeric overloading, such ultrafine particles (sized around 0.1 μm) may be designed using polymers able to be degraded *in vivo*. Such particles can be made as described, for example, by Couvreur *et al.*, Crit Rev Ther Drug Carrier Syst. 1988;5(1):1-20; zur Muhlen *et al.*, Eur J Pharm Biopharm. 1998 Mar;45(2):149-55; Zambaux *et al.* J Controlled Release. 1998 Jan 2;50(1-3):31-40; and U. S. Patent 5,145,684.

Cancer Therapeutic Methods

In further aspects of the present invention, the pharmaceutical compositions described herein may be used for the treatment of cancer, particularly for the immunotherapy of lung cancer. Within such methods, the pharmaceutical compositions described herein are administered to a patient, typically a warm-blooded animal, preferably a human. A patient may or may not be afflicted with cancer. Accordingly, the above pharmaceutical compositions may be used to prevent the development of a cancer or to treat a patient afflicted with a cancer. Pharmaceutical compositions and vaccines may be administered either prior to or following surgical removal of primary tumors and/or treatment such as administration of radiotherapy or conventional chemotherapeutic drugs. As discussed above, administration of the

pharmaceutical compositions may be by any suitable method, including administration by intravenous, intraperitoneal, intramuscular, subcutaneous, intranasal, intradermal, anal, vaginal, topical and oral routes.

Within certain embodiments, immunotherapy may be active immunotherapy, in which treatment relies on the *in vivo* stimulation of the endogenous host immune system to react against tumors with the administration of immune response-modifying agents (such as polypeptides and polynucleotides as provided herein).

Within other embodiments, immunotherapy may be passive immunotherapy, in which treatment involves the delivery of agents with established tumor-immune reactivity (such as effector cells or antibodies), that can directly or indirectly mediate antitumor effects and does not necessarily depend on an intact host immune system. Examples of effector cells include T cells as discussed above, T lymphocytes (such as CD8⁺ cytotoxic T lymphocytes and CD4⁺ T-helper tumor-infiltrating lymphocytes), killer cells (such as Natural Killer cells and lymphokine-activated killer cells), B cells and antigen-presenting cells (such as dendritic cells and macrophages) expressing a polypeptide provided herein. T cell receptors and antibody receptors specific for the polypeptides recited herein may be cloned, expressed and transferred into other vectors or effector cells for adoptive immunotherapy. The polypeptides provided herein may also be used to generate antibodies or anti-idiotypic antibodies (as described above and in U.S. Patent No. 4,918,164) for passive immunotherapy.

Effector cells may generally be obtained in sufficient quantities for adoptive immunotherapy by growth *in vitro*, as described herein. Culture conditions for expanding single antigen-specific effector cells to several billion in number with retention of antigen recognition *in vivo* are well known in the art. Such *in vitro* culture conditions typically use intermittent stimulation with antigen, often in the presence of cytokines (such as IL-2) and non-dividing feeder cells. As noted above, immunoreactive polypeptides as provided herein may be used to rapidly expand antigen-specific T cell cultures in order to generate a sufficient number of cells for

immunotherapy. In particular, antigen-presenting cells, such as dendritic, macrophage, monocyte, fibroblast and/or B cells, may be pulsed with immunoreactive polypeptides or transfected with one or more polynucleotides using standard techniques well known in the art. For example, antigen-presenting cells can be transfected with a
5 polynucleotide having a promoter appropriate for increasing expression in a recombinant virus or other expression system. Cultured effector cells for use in therapy must be able to grow and distribute widely, and to survive long term *in vivo*. Studies have shown that cultured effector cells can be induced to grow *in vivo* and to survive long term in substantial numbers by repeated stimulation with antigen supplemented
10 with IL-2 (*see, for example, Cheever et al., Immunological Reviews 157:177, 1997*).

Alternatively, a vector expressing a polypeptide recited herein may be introduced into antigen presenting cells taken from a patient and clonally propagated *ex vivo* for transplant back into the same patient. Transfected cells may be reintroduced into the patient using any means known in the art, preferably in sterile form by
15 intravenous, intracavitary, intraperitoneal or intratumor administration.

Routes and frequency of administration of the therapeutic compositions described herein, as well as dosage, will vary from individual to individual, and may be readily established using standard techniques. In general, the pharmaceutical compositions and vaccines may be administered by injection (*e.g.*, intracutaneous,
20 intramuscular, intravenous or subcutaneous), intranasally (*e.g.*, by aspiration) or orally. Preferably, between 1 and 10 doses may be administered over a 52 week period. Preferably, 6 doses are administered, at intervals of 1 month, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of a compound that, when
25 administered as described above, is capable of promoting an anti-tumor immune response, and is at least 10-50% above the basal (*i.e.*, untreated) level. Such response can be monitored by measuring the anti-tumor antibodies in a patient or by vaccine-dependent generation of cytolytic effector cells capable of killing the patient's tumor cells *in vitro*. Such vaccines should also be capable of causing an immune response that
30 leads to an improved clinical outcome (*e.g.*, more frequent remissions, complete or

partial or longer disease-free survival) in vaccinated patients as compared to non-vaccinated patients. In general, for pharmaceutical compositions and vaccines comprising one or more polypeptides, the amount of each polypeptide present in a dose ranges from about 25 µg to 5 mg per kg of host. Suitable dose sizes will vary with the
5 size of the patient, but will typically range from about 0.1 mL to about 5 mL.

In general, an appropriate dosage and treatment regimen provides the active compound(s) in an amount sufficient to provide therapeutic and/or prophylactic benefit. Such a response can be monitored by establishing an improved clinical outcome (e.g., more frequent remissions, complete or partial, or longer disease-free
10 survival) in treated patients as compared to non-treated patients. Increases in preexisting immune responses to a tumor protein generally correlate with an improved clinical outcome. Such immune responses may generally be evaluated using standard proliferation, cytotoxicity or cytokine assays, which may be performed using samples obtained from a patient before and after treatment.

15 Cancer Detection and Diagnostic Compositions, Methods and Kits

In general, a cancer may be detected in a patient based on the presence of one or more lung tumor proteins and/or polynucleotides encoding such proteins in a biological sample (for example, blood, sera, sputum urine and/or tumor biopsies) obtained from the patient. In other words, such proteins may be used as markers to
20 indicate the presence or absence of a cancer such as lung cancer. In addition, such proteins may be useful for the detection of other cancers. The binding agents provided herein generally permit detection of the level of antigen that binds to the agent in the biological sample. Polynucleotide primers and probes may be used to detect the level of mRNA encoding a tumor protein, which is also indicative of the presence or absence
25 of a cancer. In general, a lung tumor sequence should be present at a level that is at least three fold higher in tumor tissue than in normal tissue

There are a variety of assay formats known to those of ordinary skill in the art for using a binding agent to detect polypeptide markers in a sample. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory,

1988. In general, the presence or absence of a cancer in a patient may be determined by (a) contacting a biological sample obtained from a patient with a binding agent; (b) detecting in the sample a level of polypeptide that binds to the binding agent; and (c) comparing the level of polypeptide with a predetermined cut-off value.

5 In a preferred embodiment, the assay involves the use of binding agent immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a detection reagent that contains a reporter group and specifically binds to the binding agent/polypeptide complex. Such detection reagents may comprise, for example, a
10 binding agent that specifically binds to the polypeptide or an antibody or other agent that specifically binds to the binding agent, such as an anti-immunoglobulin, protein G, protein A or a lectin. Alternatively, a competitive assay may be utilized, in which a polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding agent after incubation of the binding agent with the sample. The extent to
15 which components of the sample inhibit the binding of the labeled polypeptide to the binding agent is indicative of the reactivity of the sample with the immobilized binding agent. Suitable polypeptides for use within such assays include full length lung tumor proteins and polypeptide portions thereof to which the binding agent binds, as described above.

20 The solid support may be any material known to those of ordinary skill in the art to which the tumor protein may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a
25 magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption,
30 and covalent attachment (which may be a direct linkage between the agent and

functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact
5 time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10 µg, and preferably about 100 ng to about 1 µg, is sufficient to immobilize an adequate amount of binding agent.

10 Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an
15 aldehyde group on the support with an amine and an active hydrogen on the binding partner (*see, e.g.*, Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized
20 on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a detection reagent (preferably a second antibody capable of binding to a different site on the polypeptide) containing a reporter group is added. The amount of
25 detection reagent that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such
30 as bovine serum albumin or Tween 20™ (Sigma Chemical Co., St. Louis, MO). The

immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is a period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with lung cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20™. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include those groups recited above.

The detection reagent is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound detection reagent is then removed and bound detection reagent is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of a cancer, such as lung cancer, the signal detected from the reporter group that remains bound to the solid support is

generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value for the detection of a cancer is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without the cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for the cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (i.e., sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (i.e., the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for a cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the binding agent is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized binding agent as the sample passes through the membrane. A second, labeled binding agent then binds to the binding agent-polypeptide complex as a solution containing the second binding agent flows through the membrane. The detection of bound second binding agent may then be performed as described above. In the strip test format, one end of the membrane to which binding agent is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second binding agent and to the area of immobilized binding agent. Concentration of second binding agent at the area of immobilized antibody indicates the presence of a cancer. Typically, the concentration of second binding agent at that site

generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of binding agent immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferred binding agents for use in such assays are antibodies and antigen-binding fragments thereof. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 μ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the tumor proteins or binding agents of the present invention. The above descriptions are intended to be exemplary only. For example, it will be apparent to those of ordinary skill in the art that the above protocols may be readily modified to use tumor polypeptides to detect antibodies that bind to such polypeptides in a biological sample. The detection of such tumor protein specific antibodies may correlate with the presence of a cancer.

A cancer may also, or alternatively, be detected based on the presence of T cells that specifically react with a tumor protein in a biological sample. Within certain methods, a biological sample comprising CD4⁺ and/or CD8⁺ T cells isolated from a patient is incubated with a tumor polypeptide, a polynucleotide encoding such a polypeptide and/or an APC that expresses at least an immunogenic portion of such a polypeptide, and the presence or absence of specific activation of the T cells is detected. Suitable biological samples include, but are not limited to, isolated T cells. For example, T cells may be isolated from a patient by routine techniques (such as by Ficoll/Hypaque density gradient centrifugation of peripheral blood lymphocytes). T cells may be incubated *in vitro* for 2-9 days (typically 4 days) at 37°C with polypeptide (e.g., 5 - 25 μ g/ml). It may be desirable to incubate another aliquot of a T cell sample in the absence of tumor polypeptide to serve as a control. For CD4⁺ T cells, activation is preferably detected by evaluating proliferation of the T cells. For CD8⁺ T cells,

activation is preferably detected by evaluating cytolytic activity. A level of proliferation that is at least two fold greater and/or a level of cytolytic activity that is at least 20% greater than in disease-free patients indicates the presence of a cancer in the patient.

5 As noted above, a cancer may also, or alternatively, be detected based on the level of mRNA encoding a tumor protein in a biological sample. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify a portion of a tumor cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for (*i.e.*,
10 hybridizes to) a polynucleotide encoding the tumor protein. The amplified cDNA is then separated and detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes that specifically hybridize to a polynucleotide encoding a tumor protein may be used in a hybridization assay to detect the presence of polynucleotide encoding the tumor protein in a biological sample.

15 To permit hybridization under assay conditions, oligonucleotide primers and probes should comprise an oligonucleotide sequence that has at least about 60%, preferably at least about 75% and more preferably at least about 90%, identity to a portion of a polynucleotide encoding a tumor protein of the invention that is at least 10 nucleotides, and preferably at least 20 nucleotides, in length. Preferably,
20 oligonucleotide primers and/or probes hybridize to a polynucleotide encoding a polypeptide described herein under moderately stringent conditions, as defined above. Oligonucleotide primers and/or probes which may be usefully employed in the diagnostic methods described herein preferably are at least 10-40 nucleotides in length. In a preferred embodiment, the oligonucleotide primers comprise at least 10 contiguous
25 nucleotides, more preferably at least 15 contiguous nucleotides, of a DNA molecule having a sequence as disclosed herein. Techniques for both PCR based assays and hybridization assays are well known in the art (*see*, for example, Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989).

One preferred assay employs RT-PCR, in which PCR is applied in conjunction with reverse transcription. Typically, RNA is extracted from a biological sample, such as biopsy tissue, and is reverse transcribed to produce cDNA molecules. PCR amplification using at least one specific primer generates a cDNA molecule, which
5 may be separated and visualized using, for example, gel electrophoresis. Amplification may be performed on biological samples taken from a test patient and from an individual who is not afflicted with a cancer. The amplification reaction may be performed on several dilutions of cDNA spanning two orders of magnitude. A two-fold or greater increase in expression in several dilutions of the test patient sample as
10 compared to the same dilutions of the non-cancerous sample is typically considered positive.

In another embodiment, the compositions described herein may be used as markers for the progression of cancer. In this embodiment, assays as described above for the diagnosis of a cancer may be performed over time, and the change in the
15 level of reactive polypeptide(s) or polynucleotide(s) evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, a cancer is progressing in those patients in whom the level of polypeptide or polynucleotide detected increases over time. In contrast, the cancer is not progressing when the level of reactive polypeptide or polynucleotide either
20 remains constant or decreases with time.

Certain *in vivo* diagnostic assays may be performed directly on a tumor. One such assay involves contacting tumor cells with a binding agent. The bound binding agent may then be detected directly or indirectly via a reporter group. Such binding agents may also be used in histological applications. Alternatively,
25 polynucleotide probes may be used within such applications.

As noted above, to improve sensitivity, multiple tumor protein markers may be assayed within a given sample. It will be apparent that binding agents specific for different proteins provided herein may be combined within a single assay. Further, multiple primers or probes may be used concurrently. The selection of tumor protein
30 markers may be based on routine experiments to determine combinations that results in

optimal sensitivity. In addition, or alternatively, assays for tumor proteins provided herein may be combined with assays for other known tumor antigens.

The present invention further provides kits for use within any of the above diagnostic methods. Such kits typically comprise two or more components
5 necessary for performing a diagnostic assay. Components may be compounds, reagents, containers and/or equipment. For example, one container within a kit may contain a monoclonal antibody or fragment thereof that specifically binds to a tumor protein. Such antibodies or fragments may be provided attached to a support material, as described above. One or more additional containers may enclose elements, such as
10 reagents or buffers, to be used in the assay. Such kits may also, or alternatively, contain a detection reagent as described above that contains a reporter group suitable for direct or indirect detection of antibody binding.

Alternatively, a kit may be designed to detect the level of mRNA encoding a tumor protein in a biological sample. Such kits generally comprise at least
15 one oligonucleotide probe or primer, as described above, that hybridizes to a polynucleotide encoding a tumor protein. Such an oligonucleotide may be used, for example, within a PCR or hybridization assay. Additional components that may be present within such kits include a second oligonucleotide and/or a diagnostic reagent or container to facilitate the detection of a polynucleotide encoding a tumor protein.

20 The following Examples are offered by way of illustration and not by way of limitation.

EXAMPLE 1

PREPARATION OF LUNG TUMOR-SPECIFIC CDNA SEQUENCES USING

DIFFERENTIAL DISPLAY RT-PCR

25 This example illustrates the preparation of cDNA molecules encoding lung tumor-specific polypeptides using a differential display screen.

Tissue samples were prepared from lung tumor and normal tissue of a patient with lung cancer that was confirmed by pathology after removal of samples from the patient. Normal RNA and tumor RNA was extracted from the samples and
30 mRNA was isolated and converted into cDNA using a (dT)₁₂AG (SEQ ID NO: 47)

anchored 3' primer. Differential display PCR was then executed using a randomly chosen primer (SEQ ID NO: 48). Amplification conditions were standard buffer containing 1.5 mM MgCl₂, 20 pmol of primer, 500 pmol dNTP and 1 unit of Taq DNA polymerase (Perkin-Elmer, Branchburg, NJ). Forty cycles of amplification were performed using 94 °C denaturation for 30 seconds, 42 °C annealing for 1 minute and 72 °C extension for 30 seconds. Bands that were repeatedly observed to be specific to the RNA fingerprint pattern of the tumor were cut out of a silver stained gel, subcloned into the pGEM-T vector (Promega, Madison, WI) and sequenced. The isolated 3' sequences are provided in SEQ ID NO: 1-16.

Comparison of these sequences to those in the public databases using the BLASTN program, revealed no significant homologies to the sequences provided in SEQ ID NO: 1-11. To the best of the inventors' knowledge, none of the isolated DNA sequences have previously been shown to be expressed at a greater level in human lung tumor tissue than in normal lung tissue.

15

EXAMPLE 2

USE OF PATIENT SERA TO IDENTIFY DNA SEQUENCES ENCODING
LUNG TUMOR ANTIGENS

This example illustrates the isolation of cDNA sequences encoding lung tumor antigens by expression screening of lung tumor samples with autologous patient sera.

A human lung tumor directional cDNA expression library was constructed employing the Lambda ZAP Express expression system (Stratagene, La Jolla, CA). Total RNA for the library was taken from a late SCID mouse passaged human squamous epithelial lung carcinoma and poly A+ RNA was isolated using the Message Maker kit (Gibco BRL, Gaithersburg, MD). The resulting library was screened using *E. coli*-absorbed autologous patient serum, as described in Sambrook et al., (*Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989), with the secondary antibody being goat anti-human IgG-A-M (H + L) conjugated with alkaline phosphatase, developed with NBT/BCIP (Gibco

BRL). Positive plaques expressing immunoreactive antigens were purified. Phagemid from the plaques was rescued and the nucleotide sequences of the clones was determined.

Fifteen clones were isolated, referred to hereinafter as LT86-1 – LT86-15.

5 15. The isolated cDNA sequences for LT86-1 – LT86-8 and LT86-10 – LT86-15 are provided in SEQ ID NO: 17-24 and 26-31, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 32-39 and 41-46, respectively. The determined cDNA sequence for LT86-9 is provided in SEQ ID NO: 25, with the corresponding predicted amino acid sequences from the 3' and 5' ends

10 being provided in SEQ ID NO: 40 and 65, respectively. These sequences were compared to those in the gene bank as described above. Clones LT86-3, LT86-6 – LT86-9, LT86-11 – LT86-13 and LT86-15 (SEQ ID NO: 19, 22-25, 27-29 and 31, respectively) were found to show some homology to previously identified expressed sequence tags (ESTs), with clones LT86-6, LT86-8, LT86-11, LT86-12 and LT86-15

15 appearing to be similar or identical to each other. Clone LT86-3 was found to show some homology with a human transcription repressor. Clones LT86-6, 8, 9, 11, 12 and 15 were found to show some homology to a yeast RNA Pol II transcription regulation mediator. Clone LT86-13 was found to show some homology with a *C. elegans* leucine aminopeptidase. Clone LT86-9 appears to contain two inserts, with the 5' sequence

20 showing homology to the previously identified antisense sequence of interferon alpha-induced P27, and the 3' sequence being similar to LT86-6. Clone LT86-14 (SEQ ID NO: 30) was found to show some homology to the trithorax gene and has an "RGD" cell attachment sequence and a beta-Lactamase A site which functions in hydrolysis of penicillin. Clones LT86-1, LT86-2, LT86-4, LT86-5 and LT86-10 (SEQ ID NOS: 17,

25 18, 20, 21 and 26, respectively) were found to show homology to previously identified genes. A subsequently determined extended cDNA sequence for LT86-4 is provided in SEQ ID NO: 66, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 67.

Subsequent studies led to the isolation of five additional clones, referred

30 to as LT86-20, LT86-21, LT86-22, LT86-26 and LT86-27. The determined 5' cDNA

sequences for LT86-20, LT86-22, LT86-26 and LT86-27 are provided in SEQ ID NO: 68 and 70-72, respectively, with the determined 3' cDNA sequences for LT86-21 being provided in SEQ ID NO: 69. The corresponding predicted amino acid sequences for LT86-20, LT86-21, LT86-22, LT86-26 and LT86-27 are provided in SEQ ID NO: 73-77, respectively. LT86-22 and LT86-27 were found to be highly similar to each other. Comparison of these sequences to those in the gene bank as described above, revealed no significant homologies to LT86-22 and LT86-27. LT86-20, LT86-21 and LT86-26 were found to show homology to previously identified genes.

In further studies, a cDNA expression library was prepared using mRNA from a lung small cell carcinoma cell line in the lambda ZAP Express expression vector (Stratagene), and screened as described above, with a pool of two lung small cell carcinoma patient sera. The sera pool was adsorbed with *E. coli* lysate and human PBMC lysate was added to the serum to block antibody to proteins found in normal tissue. Seventy-three clones were isolated. The determined cDNA sequences of these clones are provided in SEQ ID NO: 290-362. The sequences of SEQ ID NO: 289-292, 294, 296-297, 300, 302, 303, 305, 307-315, 317-320, 322-325, 327-332, 334, 335, 338-341, 343-352, 354-358, 360 and 362 were found to show some homology to previously isolated genes. The sequences of SEQ ID NO: 293, 295, 298, 299, 301, 304, 306, 316, 321, 326, 333, 336, 337, 342, 353, 359 and 361 were found to show some homology to previously identified ESTs.

EXAMPLE 3

USE OF MOUSE ANTISERA TO IDENTIFY DNA SEQUENCES ENCODING

LUNG TUMOR ANTIGENS

This example illustrates the isolation of cDNA sequences encoding lung tumor antigens by screening of lung tumor cDNA libraries with mouse anti-tumor sera.

A directional cDNA lung tumor expression library was prepared as described above in Example 2. Sera was obtained from SCID mice containing late passaged human squamous cell and adenocarcinoma tumors. These sera were pooled and injected into normal mice to produce anti-lung tumor serum. Approximately 200,000 PFUs were screened from the unamplified library using this antiserum. Using

a goat anti-mouse IgG-A-M (H+L) alkaline phosphatase second antibody developed with NBT/BCIP (BRL Labs.), approximately 40 positive plaques were identified. Phage was purified and phagemid excised for 9 clones with inserts in a pBK-CMV vector for expression in prokaryotic or eukaryotic cells.

5 The determined cDNA sequences for 7 of the isolated clones (hereinafter referred to as L86S-3, L86S-12, L86S-16, L86S-25, L86S-36, L86S-40 and L86S-46) are provided in SEQ ID NO: 49-55, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 56-62, respectively. The 5' cDNA sequences for the remaining 2 clones (hereinafter referred to as L86S-30 and L86S-41) are
10 provided in SEQ ID NO: 63 and 64. L86S-36 and L86S-46 were subsequently determined to represent the same gene. Comparison of these sequences with those in the public database as described above, revealed no significant homologies to clones L86S-30, L86S-36 and L86S-46 (SEQ ID NO: 63, 53 and 55, respectively). L86S-16 (SEQ ID NO: 51) was found to show some homology to an EST previously identified in
15 fetal lung and germ cell tumor. The remaining clones were found to show at least some degree of homology to previously identified human genes. Subsequently determined extended cDNA sequences for L86S-12, L86S-36 and L86S-46 are provided in SEQ ID NO: 78-80, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 81-83.

20 Subsequent studies led to the determination of 5' cDNA sequences for an additional nine clones, referred to as L86S-6, L86S-11, L86S-14, L86S-29, L86S-34, L86S-39, L86S-47, L86S-49 and L86S-51 (SEQ ID NO: 84-92, respectively). The corresponding predicted amino acid sequences are provided in SEQ ID NO: 93-101, respectively. L86S-30, L86S-39 and L86S-47 were found to be similar to each other.
25 Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to L86S-14. L86S-29 was found to show some homology to a previously identified EST. L86S-6, L86S-11, L86S-34, L86S-39, L86S-47, L86S-49 and L86S-51 were found to show some homology to previously identified genes.

In further studies, a directional cDNA library was constructed using a Stratagene kit with a Lambda Zap Express vector. Total RNA for the library was isolated from two primary squamous lung tumors and poly A+ RNA was isolated using an oligo dT column. Antiserum was developed in normal mice using a pool of sera
5 from three SCID mice implanted with human squamous lung carcinomas. Approximately 700,000 PFUs were screened from the unamplified library with *E. coli* absorbed mouse anti-SCID tumor serum. Positive plaques were identified as described above. Phage was purified and phagemid excised for 180 clones with inserts in a pBK-CMV vector for expression in prokaryotic or eukaryotic cells.

10 The determined cDNA sequences for 23 of the isolated clones are provided in SEQ ID NO: 126-148. Comparison of these sequences with those in the public database as described above revealed no significant homologies to the sequences of SEQ ID NO: 139 and 143-148. The sequences of SEQ ID NO: 126-138 and 140-142 were found to show homology to previously identified human polynucleotide
15 sequences.

EXAMPLE 4

USE OF MOUSE ANTISERA TO SCREEN LUNG TUMOR LIBRARIES

PREPARED FROM SCID MICE

This example illustrates the isolation of cDNA sequences encoding lung
20 tumor antigens by screening of lung tumor cDNA libraries prepared from SCID mice with mouse anti-tumor sera.

A directional cDNA lung tumor expression library was prepared using a Stratagene kit with a Lambda Zap Express vector. Total RNA for the library was taken from a late passaged lung adenocarcinoma grown in SCID mice. Poly A+ RNA was
25 isolated using a Message Maker Kit (Gibco BRL). Sera was obtained from two SCID mice implanted with lung adenocarcinomas. These sera were pooled and injected into normal mice to produce anti-lung tumor serum. Approximately 700,000 PFUs were screened from the unamplified library with *E. coli*-absorbed mouse anti-SCID tumor serum. Positive plaques were identified with a goat anti-mouse IgG-A-M (H+L)
30 alkaline phosphatase second antibody developed with NBT/BCIP (Gibco BRL). Phage

was purified and phagemid excised for 100 clones with insert in a pBK-CMV vector for expression in prokaryotic or eukaryotic cells.

The determined 5' cDNA sequences for 33 of the isolated clones are provided in SEQ ID NO: 149-181. The corresponding predicted amino acid sequences for SEQ ID NO: 149, 150, 152-154, 156-158 and 160-181 are provided in SEQ ID NO: 182, 183, 186, 188-193 and 194-215, respectively. The clone of SEQ ID NO: 151 (referred to as SAL-25) was found to contain two open reading frames (ORFs). The predicted amino acid sequences encoded by these ORFs are provided in SEQ ID NO: 184 and 185. The clone of SEQ ID NO: 153 (referred to as SAL-50) was found to contain two open reading frames encoding the predicted amino acid sequences of SEQ ID NO: 187 and 216. Similarly, the clone of SEQ ID NO: 155 (referred to as SAL-66) was found to contain two open reading frames encoding the predicted amino acid sequences of SEQ ID NO: 189 and 190. Comparison of the isolated sequences with those in the public database revealed no significant homologies to the sequences of SEQ ID NO: 151, 153 and 154. The sequences of SEQ ID NO: 149, 152, 156, 157 and 158 were found to show some homology to previously isolated expressed sequence tags (ESTs). The sequences of SEQ ID NO: 150, 155 and 159-181 were found to show homology to sequences previously identified in humans.

Using the procedures described above, two directional cDNA libraries (referred to as LT46-90 and LT86-21) were prepared from two late passaged lung squamous carcinomas grown in SCID mice and screened with sera obtained from SCID mice implanted with human squamous lung carcinomas. The determined cDNA sequences for the isolated clones are provided in SEQ ID NO: 217-237 and 286-289. SEQ ID NO: 286 was found to be a longer sequence of LT4690-71 (SEQ ID NO: 237). Comparison of these sequences with those in the public databases revealed no known homologies to the sequences of SEQ ID NO: 219, 220, 225, 226, 287 and 288. The sequences of SEQ ID NO: 218, 221, 222 and 224 were found to show some homology to previously identified sequences of unknown function. The sequence of SEQ ID NO: 236 was found to show homology to a known mouse mRNA sequence. The sequences

of SEQ ID NO: 217, 223, 227-237, 286 and 289 showed some homology to known human DNA and/or RNA sequences.

In further studies using the techniques described above, one of the cDNA libraries described above (LT86-21) was screened with *E. coli*-absorbed mouse anti-SCID tumor serum. This serum was obtained from normal mice immunized with a pool of 3 sera taken from SCID mice implanted with human squamous lung carcinomas. The determined cDNA sequences for the isolated clones are provided in SEQ ID NO: 238-285. Comparison of these sequences with those in the public databases revealed no significant homologies to the sequences of SEQ ID NO: 253, 260, 277 and 285. The sequences of SEQ ID NO: 249, 250, 256, 266, 276 and 282 were found to show some homology to previously isolated expressed sequence tags (ESTs). The sequences of SEQ ID NO: 238-248, 251, 252, 254, 255, 257-259, 261-263, 265, 267-275, 278-281, 283 and 284 were found to show some homology to previously identified DNA or RNA sequences.

The expression levels of certain of the isolated antigens in lung tumor tissues compared to expression levels in normal tissues was determined by microarray technology. The results of these studies are shown below in Table 2, together with the databank analyses for these sequences.

TABLE 2

Clone	SEQ ID NO:	Description	LT+F/N	SCC+M/N	Squa/N	Adeno/N
2LT-3	238	Unknown (KIAA0712)	2.2	3.8	3.3	-
2LT-6	239	Lactate DH B	2.3	3.8	4.1	-
2LT-22	240	Fumarate hydratase	-	3.0	-	-
2LT-26	242	CG1-39	-	-	12.8	-
2LT-31	243	ADH7	-	-	8.4	2.2
2LT-36	244	ADH7	-	2.4	2.0	-
2LT-42	245	HMG-CoA synthase	2.2	2.6	2.2	-
2LT-54	247	(Mus) ninein	-	2.1	-	-
2LT-55	248	Ubiquitin	2.2	-	2.5	2.0
2LT-57	249	Novel	2.1	2.9	2.4	-

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2LT-58	250	Novel	2.3	4.0	2.9	-
2LT-59	251	Unknown KIAA0784	2.4	3.0	2.3	2.0
2LT-62	252	Nuc Pore Cmplx- ass.pro TPR	-	-	-	2.1
2LT-70	256	Unknown KIAA0871	-	2.5	2.2	2.1
2LT-73	257	Mus polyadenylate- binding	-	2.0	-	-
2LT-76	259	Trans-Golgi p230	2.1	-	2.6	-
2LT-85	263	Ribosomal protein (LS29)	-	-	-	2.1
2LT-89	265	Unknown PAC212G6	-	2.0	-	-
2LT-98	268	Melanoma diff assoc pro 9	-	-	-	2.2
2LT-100	269	Mus Collagen alpha VI	-	-	-	2.1
2LT-105	271	NY-CO-7 antigen	-	3.2	-	-
2LT-108	273	Unknown RG363M04	-	3.1	-	-
2LT-124	279	Galectin-9 (secreted)	2.3	2.7	2.0	-
2LT-126	280	L1 element L1.33 p40	2.5	-	3.1	-
2LT-128	282	Novel (kappa B- ras 2)	2.3+	-	20.4	2.5
2LT-133	284	alpha II spectrin	-	2.3	-	-

LT+F/N = Lung Tumor plus Fetal tissue over Normal tissues

SC+M/N = Lung Small Cell carcinoma plus Metastatic over Normal tissues

Squa/N = Squamous lung tumor over Normal tissues

5 Aden/N = Adenocarcinoma over Normal tissues

Full-length sequencing studies on antigen 2LT-128 (SEQ ID NO: 282) resulted in the isolation of the full-length cDNA sequence provided in SEQ ID NO: 392. This amino acid sequence encoded by this full-length cDNA sequence is provided in SEQ ID NO: 393. This antigen shows 20-fold over-expression in squamous cell carcinoma and 2.5-fold over-expression in lung adenocarcinoma. This gene has been described as a potential ras oncogene (Fenwick et al. *Science*, 287:869-873, 2000).

Extended sequence information was obtained for clones 2LT-3 (SEQ ID NO:238), 2LT-26 (SEQ ID NO:242), 2LT-57 (SEQ ID NO: 249), 2LT-58 (SEQ ID NO:250), 2LT-98 (SEQ ID NO:268) and 2LT-124 (SEQ ID NO:279). The extended cDNA sequences for these clones are set forth in SEQ ID NOs:428-433, respectively, encoding the polypeptide sequences set forth in SEQ ID NOs: 434-439, respectively.

EXAMPLE 5

DETERMINATION OF TISSUE SPECIFICITY OF LUNG TUMOR POLYPEPTIDES

Using gene specific primers, mRNA expression levels for representative lung tumor polypeptides were examined in a variety of normal and tumor tissues using RT-PCR.

Briefly, total RNA was extracted from a variety of normal and tumor tissues using Trizol reagent. First strand synthesis was carried out using 2 µg of total RNA with SuperScript II reverse transcriptase (BRL Life Technologies) at 42°C for one hour. The cDNA was then amplified by PCR with gene-specific primers. To ensure the semi-quantitative nature of the RT-PCR, β-actin was used as an internal control for each of the tissues examined. 1 µl of 1:30 dilution of cDNA was employed to enable the linear range amplification of the β-actin template and was sensitive enough to reflect the differences in the initial copy numbers. Using these conditions, the β-actin levels were determined for each reverse transcription reaction from each tissue. DNA contamination was minimized by DNase treatment and by assuring a negative PCR result when using first strand cDNA that was prepared without adding reverse transcriptase.

mRNA Expression levels were examined in five different types of tumor tissue (lung squamous tumor from 3 patients, lung adenocarcinoma, prostate tumor, colon tumor and lung tumor), and different normal tissues, including lung from four patients, prostate, brain, kidney, liver, ovary, skeletal muscle, skin, small intestine, myocardium, retina and testes. L86S-46 was found to be expressed at high levels in lung squamous tumor, colon tumor and prostate tumor, and was undetectable in the other tissues examined. L86S-5 was found to be expressed in the lung tumor samples and in 2 out of 4 normal lung samples, but not in the other normal or tumor tissues

tested. L86S-16 was found to be expressed in all tissues except normal liver and normal stomach. Using real-time PCR, L86S-46 was found to be over-expressed in lung squamous tissue and normal tonsil, with expression being low or undetectable in all other tissues examined.

5

EXAMPLE 6

ISOLATION OF DNA SEQUENCES ENCODING LUNG TUMOR ANTIGENS

DNA sequences encoding antigens potentially involved in squamous cell lung tumor formation were isolated as follows.

A lung tumor directional cDNA expression library was constructed
10 employing the Lambda ZAP Express expression system (Stratagene, La Jolla, CA). Total RNA for the library was taken from a pool of two human squamous epithelial lung carcinomas and poly A+ RNA was isolated using oligo-dT cellulose (Gibco BRL, Gaithersburg, MD). Phagemid were rescued at random and the cDNA sequences of isolated clones were determined.

15 The determined cDNA sequence for the clone SLT-T1 is provided in SEQ ID NO: 102, with the determined 5' cDNA sequences for the clones SLT-T2, SLT-T3, SLT-T5, SLT-T7, SLT-T9, SLT-T10, SLT-T11 and SLT-T12 being provided in SEQ ID NO: 103-110, respectively. The corresponding predicted amino acid
20 sequence for SLT-T1, SLT-T2, SLT-T3, SLT-T10 and SLT-T12 are provided in SEQ ID NO: 111-115, respectively. Comparison of the sequences for SLT-T2, SLT-T3, SLT-T5, SLT-T7, SLT-T9 and SLT-T11 with those in the public databases as described above, revealed no significant homologies. The sequences for SLT-T10 and SLT-T12 were found to show some homology to sequences previously identified in humans.

The sequence of SLT-T1 was determined to show some homology to a
25 PAC clone of unknown protein function. The cDNA sequence of SLT-T1 (SEQ ID NO: 102) was found to contain a mutator (MUT) domain. Such domains are known to function in removal of damaged guanine from DNA that can cause A to G transversions (see, for example, el-Deiry, W.S., 1997 *Curr. Opin. Oncol.* 9:79-87; Okamoto, K. et al. 1996 *Int. J. Cancer* 65:437-41; Wu, C. et al. 1995 *Biochem. Biophys. Res. Commun.*
30 214:1239-45; Porter, D.W. et al. 1996 *Chem. Res. Toxicol.* 9:1375-81). SLT-T1 may

thus be of use in the treatment, by gene therapy, of lung cancers caused by, or associated with, a disruption in DNA repair.

In further studies, DNA sequences encoding antigens potentially involved in adenocarcinoma lung tumor formation were isolated as follows. A human
5 lung tumor directional cDNA expression library was constructed employing the Lambda ZAP Express expression system (Stratagene, La Jolla, CA). Total RNA for the library was taken from a late SCID mouse passaged human adenocarcinoma and poly A+ RNA was isolated using the Message Maker kit (Gibco BRL, Gaithersburg, MD). Phagemid were rescued at random and the cDNA sequences of isolated clones were
10 determined.

The determined 5' cDNA sequences for five isolated clones (referred to as SALT-T3, SALT-T4, SALT-T7, SALT-T8, and SALT-T9) are provided in SEQ ID NO: 116-120, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 121-125. SALT-T3 was found to show 98% identity to the previously
15 identified human transducin-like enhancer protein TLE2. SALT-T4 appears to be the human homologue of the mouse H beta 58 gene. SALT-T7 was found to have 97% identity to human 3-mercaptopyruvate sulfurtransferase and SALT-T8 was found to show homology to human interferon-inducible protein 1-8U. SALT-T9 shows approximately 90% identity to human mucin MUC 5B.

20 cDNA sequences encoding antigens potentially involved in small cell lung carcinoma development were isolated as follows. cDNA expression libraries were constructed with mRNA from the small cell lung carcinoma cell lines NCIH69, NCIH128 and DMS79 (all available from the American Type Culture Collection, Manassas, VA) employing the Lambda ZAP Express expression system (Stratagene, La
25 Jolla, CA). Phagemid were rescued at random and the cDNA sequences of 27 isolated clones were determined. Comparison of the determined cDNA sequences revealed no significant homologies to the sequences of SEQ ID NO: 372 and 373. The sequences of SEQ ID NO: 364, 369, 377, 379 and 386 showed some homology to previously isolated ESTs. The sequences of the remaining 20 clones showed some homology to previously
30 identified genes. The cDNA sequences of these clones are provided in SEQ ID NO:

363, 365-368, 370, 371, 374-376, 378, 380-385 and 387-389, wherein SEQ ID NO: 363, 366-368, 370, 375, 376, 378, 380-382, 384 and 385 are full-length sequences.

Comparison of the cDNA sequence of SEQ ID NO: 372 indicated that this clone (referred to as 128T1) is a novel member of a family of putative seven pass transmembrane proteins. Specifically, using the computer algorithm PSORT, the protein was predicted to be a type IIIA plasma membrane seven pass transmembrane protein. A genomic clone was identified in the Genbank database which contained the predicted N-terminal 58 amino acids missing from the amino acid sequence encoded by SEQ ID NO: 372. The determined full-length cDNA sequence for the 128T1 clone is provided in SEQ ID NO: 390, with the corresponding amino acid sequence being provided in SEQ ID NO: 391.

The expression levels of certain of the isolated antigens in lung tumor tissues compared to expression levels in normal tissues was determined by microarray technology. The results of these studies are shown below in Table 3, together with the databank analyses for these sequences.

TABLE 3

Clone	SEQ ID NO:	Description	LT+F/N	SCC+M/N	Squa/N	Adeno/N
DMS79-T1	363	STAT-ind inhib of cytokine	-	2.0	-	-
DMS79-T6	367	Neuronal cell death related	-	2.2	-	-
DMS79-T9	369	Novel	-	2.2	-	-
DMS79-T10	370	Ubiquitin carrier protein	-	3.9	2.2	-
DMS79-T11	371	HPV16E1 pro binding protein	-	2.1	-	-
128-T9	378	Elongation factor 1 alpha	-	2.7	-	-
128T11	380	Malate dehydrogenase	-	2.3	2.0	-
128-T12	381	Apurinic/apyrim endonuclease	-	5.4	-	-
NCIH69-	382	Sm-like protein	-	-	2.4	-

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T3		CaSm				
NCIH69-T6	384	Transcription factor BTF3a	-	2.5	-	-

LT+F/N = Lung Tumor plus Fetal tissue over Normal tissues

SC+M/N = Lung Small Cell carcinoma plus Metastatic over Normal tissues

Squa/N = Squamous lung tumor over Normal tissues

5 Aden/N = Adenocarcinoma over Normal tissues

EXAMPLE 7

SYNTHESIS OF POLYPEPTIDES

Polypeptides may be synthesized on a Perkin Elmer/Applied Biosystems Division 430A peptide synthesizer using Fmoc chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol
 15 (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following lyophilization of
 20 the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

EXAMPLE 8

ISOLATION AND CHARACTERIZATION OF DNA SEQUENCES ENCODING LUNG TUMOR

ANTIGENS BY T-CELL EXPRESSION CLONING

25 Lung tumor antigens may also be identified by T cell expression cloning. One source of tumor specific T cells is from surgically excised tumors from human patients.

A non-small cell lung carcinoma was minced and enzymatically digested for several hours to release tumor cells and infiltrating lymphocytes (tumor infiltrating T cells, or TILs). The cells were washed in HBSS buffer and passed over a Ficoll (100%/75%/HBSS) discontinuous gradient to separate tumor cells and lymphocytes from non-viable cells. Two bands were harvested from the interfaces; the upper band at the 75%/HBSS interface contained predominantly tumor cells, while the lower band at the 100%/75%/HBSS interface contained a majority of lymphocytes. The TILs were expanded in culture, either in 24-well plates with culture media supplemented with 10 ng/ml IL-7 and 100 U/ml IL-2, or alternatively, 24-well plates that have been pre-coated with the anti-CD3 monoclonal antibody OKT3. The resulting TIL cultures were analyzed by FACS to confirm that a high percentage were CD8+ T-cells (>90% of gated population) with only a small percentage of CD4+ cells.

In addition, non-small cell lung carcinoma cells were expanded in culture using standard techniques to establish a tumor cell line (referred to as LT391-06), which was later confirmed to be a lung carcinoma cell line by immunohistochemical analysis. This tumor cell line was transduced with a retroviral vector to express human CD80, and characterized by FACS analysis to confirm high expression levels of CD80, class I MHC and class II MHC molecules.

The ability of the TIL lines to specifically recognize autologous lung tumor was demonstrated by cytokine release assays (IFN- γ and TNF- α) as well as ^{51}Cr release assays. Briefly, TIL cells from day 21 cultures were co-cultured with either autologous or allogeneic tumor cells, EBV-immortalized LCL, or control cell lines Daudi and K562, and the culture supernatant monitored by ELISA for the presence of cytokines. The TIL specifically recognized autologous tumor but not allogeneic tumor. In addition, there was no recognition of EBV-immortalized LCL or the control cell lines, indicating that the TIL lines are tumor specific and are potentially recognizing a tumor antigen presented by autologous MHC molecules.

The characterized tumor-specific TIL lines were expanded to suitable numbers for T cell expression cloning using soluble anti-CD3 antibody in culture with irradiated EBV transformed LCLs and PBL feeder cells in the presence of 20 U/ml IL-

2. Clones from the expanded TIL lines were generated by standard limiting dilution techniques. Specifically, TIL cells were seeded at 0.5 cells/well in a 96-well U bottom plate and stimulated with CD-80-transduced autologous tumor cells, EBV transformed LCL, and PBL feeder cells in the presence of 50 U/ml IL-2. The specificity of these
5 clones for autologous tumor was confirmed by ^{51}Cr microcytotoxicity and IFN- γ bioassays.

These CTL clones were demonstrated to be HLA-B/C restricted by antibody blocking experiments. A representative CTL clone was tested on a panel of allogeneic lung carcinomas and it recognized both autologous tumor and a lung
10 squamous cell carcinoma (936T). As the only class I MHC molecule shared among these tumors was HLA-Cw1203, this indicated that this was the restriction element used by the CTL. This finding was confirmed by the recognition of a number of allogeneic lung carcinomas transduced with a retroviral vector encoding HLA-Cw1203 by the CTL.

15 PolyA mRNA was prepared from a lung tumor cell line referred to as LT391-06 using Message Maker (Life Technologies; Rockville, MD). The subsequent steps involving cDNA synthesis were performed according to Life Technologies cloning manual (SuperScript Plasmid System for cDNA Synthesis and Plasmid Cloning). Modifications to the protocol were made as follows. At the adapter addition
20 step, EcoRI-XmnI adapters (New England Biolabs; Beverly, MA) were substituted. Size fractionated cDNAs were ligated into the expression vector system HisMax A, B, C (Invitrogen; Carlsbad, CA) to optimize for protein expression in all three coding frames. Library plasmids were then aliquotted at approximately 100 CFU/well into a 96-well block for overnight liquid amplification. From these cultures, glycerol stocks
25 were made and pooled plasmid was prepared by automated robot (Qiagen; Valencia, CA). The concentration of the plasmid DNA in each well of the library plates was determined to be approximately 150 ng/ul. Initial characterization of the cDNA expression library was performed by randomly sequencing 24 primary transformants and subjecting the resulting sequences to BLAST searches against available databases.

The determined cDNA sequences are provided in SEQ ID NO: 443-480, with the results of the BLAST searches being provided in Table 4.

TABLE 4

Clone	SEQ ID NO:	GenBank Accession	Description
55163	458, 459		<i>Novel in Genbank</i>
55158	452		<i>Novel in Genbank</i>
Homology to known sequences with unknown function			
55153	443, 444	7018516	H. sapiens mRNA; cDNA DKFZp434M035
55154	445, 446	6437562	H. sapiens Chr 22q11 PAC Clone p393
55157	450, 451	2887408	H. sapiens KIAA0417 mRNA
55165	462, 463	3970871	H. sapiens HRIHFB2122 mRNA
Homology to known sequences with known function			
55155	447	7677405	H. sapiens F-box protein FBS (FBS)
55156	448, 449	3929584	H. sapiens EEN pseudogene
55161	454, 455	4503350	H. sapiens DNA (cytosine-5-)-methyltransferase 1 (DNMT1)
55162	456, 457	31220	ERK1 mRNA for protein serine/threonine kinase
55164	460, 461	6677666	H. sapiens RNA-binding protein (autoantigenic) (RALY)
55166	464, 465	3249540	H. sapiens ribonuclease P protein subunit p40 (RPP40)
55167	466, 467	7657497	H. sapiens renal tumor antigen (RAGE)
55168	468, 469	2873376	H. sapiens exportin t mRNA
55169	470, 471	3135472	H. sapiens Cre binding protein-like 2 mRNA
55171	474	4759151	H. sapiens spermine synthase (SMS)
55173	476	6688148	H. sapiens partial mRNA for NICE-3 protein
55174	477, 478	531394	Human transcriptional coactivator PC4
55175	479	6563201	H. sapiens translation initiation factor eIF-2b delta subunit
55176	480	29860	hCENP-Bgene, for centromere autoantigen B (CENP-B)
Homology to Ribosomal Protein			
55159	453	337494	Ribosomal protein L7a (surf 3) large subunit mRNA
55170	472, 473	4506648	H.sapiens mRNA for ribosomal protein L3

Clone	SEQ ID NO:	GenBank Accession	Description
55172	475	388031	H. sapiens ribosomal protein L11

For T cell screening, approximately 80 ng of the library plasmid DNA and 80 ng of HLA-Cw1203 plasmid DNA was mixed with the lipid Fugene according to the manufacturers' instructions and transfected in duplicate into COS-7 cells. After
5 incubation at 37 °C for 48 hours, the transfection mixture was removed and 10,000 LT391-06 CTL were added to each well in fresh media containing human serum.

The ability of T cells to recognize an antigen in the library was assessed by cytokine release after 6 hours (TNF-alpha, WEHI bio-assay) or after 24 hours (IFN-gamma, ELISA). Approximately 2.0×10^5 clones (in plasmid pools of 100) were
10 screened using this system in COS-7 cells. Three plasmid pools were identified (referred to as 14F10, 19A4, and 20E10) that were recognized by LT391-06 CTL. Transfection of these plasmid pools into COS-7 cells led to production of both IFN-gamma and TNF-alpha from the LT391-06 CTL at levels significantly above
background. Pools 14F10, 19A4 and 20E10 were "broken down" into several hundred
15 individual plasmid DNAs and retested. The sequences of 24 novel clones isolated from pool 14F10 are provided in SEQ ID NO: 481-511.

One plasmid (3D9) from pool 14F10, one plasmid from pool 20E10 and
5 plasmids (2A6, 2E11, 2F12, 3F4, 3H8) from pool 19A4 were capable of reconstituting T cell recognition. Sequencing of these plasmids led to the identification
20 of a 7.8 kB cDNA insert (referred to as clone 14F10), a 2.2 kB cDNA insert (referred to as clone 19A4; SEQ ID NO:440), and a clone referred to as 20E10. The full-length cDNA sequence for 14F10 is provided in SEQ ID NO: 441. Clone 14F10 does not contain the first two "G" nucleotides found at the 5' end of 19A4, and the 3'-proximal
24 bp of 19A4 differ from the corresponding region of 14F10 (nucleotides 2145-2165).
25 Furthermore, 3837 bp of 3' additional sequence was isolated for clone 14F10. The 5' terminal cDNA sequence (337 bp) of clone 20E10 is provided in SEQ ID NO: 442. 20E10 contains an additional 3 nucleotides (as compared to 19A4) at the 5'-most end. The additional sequence from the 5' end of clone 20E10 contains an "ATG" and

therefore appears to contain the translational start site of a novel open reading frame. BLAST search analysis against the GenBank database identified these sequences as having significant homology with a truncated human cystine/glutamate transporter gene. Unlike the published sequence, however, clones 14F10 and 19A4 contain a
5 unique 5' terminus consisting of 181 nucleotides. This novel sequence replaces the published 5' region and results in the removal of the reported initiating methionine (start codon) and an additional two amino acids of the reported transporter protein. Therefore, the translated product of clones 14F10 and 19A4 is different than the cystine/glutamate transporter protein. Furthermore, T cell recognition of other lung
10 tumors demonstrates that this antigen is expressed by other tumors as well.

The epitope and amino acid sequence encoded within clones 19A4 and 14F10 which reconstitutes T cell recognition of anti-LT391-06 cells were mapped as follows. Cos-7 cells were transfected with 80 ng/well HLA-Cw1203 along with titrated amounts of cDNA encoding clone 19A4, a potential open reading frame located in the
15 unique 5' terminus of 19A4, or the open reading frame from the cystine/glutamate (Cys-Glu) transporter gene, cloned into a eukaryotic expression vector and tested for stimulation of anti-LT391-06 T cells in a TNF assay. As a positive control Cos-7 cells were co-transfected with HLA-Cw1203 and the positive plasmid clone 19A4 described above. The Cys-Glu transporter expression construct was isolated by PCR using 5' and
20 3' primers specific for the known ORF of the transporter with 19A4 as template. In addition, each 5' primer contained a Kozak translation initiation site and starting methionine to drive translation of the polypeptide. CTL against LT391-06 did not recognize transfectants expressing the Cys-Glu transporter construct, but did recognize transfectants expressing 19A4 and the 5' ORF from 19A4.

25 In subsequent experiments, Cos-7 cells were co-transfected with 80 ng/well HLA-Cw1203 along with titrated amounts of DNA of transposition mutants F10 and C12, respectively, and tested for stimulation of anti-LT391-06 T cells in a TNF assay. As a positive control, Cos-7 cells were co-transfected with HLA-Cw1203 and clones of the 5' ORF of 19A4. Transposition mutants F10 and C12 were obtained by
30 transposon-mediated mutation of the 14F10 clone and screening for insertion site by

sequence analyses. The transposon of mutant F10 is inserted approximately 304 bp from the 5' EcoRI cloning site of the 14F10 cDNA. This mutation did not disrupt translation of the T cell epitope. By contrast, the transposon of mutant C12, which is inserted approximately 116 bp from the 5' EcoRI cloning site of the 14F10 cDNA, was found to interrupt translation of the T cell epitope. Thus the epitope in 14F10 maps between these two transposon insertion sites. The amino acid sequence of the region between the C12 and F10 transposon insertion sites is provided in SEQ ID NO: 586.

A series of 11 overlapping 16-mer and 15-mer peptides for the region shown in SEQ ID NO: 586 were prepared and tested for stimulation of anti-LT391-06 cells, as determined by cytokine release in TNF and IFN- γ assays. Only the peptide provided in SEQ ID NO: 587 (corresponding to residues 5-20 of SEQ ID NO: 586) stimulated cytokine release. These studies demonstrate that the HLA-Cw1203 restricted epitope of the LT391-06 antigen is contained within SEQ ID NO: 587.

EXAMPLE 9

ISOLATION AND CHARACTERIZATION OF DNA SEQUENCES ENCODING LUNG TUMOR ANTIGENS BY PCR SUBTRACTION

This example describes the isolation and characterization of cDNA clones from a PCR subtracted expression library prepared from the human lung tumor cell line LT391-06 described above.

Tester poly A mRNA was prepared from the cell line LT391-06 as described above. Driver poly A mRNA was isolated from a human acute T cell leukemia/T lymphocyte cell line (Jurkat) which is derived from non-lung cells and is not recognized by LT391-06 reactive T cells. The subtraction was performed according to the method of Clontech (Palo Alto, CA) with the following changes: 1) a second restriction digestion reaction of cDNA was completed using a pool of enzymes (MscI, PvuII, StuI and DraI). This was in addition to, and separate from, the Clontech recommended single restriction enzyme digestion with RsaI. Each restriction digest set was treated as a separate library to ensure that the final mixed library contained overlapping fragments. Thus, the epitope recognized by the T cells should be represented on a fragment within the library and not destroyed by the presence of a

single restriction site within it. 2) The ratio of driver to tester cDNA was increased in the hybridization steps to increase subtraction stringency. To analyze the efficiency of the subtraction, actin was PCR amplified from dilutions of subtracted, as well as unsubtracted, PCR samples. The second amplification step utilized primers that were modified from those normally used. Three nested PCR primers were engineered to contain a cleavable EcoRI site (not utilized during cloning) that was in one of three frames. Thus, secondary amplification with these primers resulted in products that could be ligated directly into the eukaryotic expression plasmid pcDNA4His/Max-Topo (Invitrogen). This resulted in the PCR subtracted and amplified fragments being represented in-frame somewhere within the library. Due to the mechanics of the subtraction only 50% of fragments will be in the correct orientation. The complexity and redundancy of the library was characterized by sequencing 96 randomly picked clones from the final pooled PCR subtraction expression library, referred to as LT391-06PCR. These sequences (SEQ ID NO: 512-581) were analyzed by comparison to sequences in publicly available databases (Table 5).

TABLE 5

Clone	SEQ ID NO:	GenBank Accession	Description
57235	532		<i>Novel in Genbank</i>
57255	547		<i>Novel in Genbank</i>
57264	554		<i>Novel in Genbank</i>
Homology to known sequences with unknown function			
57215	518	5689540	H. sapiens mRNA for KIAA1102 protein
57223	522	2341006	Human Xq13 3' end of PAC 92E23
57227	524	7022540	H. sapiens cDNA FLJ10480 fis, clone NT2RP2000126
57238	535	6807795	H. sapiens mRNA; cDNA DKFZp761G02121
57239	536	5757546	H. sapiens clone DJ0823F17
57243	539	7023805	H. sapiens cDNA FLJ11259 fis, clone PLACE1009045
57245	540	4884472	H. sapiens mRNA; cDNA DKFZp586O2223
57267	557	6808218	H. sapiens mRNA; cDNA DKFZp434O1519
57268	558	10040400	Sequence 12 from Patent WO9954460

Clone	SEQ ID NO:	GenBank Accession	Description
57270	560	7959775	H. sapiens PRO1489 mRNA
57271	561	4500158	H. sapiens mRNA; cDNA DKFZp586B0918
57281	567	6560920	H. sapiens clone RP11- 50107
57283	569	285962	Human mRNA for KIAA0108 gene
57285	570	7019813	H. sapiens cDNA FLJ20002 fis, clone ADKA01577
Homology to known sequences with known function			
57207	512	517176	H. sapiens YAP65 mRNA
57210	514	6841233	H. sapiens HSPC292 mRNA
57211	515	2606093	H. sapiens Cyr61 protein (CYR61) mRNA
57212	516	339648	Human thioredoxin (TXN) mRNA
57219	519	4504616	H. sapiens insulin- like growth factor binding protein 3 (IGFBP3)
57221	520	7274241	H. sapiens novel retinal pigment epithelial cell protein (NORPEG)
57222	521	189564	Human, plasminogen activator inhibitor- 1 gene
57228	525	4757755	H. sapiens annexin A2 (ANXA2)
57230	527	180800	Human alpha- 1 collagen type IV gene, exon 52
57232	529	6729061	H. sapiens clone RPC11- 98D12 from 7q31
57233	530	338391	Spermidine/ spermine N1- acetyltransferase
57234	531	7305302	H. sapiens NCK- associated protein 1 (NCKAP1)
57236	533	4929722	H. sapiens CGI- 127 protein
57242	538	4503558	H. sapiens epithelial membrane protein 1 (EMP1)
57248	541	183585	Human pregnancy- specific beta- glycoprotein c
57250	543	4759283	H. sapiens ubiquitin carboxyl- terminal esterase L1 (UCHL1)
57251	544	1236321	Human laminin gamma2 chain gene (LAMC2)
57253	545	213831	H. sapiens lysyl hydroxylase isoform 2 (PLOD2)
57254	546	536897	Human follistatin- related protein precursor mRNA
57257	548	339656	Human endothelial cell thrombomodulin
57258	549	190467	Human prion protein (PrP) mRNA
57261	551	338031	Human serglycin gene
57262	552	178430	Human alphoid DNA (alphoid repetitive

Clone	SEQ ID NO:	GenBank Accession	Description
			sequence)
57265	555	4502562	H. sapiens calpain, large polypeptide L2 (CAPN2)
57266	556	398163	H. sapiens mRNA for insulin- like growth factor binding protein- 3
57269	559	7262375	H. carboxylesterase 2 (intestine, liver) (CES2)
57272	562	467560	H. sapiens mRNA for cysteine dioxygenase type 1
57274	563	482664	H. sapiens annexin A3 (ANXA3)
57275	564	2281904	H. sapiens Bruton's tyr. kinase (BTK), alpha- D- galactosidase A (GLA)
57277	565	4557498	H. sapiens C- terminal binding protein 2 (CTBP2)
57282	568	189245	Human, NAD(P) H: menadione oxidoreductase mRNA
57287	571	28525	Human mRNA for amyloid A4 precursor of Alzheimer's disease
57288	572	4757755	H. sapiens annexin A2 (ANXA2)
57289	573	5729841	H. sapiens glyoxalase I (GLO1) mRNA
57290	574	6103642	H. sapiens F- box protein FBX3 mRNA
57295	576	182513	Human ferritin L chain mRNA
57299	579	37137	Human mRNA for thrombospondin
57301	580	179682	Human (clone A12) C4b- binding protein beta- chain
57302	581	6042205	H. sapiens membrane metallo- endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10) (MME).
57213	517	2665791	H. sapiens caveolin- 2 mRNA
57259	550	2665791	H. sapiens caveolin- 2 mRNA
57225	523	179765	Human calcyclin gene
57229	526	179765	Human calcyclin gene
57237	534	186962	Human laminin B2 chain gene
57249	542	186962	Human laminin B2 chain gene
57231	528	4972626	H. sapiens caveolin 1 (CAV1) gene
57296	577	4972626	H. sapiens caveolin 1 (CAV1) gene
57297	578	4972626	H. sapiens caveolin 1 (CAV1) gene
57240	537	266237	insulin- like growth factor binding protein 3
57292	575	184522	Human insulin- like growth factor- binding protein- 3 gene
57263	553	4504618	H. sapiens insulin- like growth factor

Clone	SEQ ID NO:	GenBank Accession	Description
			binding protein 7 (IGFBP7)
57280	566	4504618	H. sapiens insulin- like growth factor binding protein 7 (IGFBP7)
Homology to Ribosomal Protein			
57209	513	337504	Human ribosomal protein S24 mRNA

EXAMPLE 10

ISOLATION AND CHARACTERIZATION OF T CELL RECEPTORS FROM T CELL CLONES
SPECIFIC FOR LUNG TUMOR ANTIGENS

5 This example describes the cloning and sequencing of T cell receptor (TCR) alpha and beta chains from a CD8 T cell clone specific for an antigen expressed by the lung tumor cell line LT391-06. T cells have a limited lifespan. Cloning of TCR chains and subsequent transfer would essentially enable infinite propagation of the T cell specificity. Cloning of tumor antigen TCR chains allows the transfer of the

10 specificity into T cells isolated from patients that share TCR MHC-restricting alleles. Such T cells can then be expanded and used in adoptive transfer techniques to introduce the tumor antigen specificity into patients carrying tumors that express the antigen (see, for example, Clay et al. *J. Immunol.* 163:507 (1999)).

Cytotoxic T lymphocyte (CTL) clones specific for the lung tumor cell

15 line LT391-06 were generated. Total mRNA from 2×10^6 cells from 15 such clones was isolated using Trizol reagent and cDNA was synthesized using Ready-to-Go kits (Pharmacia). To determine Va and Vb sequences in these clones, a panel of Va and Vb subtype-specific primers was synthesized and used in RT-PCR reactions with cDNA generated from each of the clones. The RT-PCR reactions demonstrated that each of

20 the clones expressed a common Vb sequence that corresponded to the Vb13 subfamily. Using cDNA generated from one of the clones (referred to as 1105), the Va sequence expressed was determined to be Va22. To clone the full TCR alpha and beta chains from clone 1105, primers were designed that spanned the initiator and terminator-coding TCR nucleotides. Standard 35-cycle RT-PCR reactions were established using

25 cDNA synthesized from the CTL clone and the primers, with PWO (BMB) as the

thermostable polymerase. The resultant specific bands (approximately 850 bp for the alpha chain and approximately 950 bp for the beta chain) were ligated into the PCR blunt vector (Invitrogen) and transformed into *E. coli*. *E. coli* transformed with plasmids containing the full-length alpha and beta chains were identified, and large
5 scale preparations of the corresponding plasmids were generated. Plasmids containing full-length TCR alpha and beta chains were sequenced. The determined cDNA sequences for the alpha and beta chains are provided in SEQ ID NO: 583 and 582, respectively, with the corresponding amino acid sequences being provided in SEQ ID NO: 584 and 585, respectively.

10 From the foregoing it will be appreciated that, although specific embodiments of the invention have been described herein for purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention. Accordingly, the invention is not limited except as by the appended claims.

CLAIMS

What is Claimed:

1. An isolated polynucleotide comprising a sequence selected from the group consisting of:

- (a) sequences provided in SEQ ID NO: 390, 392, 394, 396, 398-420, 422-424, 428-433 and 440-583;
- (b) complements of the sequences provided in SEQ ID NO: 390, 392, 394, 396, 398-420, 422-424, 428-433 and 440-583;
- (c) sequences consisting of at least 20 contiguous residues of a sequence provided in SEQ ID NO: 390, 392, 394, 396, 398-420, 422-424, 428-433 and 440-583;
- (d) sequences that hybridize to a sequence provided in SEQ ID NO: 390, 392, 394, 396, 398-420, 422-424, 428-433 and 440-583, under moderately stringent conditions;
- (e) sequences having at least 75% identity to a sequence of SEQ ID NO: 390, 392, 394, 396, 398-420, 422-424, 428-433 and 440-583;
- (f) sequences having at least 90% identity to a sequence of SEQ ID NO: 390, 392, 394, 396, 398-420, 422-424, 428-433 and 440-583; and
- (g) degenerate variants of a sequence provided in SEQ ID NO: 390, 392, 394, 396, 398-420, 422-424, 428-433 and 440-583.

2. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:

- (a) SEQ ID NO: 584-587;
- (b) sequences encoded by a polynucleotide of claim 1; and
- (c) sequences having at least 70% identity to a sequence encoded by a polynucleotide of claim 1; and
- (d) sequences having at least 90% identity to a sequence encoded by a polynucleotide of claim 1.

3. An expression vector comprising a polynucleotide of claim 1 operably linked to an expression control sequence.
4. A host cell transformed or transfected with an expression vector according to claim 3.
5. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to a polypeptide of claim 2.
6. A method for detecting the presence of a cancer in a patient, comprising the steps of:
 - (a) obtaining a biological sample from the patient;
 - (b) contacting the biological sample with a binding agent that binds to a polypeptide of claim 2;
 - (c) detecting in the sample an amount of polypeptide that binds to the binding agent; and
 - (d) comparing the amount of polypeptide to a predetermined cut-off value and therefrom determining the presence of a cancer in the patient.
7. A fusion protein comprising at least one polypeptide according to claim 2.
8. An oligonucleotide that hybridizes to a sequence recited in SEQ ID NO: 390, 392, 394, 396, 398-420, 422-424, 428-433 and 440-583 under moderately stringent conditions.
9. A method for stimulating and/or expanding T cells specific for a tumor protein, comprising contacting T cells with at least one component selected from the group consisting of:
 - (a) polypeptides according to claim 2;

- (b) polynucleotides according to claim 1; and
 - (c) antigen-presenting cells that express a polypeptide according to claim 1,
- under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells.

10. An isolated T cell population, comprising T cells prepared according to the method of claim 9.

11. A composition comprising a first component selected from the group consisting of physiologically acceptable carriers and immunostimulants, and a second component selected from the group consisting of:

- (a) polypeptides according to claim 2;
- (b) polynucleotides according to claim 1;
- (c) antibodies according to claim 5;
- (d) fusion proteins according to claim 7;
- (e) T cell populations according to claim 10; and
- (f) antigen presenting cells that express a polypeptide according to claim 2.

12. A method for stimulating an immune response in a patient, comprising administering to the patient a composition of claim 11.

13. A method for the treatment of a cancer in a patient, comprising administering to the patient a composition of claim 11.

14. A method for determining the presence of a cancer in a patient, comprising the steps of:

- (a) obtaining a biological sample from the patient;

(b) contacting the biological sample with an oligonucleotide according to claim 8;

(c) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; and

(d) compare the amount of polynucleotide that hybridizes to the oligonucleotide to a predetermined cut-off value, and therefrom determining the presence of the cancer in the patient.

15. A diagnostic kit comprising at least one oligonucleotide according to claim 8.

16. A diagnostic kit comprising at least one antibody according to claim 5 and a detection reagent, wherein the detection reagent comprises a reporter group.

17. A method for inhibiting the development of a cancer in a patient, comprising the steps of:

(a) incubating CD4+ and/or CD8+ T cells isolated from a patient with at least one component selected from the group consisting of: (i) polypeptides according to claim 2; (ii) polynucleotides according to claim 1; and (iii) antigen presenting cells that express a polypeptide of claim 2, such that T cell proliferate;

(b) administering to the patient an effective amount of the proliferated T cells,

and thereby inhibiting the development of a cancer in the patient.

SEQUENCE LISTING

<110> Corixa Corporation
 Reed, Steven G.
 Henderson, Robert A.
 Lodes, Michael J.
 Fling, Steven P.
 Mohamath, Raodoh
 Algate, Paul A.
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 Elliot, Mark
 Mannion, Jane
 Kalos, Michael D.

<120> COMPOSITIONS AND METHODS FOR
 THE THERAPY AND DIAGNOSIS OF LUNG CANCER

<130> 210121.47501PC

<140> PCT

<141> 2001-03-38

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<210> 20
 <211> 488
 <212> DNA
 <213> Homo sapien

<400> 20						
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<210> 21
 <211> 391
 <212> DNA
 <213> Homo sapien

<400> 21						
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<210> 22
 <211> 1320
 <212> DNA
 <213> Homo sapien

<400> 22

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<210> 23
 <211> 633
 <212> DNA
 <213> Homo sapien

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<210> 24
 <211> 1328
 <212> DNA
 <213> Homo sapien

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<210> 25

<211> 1758

<212> DNA

<213> Homo sapien

<400> 25

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<210> 26

<211> 493

<212> DNA

<213> Homo sapien

<400> 26

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<210> 27
 <211> 1331
 <212> DNA
 <213> Homo sapien

<400> 27						
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<210> 28
 <211> 1333
 <212> DNA
 <213> Homo sapien

<400> 28						
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<210> 29

<211> 813

<212> DNA

<213> Homo sapien

<400> 29

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<210> 30

<211> 1316

<212> DNA

<213> Homo sapien

<400> 30

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gcaaaggcag	atgaagcagc	agcttgaggc	acttgagac	ttacaacaaa	gcttgtgtctc	900
atttcaagaa	aatggggacc	tggactgtctc	aagttctaca	tcaggatcct	tgctacctcc	960
tgaggaccac	cagtaaaagc	tgctctcctc	gaaaactgga	tggggcctcc	atgttctcca	1020
aggatcgagg	aagctcttct	gcctaccctg	cccacccag	tcaagggcag	caacaccaga	1080
gctttgtctc	gccttaaatg	gaatcttaga	gcttctctct	gcttctgcta	ctcctacaga	1140
tggcctcatc	atggtctcca	ctcagtatta	ataactccat	cagcatagag	caaactcaac	1200
actgtgcatt	gcacactgtt	accatgggtt	tatgtctact	atcatatcac	attgccaaata	1260

tttagcacac ttaataaatg cttgtcaaaa cccaaaaaaa aaaaaaaaaa ctcgag 1316

<210> 31
 <211> 1355
 <212> DNA
 <213> Homo sapien

<400> 31
 cggcggtgga tatccgagac aatctgctgg gaatttcttg ggttgacagc tcttgatcc 60
 ctattttgaa cagtggtagt gtcctggatt acttttcaga aagaagtaat cctttttatg 120
 acagaacatg taataatgaa gtggtcaaaa tgcagaggct aacattagaa cacttgaatc 180
 agatggttgg aatcgagtac atccttttgc atgctcaaga gccatttctt ttcattcattc 240
 ggaagcaaca gcggcagtc cctgcccagg ttatcccact agctgattac tatatcattg 300
 ctggagtgat ctatcaggca ccagacttgg gatcagttat aaactctaga gtgcttactg 360
 cagtgcagtg tattcagtc gcttttgatg aagctatgct atactgtcga tatcatcctt 420
 ccaaagggtg ttggtggcac ttcaaagatc atgaagagca agataaagtc agacctaaag 480
 ccaaaaggaa agaagaacca agctctatct ttcagagaca acgtgtggat gctttacttt 540
 tagacctcag acaaaaatct ccaccccaat ttgtgcagct aaagcctgga gaaaagcctg 600
 ttccagtggg tcaaacaag aaagaggcag aacctatacc agaaactgta aaacctgagg 660
 agaaggagac cacaaagaat gtacaacaga cagtgaagtc taaaggcccc cctgaaaaac 720
 ggatgagact tcagtgaag ctggacaaaa gagaagcctg gaagactcct catgctagtt 780
 atcatacctc agtactgtgg ctcttgagct ttgaagtact ttattgtaac cttcttattt 840
 gtatggaatg cgcttatttt ttgaaaggat attaggccgg atgtggtggc tcacgcctgt 900
 aatcccagca ctttgggagg ccatggcggg tggatcactt gaggtcagaa gttcaagacc 960
 agcctgacca atatggtgaa acccgcgtct tactaaaaat acaaaaatta gccgggcgtg 1020
 gtggcgggag cccatagtc cagctactcg ggaggctgag acaggagact tgcttgaacc 1080
 cgggaggttg aggttgccct gagctgatta tcatgctgtt gcactccagc ttgggcgaca 1140
 gaacgagact ttgtctcaaa aaaagaagaa aagatattat tcccatcatg atttcttgtg 1200
 aatatttgtt atatgtcttc tggtaacctt tctctcccg gacttgaagc aacctcacac 1260
 actcacatgt ttactggtag atatgtttta aaagcaaat aaaggatatt gtttttccaa 1320
 aaaaaaaaaa aaaaaaaaaa aaaaaaaac tcgag 1355

<210> 32
 <211> 80
 <212> PRT
 <213> Homo sapien

<400> 32
 Val Ser Arg Ile Arg Gly Gly Ala Lys Lys Arg Lys Lys Lys Ser Tyr
 1 5 10 15
 Thr Thr Pro Lys Lys Asp Lys His Gln Arg Lys Lys Val Gln Pro Ala
 20 25 30
 Val Leu Lys Tyr Tyr Lys Val Asp Glu Asn Gly Lys Ile Ser Cys Leu
 35 40 45
 Arg Arg Glu Cys Pro Ser Asp Glu Cys Gly Ala Gly Val Phe Met Ala
 50 55 60
 Ser His Phe Asp Arg His Tyr Cys Gly Lys Cys Cys Leu Thr His Cys
 65 70 75 80

<210> 33
 <211> 130
 <212> PRT
 <213> Homo sapien

<400> 33
 Glu Ile Ser Asn Glu Val Arg Lys Phe Arg Thr Leu Thr Glu Leu Ile
 1 5 10 15
 Leu Asp Ala Gln Glu His Val Lys Asn Pro Tyr Lys Gly Lys Lys Leu

20 25 30
 Lys Lys His Pro Asp Phe Pro Lys Lys Pro Leu Thr Pro Tyr Phe Arg
 35 40 45
 Phe Phe Met Glu Lys Arg Ala Lys Tyr Ala Lys Leu His Pro Gln Met
 50 55 60
 Ser Asn Leu Asp Leu Thr Lys Ile Leu Ser Lys Lys Tyr Lys Glu Leu
 65 70 75 80
 Pro Glu Lys Lys Lys Met Lys Tyr Val Pro Asp Phe Gln Arg Arg Glu
 85 90 95
 Thr Gly Val Arg Ala Lys Pro Gly Pro Ile Gln Gly Gly Ser Pro Pro
 100 105 110
 Pro Tyr Pro Glu Cys Gln Glu Ser Asp Ile Pro Glu Lys Pro Gln Asp
 115 120 125
 Pro Pro
 130

<210> 34
 <211> 506
 <212> PRT
 <213> Homo sapien

<400> 34
 Asn Ser Glu Lys Glu Ile Pro Val Leu Asn Glu Leu Pro Val Pro Met
 1 5 10 15
 Val Ala Arg Tyr Ile Arg Ile Asn Pro Gln Ser Trp Phe Asp Asn Gly
 20 25 30
 Ser Ile Cys Met Arg Met Glu Ile Leu Gly Cys Pro Leu Pro Asp Pro
 35 40 45
 Asn Asn Tyr Tyr His Arg Arg Asn Glu Met Thr Thr Thr Asp Asp Leu
 50 55 60
 Asp Phe Lys His His Asn Tyr Lys Glu Met Arg Gln Leu Met Lys Val
 65 70 75 80
 Val Asn Glu Met Cys Pro Asn Ile Thr Arg Ile Tyr Asn Ile Gly Lys
 85 90 95
 Ser His Gln Gly Leu Lys Leu Tyr Ala Val Glu Ile Ser Asp His Pro
 100 105 110
 Gly Glu His Glu Val Gly Glu Pro Glu Phe His Tyr Ile Ala Gly Ala
 115 120 125
 His Gly Asn Glu Val Leu Gly Arg Glu Leu Leu Leu Leu Leu His
 130 135 140
 Phe Leu Cys Gln Glu Tyr Ser Ala Gln Asn Ala Arg Ile Val Arg Leu
 145 150 155 160
 Val Glu Glu Thr Arg Ile His Ile Leu Pro Ser Leu Asn Pro Asp Gly
 165 170 175
 Tyr Glu Lys Ala Tyr Glu Gly Gly Ser Glu Leu Gly Gly Trp Ser Leu
 180 185 190
 Gly Arg Trp Thr His Asp Gly Ile Asp Ile Asn Asn Asn Phe Pro Asp
 195 200 205
 Leu Asn Ser Leu Leu Trp Glu Ala Glu Asp Gln Gln Asn Ala Pro Arg
 210 215 220
 Lys Val Pro Asn His Tyr Ile Ala Ile Pro Glu Trp Phe Leu Ser Glu
 225 230 235 240
 Asn Ala Thr Val Ala Thr Glu Thr Arg Ala Val Ile Ala Trp Met Glu
 245 250 255
 Lys Ile Pro Phe Val Leu Gly Gly Asn Leu Gln Gly Gly Glu Leu Val
 260 265 270
 Val Ala Tyr Pro Tyr Asp Met Val Arg Ser Leu Trp Lys Thr Gln Glu
 275 280 285

His Thr Pro Thr Pro Asp Asp His Val Phe Arg Trp Leu Ala Tyr Ser
 290 295 300
 Tyr Ala Ser Thr His Arg Leu Met Thr Asp Ala Arg Arg Arg Val Cys
 305 310 315 320
 His Thr Glu Asp Phe Gln Lys Glu Glu Gly Thr Val Asn Gly Ala Ser
 325 330 335
 Trp His Thr Val Ala Gly Ser Leu Asn Asp Phe Ser Tyr Leu His Thr
 340 345 350
 Asn Cys Phe Glu Leu Ser Ile Tyr Val Gly Cys Asp Lys Tyr Pro His
 355 360 365
 Glu Ser Glu Leu Pro Glu Glu Trp Glu Asn Asn Arg Glu Ser Leu Ile
 370 375 380
 Val Phe Met Glu Gln Val His Arg Gly Ile Lys Gly Ile Val Arg Asp
 385 390 395 400
 Leu Gln Gly Lys Gly Ile Ser Asn Ala Val Ile Ser Val Glu Gly Val
 405 410 415
 Asn His Asp Ile Arg Thr Ala Ser Asp Gly Asp Tyr Trp Arg Leu Leu
 420 425 430
 Asn Pro Gly Glu Tyr Val Val Thr Ala Lys Ala Glu Gly Phe Ile Thr
 435 440 445
 Ser Thr Lys Asn Cys Met Val Gly Tyr Asp Met Gly Ala Thr Arg Cys
 450 455 460
 Asp Phe Thr Leu Thr Lys Thr Asn Leu Ala Arg Ile Arg Glu Ile Met
 465 470 475 480
 Glu Thr Phe Gly Lys Gln Pro Val Ser Leu Pro Ser Arg Arg Leu Lys
 485 490 495
 Leu Arg Gly Arg Lys Arg Arg Gln Arg Gly
 500 505

<210> 35
 <211> 96
 <212> PRT
 <213> Homo sapien

<400> 35
 Met Asn Gly Glu Ala Asp Cys Pro Thr Asp Leu Glu Met Ala Ala Pro
 1 5 10 15
 Arg Gly Gln Asp Arg Trp Ser Gln Glu Asp Met Leu Thr Leu Leu Glu
 20 25 30
 Cys Met Lys Asn Asn Leu Pro Ser Asn Asp Ser Ser Gln Phe Lys Thr
 35 40 45
 Thr Gln Thr His Met Asp Arg Glu Lys Val Ala Leu Lys Asp Phe Ser
 50 55 60
 Gly Asp Met Cys Lys Leu Lys Trp Val Glu Ile Ser Asn Glu Val Arg
 65 70 75 80
 Lys Phe Arg Thr Leu Thr Glu Leu Ile Leu Asp Thr Gln Glu His Val
 85 90 95

<210> 36
 <211> 129
 <212> PRT
 <213> Homo sapien

<400> 36
 Gly Ile Val Val Phe Ser Leu Gly Ser Met Val Ser Glu Ile Pro Glu
 1 5 10 15
 Lys Lys Ala Val Ala Ile Ala Asp Ala Leu Gly Lys Ile Pro Gln Thr
 20 25 30

Val Leu Trp Arg Tyr Thr Gly Thr Arg Pro Ser Asn Leu Ala Asn Asn
 35 40 45
 Thr Ile Leu Val Gln Trp Leu Pro Gln Asn Asp Leu Leu Gly His Pro
 50 55 60
 Met Thr Arg Ala Phe Ile Thr His Ala Ser Ser His Gly Val Asn Glu
 65 70 75 80
 Ser Ile Cys Asn Gly Val Pro Met Val Met Ile Pro Leu Phe Gly Asp
 85 90 95
 Gln Met Asp Asn Ala Lys Arg Arg Glu Thr Lys Gly Ala Gly Val Thr
 100 105 110
 Leu Asn Val Leu Glu Met Thr Ser Glu Asp Leu Glu Asp Ala Leu Lys
 115 120 125
 Ser

<210> 37
 <211> 238
 <212> PRT
 <213> Homo sapien

<400> 37
 Asn Leu Leu Gly Ile Ser Trp Val Asp Ser Ser Trp Ile Pro Ile Leu
 1 5 10 15
 Asn Ser Gly Ser Val Leu Asp Tyr Phe Ser Glu Arg Ser Asn Pro Phe
 20 25 30
 Tyr Asp Arg Thr Cys Asn Asn Glu Val Val Lys Met Gln Arg Leu Thr
 35 40 45
 Leu Glu His Leu Asn Gln Met Val Gly Ile Glu Tyr Ile Leu Leu His
 50 55 60
 Ala Gln Glu Pro Ile Leu Phe Ile Ile Arg Lys Gln Gln Arg Gln Ser
 65 70 75 80
 Pro Ala Gln Val Ile Pro Leu Ala Asp Tyr Tyr Ile Ile Ala Gly Val
 85 90 95
 Ile Tyr Gln Ala Pro Asp Leu Gly Ser Val Ile Asn Ser Arg Val Leu
 100 105 110
 Thr Ala Val His Gly Ile Gln Ser Ala Phe Asp Glu Ala Met Ser Tyr
 115 120 125
 Cys Arg Tyr His Pro Ser Lys Gly Tyr Trp Trp His Phe Lys Asp His
 130 135 140
 Glu Glu Gln Asp Lys Val Arg Pro Lys Ala Lys Arg Lys Glu Glu Pro
 145 150 155 160
 Ser Ser Ile Phe Gln Arg Gln Arg Val Asp Ala Leu Leu Leu Asp Leu
 165 170 175
 Arg Gln Lys Phe Pro Pro Lys Phe Val Gln Leu Lys Pro Gly Glu Lys
 180 185 190
 Pro Val Pro Val Asp Gln Thr Lys Lys Glu Ala Glu Pro Ile Pro Glu
 195 200 205
 Thr Val Lys Pro Glu Glu Lys Glu Thr Thr Lys Asn Val Gln Gln Thr
 210 215 220
 Val Ser Ala Lys Gly Pro Pro Glu Lys Arg Met Arg Leu Gln
 225 230 235

<210> 38
 <211> 202
 <212> PRT
 <213> Homo sapien

<400> 38

Lys Gly Ser Glu Gly Glu Asn Pro Leu Thr Val Pro Gly Arg Glu Lys
 1 5 10 15
 Glu Gly Met Leu Met Gly Val Lys Pro Gly Glu Asp Ala Ser Gly Pro
 20 25 30
 Ala Glu Asp Leu Val Arg Arg Ser Glu Lys Asp Thr Ala Ala Val Val
 35 40 45
 Ser Arg Gln Gly Ser Ser Leu Asn Leu Phe Glu Asp Val Gln Ile Thr
 50 55 60
 Glu Pro Glu Ala Glu Pro Glu Ser Lys Ser Glu Pro Arg Pro Pro Ile
 65 70 75 80
 Ser Ser Pro Arg Ala Pro Gln Thr Arg Ala Val Lys Pro Arg Leu His
 85 90 95
 Pro Val Lys Pro Met Asn Ala Thr Ala Thr Lys Val Ala Asn Cys Ser
 100 105 110
 Leu Gly Thr Ala Thr Ile Ile Gly Glu Asn Leu Asn Asn Glu Val Met
 115 120 125
 Met Lys Lys Tyr Ser Pro Ser Asp Pro Ala Phe Ala Tyr Ala Gln Leu
 130 135 140
 Thr His Asp Glu Leu Ile Gln Leu Val Leu Lys Gln Lys Glu Thr Ile
 145 150 155 160
 Ser Lys Lys Glu Phe Gln Val Arg Glu Leu Glu Asp Tyr Ile Asp Asn
 165 170 175
 Leu Leu Val Arg Val Met Glu Glu Thr Pro Asn Ile Leu Arg Ile Pro
 180 185 190
 Thr Gln Val Gly Lys Lys Ala Gly Lys Met
 195 200

<210> 39
 <211> 243
 <212> PRT
 <213> Homo sapien

<400> 39
 Val Asn Ala Leu Gly Ile Met Ala Ala Val Asp Ile Arg Asp Asn Leu
 1 5 10 15
 Leu Gly Ile Ser Trp Val Asp Ser Ser Trp Ile Pro Ile Leu Asn Ser
 20 25 30
 Gly Ser Val Leu Asp Tyr Phe Ser Glu Arg Ser Asn Pro Phe Tyr Asp
 35 40 45
 Arg Thr Cys Asn Asn Glu Val Lys Met Gln Arg Leu Thr Leu Glu
 50 55 60
 His Leu Asn Gln Met Val Gly Ile Glu Tyr Ile Leu Leu His Ala Gln
 65 70 75 80
 Glu Pro Ile Leu Phe Ile Ile Arg Lys Gln Gln Arg Gln Ser Pro Ala
 85 90 95
 Gln Val Ile Pro Leu Ala Asp Tyr Tyr Ile Ile Ala Gly Val Ile Tyr
 100 105 110
 Gln Ala Pro Asp Leu Gly Ser Val Ile Asn Ser Arg Val Leu Thr Ala
 115 120 125
 Val His Gly Ile Gln Ser Ala Phe Asp Glu Ala Met Ser Tyr Cys Arg
 130 135 140
 Tyr His Pro Ser Lys Gly Tyr Trp Trp His Phe Lys Asp His Glu Glu
 145 150 155 160
 Gln Asp Lys Val Arg Pro Lys Ala Lys Arg Lys Glu Glu Pro Ser Ser
 165 170 175
 Ile Phe Gln Arg Gln Arg Val Asp Ala Leu Leu Leu Asp Leu Arg Gln
 180 185 190
 Lys Ile Ser Thr Gln Ile Cys Ala Val Asp Gln Thr Lys Lys Glu Ala

195 200 205
 Glu Pro Ile Pro Glu Thr Val Lys Pro Glu Glu Lys Glu Thr Thr Lys
 210 215 220
 Asn Val Gln Gln Thr Val Ser Ala Lys Gly Pro Pro Glu Lys Arg Met
 225 230 235 240
 Arg Leu Gln

<210> 40
 <211> 245
 <212> PRT
 <213> Homo sapien

<400> 40
 Ala Ala Val Asp Ile Arg Asp Asn Leu Leu Gly Ile Ser Trp Val Asp
 1 5 10 15
 Ser Ser Trp Ile Pro Ile Leu Asn Ser Ser Gly Ser Val Leu Asp Tyr Phe
 20 25 30
 Ser Glu Arg Ser Asn Pro Phe Tyr Asp Arg Thr Cys Asn Asn Glu Val
 35 40 45
 Val Lys Met Gln Arg Leu Thr Leu Glu His Leu Asn Gln Met Val Gly
 50 55 60
 Ile Glu Tyr Ile Leu Leu His Ala Gln Glu Pro Ile Leu Phe Ile Ile
 65 70 75 80
 Arg Lys Gln Gln Arg Gln Ser Pro Ala Gln Val Ile Pro Leu Ala Asp
 85 90 95
 Tyr Tyr Ile Ile Ala Gly Val Ile Tyr Gln Ala Pro Asp Leu Gly Ser
 100 105 110
 Val Ile Asn Ser Arg Val Leu Thr Ala Val His Gly Ile Gln Ser Ala
 115 120 125
 Phe Asp Glu Ala Met Ser Tyr Cys Arg Tyr His Pro Ser Lys Gly Tyr
 130 135 140
 Trp Trp His Phe Lys Asp His Glu Glu Gln Asp Lys Val Arg Pro Lys
 145 150 155 160
 Ala Lys Arg Lys Glu Glu Pro Ser Ser Ile Phe Gln Arg Gln Arg Val
 165 170 175
 Asp Ala Leu Leu Leu Asp Leu Arg Gln Lys Phe Pro Pro Lys Phe Val
 180 185 190
 Gln Leu Lys Pro Gly Glu Lys Pro Val Pro Val Asp Gln Thr Lys Lys
 195 200 205
 Glu Ala Glu Pro Ile Pro Glu Thr Val Lys Pro Glu Glu Lys Glu Thr
 210 215 220
 Thr Lys Asn Val Gln Gln Thr Val Ser Ala Lys Gly Pro Pro Glu Lys
 225 230 235 240
 Arg Met Arg Leu Gln
 245

<210> 41
 <211> 163
 <212> PRT
 <213> Homo sapien

<400> 41
 Gly Glu Arg Gln Gly Leu Val Ala Arg Ala Arg Leu Ser Leu Arg Pro
 1 5 10 15
 Ser Ile Pro Glu Leu Ser Glu Arg Thr Ser Arg Pro Cys Arg Ala Ser
 20 25 30
 Pro Ala Ser Leu Pro Ser Gln His Thr Ser Ser Pro Ala Gln Ala Arg

```

      35      40      45
Val Arg Asn Leu Ala Gln Ser Thr Phe Pro Leu Ala Ala Gln Glu Thr
  50      55      60
Pro Gly Arg Ala Pro Ala His Ala Pro Leu Ser Ser Phe Val Pro Gly
  65      70      75      80
Val Gly Gly Arg Ser Pro Ala Ser Val Gly Ile Ser Ala Pro Gly Gly
      85      90      95
Gly Pro Ser Gly Ala Ala Ala Lys Ile Pro Leu Glu Leu Thr Gln Ser
      100      105      110
Arg Val Gln Lys Ile Trp Val Pro Val Asp His Arg Pro Ser Leu Pro
      115      120      125
Arg Ser Cys Gly Pro Lys Leu Thr Asn Ser Pro Ala Val Phe Val Met
      130      135      140
Val Gly Leu Pro Arg Pro Gly Gln Asp Leu Leu Leu His Glu Ser Leu
  145      150      155      160
Leu Ala Ala

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<210> 42
<211> 243
<212> PRT
<213> Homo sapien

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      <400> 42
Val Asp Ile Arg Asp Asn Leu Leu Gly Ile Ser Trp Val Asp Ser Ser
  1      5      10      15
Trp Ile Pro Ile Leu Asn Ser Gly Ser Val Leu Asp Tyr Phe Ser Glu
      20      25      30
Arg Ser Asn Pro Phe Tyr Asp Arg Thr Cys Asn Asn Glu Val Val Lys
      35      40      45
Met Gln Arg Leu Thr Leu Glu His Leu Asn Gln Met Val Gly Ile Glu
  50      55      60
Tyr Ile Leu Leu His Ala Gln Glu Pro Ile Leu Phe Ile Ile Arg Lys
  65      70      75      80
Gln Gln Arg Gln Ser Pro Ala Gln Val Ile Pro Leu Ala Asp Tyr Tyr
      85      90      95
Ile Ile Ala Gly Val Ile Tyr Gln Ala Pro Asp Leu Gly Ser Val Ile
      100      105      110
Asn Ser Arg Val Leu Thr Ala Val His Gly Ile Gln Ser Ala Phe Asp
      115      120      125
Glu Ala Met Ser Tyr Cys Arg Tyr His Pro Ser Lys Gly Tyr Trp Trp
  130      135      140
His Phe Lys Asp His Glu Glu Gln Asp Lys Val Arg Pro Lys Ala Lys
  145      150      155      160
Arg Lys Glu Glu Pro Ser Ser Ile Phe Gln Arg Gln Arg Val Asp Ala
      165      170      175
Leu Leu Leu Asp Leu Arg Gln Lys Phe Pro Pro Lys Phe Val Gln Leu
      180      185      190
Lys Pro Gly Glu Lys Pro Val Pro Val Asp Gln Thr Lys Lys Glu Ala
      195      200      205
Glu Pro Ile Pro Glu Thr Val Lys Pro Glu Glu Lys Glu Thr Thr Lys
      210      215      220
Asn Val Gln Gln Thr Val Ser Ala Lys Gly Pro Pro Glu Lys Arg Met
  225      230      235      240
Arg Leu Gln

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<210> 43

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<211> 244
 <212> PRT
 <213> Homo sapien

<400> 43
 Ala Val Asp Ile Arg Asp Asn Leu Leu Gly Ile Ser Trp Val Asp Ser
 1 5 10 15
 Ser Trp Ile Pro Ile Leu Asn Ser Gly Ser Val Leu Asp Tyr Phe Ser
 20 25 30
 Glu Arg Ser Asn Pro Phe Tyr Asp Arg Thr Cys Asn Asn Glu Val Val
 35 40 45
 Lys Met Gln Arg Leu Thr Leu Glu His Leu Asn Gln Met Val Gly Ile
 50 55 60
 Glu Tyr Ile Leu Leu His Ala Gln Glu Pro Ile Leu Phe Ile Ile Arg
 65 70 75 80
 Lys Gln Gln Arg Gln Ser Pro Ala Gln Val Ile Pro Leu Ala Asp Tyr
 85 90 95
 Tyr Ile Ile Ala Gly Val Ile Tyr Gln Ala Pro Asp Leu Gly Ser Val
 100 105 110
 Ile Asn Ser Arg Val Leu Thr Ala Val His Gly Ile Gln Ser Ala Phe
 115 120 125
 Asp Glu Ala Met Ser Tyr Cys Arg Tyr His Pro Ser Lys Gly Tyr Trp
 130 135 140
 Trp His Phe Lys Asp His Glu Glu Gln Asp Lys Val Arg Pro Lys Ala
 145 150 155 160
 Lys Arg Lys Glu Glu Pro Ser Ser Ile Phe Gln Arg Gln Arg Val Asp
 165 170 175
 Ala Leu Leu Leu Asp Leu Arg Gln Lys Phe Pro Pro Lys Phe Val Gln
 180 185 190
 Leu Lys Pro Gly Glu Lys Pro Val Pro Val Asp Gln Thr Lys Lys Glu
 195 200 205
 Ala Glu Pro Ile Pro Glu Thr Val Lys Pro Glu Glu Lys Glu Thr Thr
 210 215 220
 Lys Asn Val Gln Gln Thr Val Ser Ala Lys Gly Pro Pro Glu Lys Arg
 225 230 235 240
 Met Arg Leu Gln

<210> 44
 <211> 109
 <212> PRT
 <213> Homo sapien

<400> 44
 Glu Leu His Phe Ser Glu Phe Thr Ser Ala Val Ala Asp Met Lys Asn
 1 5 10 15
 Ser Val Ala Asp Arg Asp Asn Ser Pro Ser Ser Cys Ala Gly Leu Phe
 20 25 30
 Ile Ala Ser His Ile Gly Phe Asp Trp Pro Gly Val Trp Val His Leu
 35 40 45
 Asp Ile Ala Ala Pro Val His Ala Gly Glu Arg Ala Thr Gly Phe Gly
 50 55 60
 Val Ala Leu Leu Leu Ala Leu Phe Gly Arg Ala Ser Glu Asp Pro Leu
 65 70 75 80
 Leu Asn Leu Val Ser Pro Leu Asp Cys Glu Val Asp Ala Gln Glu Gly
 85 90 95
 Asp Asn Met Gly Arg Asp Ser Lys Arg Arg Arg Leu Val
 100 105

<210> 45
 <211> 324
 <212> PRT
 <213> Homo sapien

<400> 45
 Arg Arg Pro Val Met Ala Gln Glu Thr Ala Pro Pro Cys Gly Pro Val
 1 5 10 15
 Ser Arg Gly Asp Ser Pro Ile Ile Glu Lys Met Glu Lys Arg Thr Cys
 20 25 30
 Ala Leu Cys Pro Glu Gly His Glu Trp Ser Gln Ile Tyr Phe Ser Pro
 35 40 45
 Ser Gly Asn Ile Val Ala His Glu Asn Cys Leu Leu Tyr Ser Ser Gly
 50 55 60
 Leu Val Glu Cys Glu Thr Leu Asp Leu Arg Asn Thr Ile Arg Asn Phe
 65 70 75 80
 Asp Val Lys Ser Val Lys Lys Glu Ile Trp Arg Gly Arg Arg Leu Lys
 85 90 95
 Cys Ser Phe Cys Asn Lys Gly Gly Ala Thr Val Gly Cys Asp Leu Trp
 100 105 110
 Phe Cys Lys Lys Ser Tyr His Tyr Val Cys Ala Lys Lys Asp Gln Ala
 115 120 125
 Ile Leu Gln Val Asp Gly Asn His Gly Thr Tyr Lys Leu Phe Cys Pro
 130 135 140
 Glu His Ser Pro Glu Gln Glu Ala Thr Glu Ser Ala Asp Asp Pro
 145 150 155 160
 Ser Met Lys Lys Lys Arg Gly Lys Asn Lys Arg Leu Ser Ser Gly Pro
 165 170 175
 Pro Ala Gln Pro Lys Thr Met Lys Cys Ser Asn Ala Lys Arg His Met
 180 185 190
 Thr Glu Glu Pro His Gly His Thr Asp Ala Ala Val Lys Ser Pro Phe
 195 200 205
 Leu Lys Lys Cys Gln Glu Ala Gly Leu Leu Thr Glu Leu Phe Glu His
 210 215 220
 Ile Leu Glu Asn Met Asp Ser Val His Gly Arg Leu Val Asp Glu Thr
 225 230 235 240
 Ala Ser Glu Ser Asp Tyr Glu Gly Ile Glu Thr Leu Leu Phe Asp Cys
 245 250 255
 Gly Leu Phe Lys Asp Thr Leu Arg Lys Phe Gln Glu Val Ile Lys Ser
 260 265 270
 Lys Ala Cys Glu Trp Glu Glu Arg Gln Arg Gln Met Lys Gln Gln Leu
 275 280 285
 Glu Ala Leu Ala Asp Leu Gln Gln Ser Leu Cys Ser Phe Gln Glu Asn
 290 295 300
 Gly Asp Leu Asp Cys Ser Ser Ser Thr Ser Gly Ser Leu Leu Pro Pro
 305 310 315 320
 Glu Asp His Gln

<210> 46
 <211> 244
 <212> PRT
 <213> Homo sapien

<400> 46
 Ala Val Asp Ile Arg Asp Asn Leu Leu Gly Ile Ser Trp Val Asp Ser
 1 5 10 15

Ser Trp Ile Pro Ile Leu Asn Ser Gly Ser Val Leu Asp Tyr Phe Ser
 20 25 30
 Glu Arg Ser Asn Pro Phe Tyr Asp Arg Thr Cys Asn Asn Glu Val Val
 35 40 45
 Lys Met Gln Arg Leu Thr Leu Glu His Leu Asn Gln Met Val Gly Ile
 50 55 60
 Glu Tyr Ile Leu Leu His Ala Gln Glu Pro Ile Leu Phe Ile Ile Arg
 65 70 75 80
 Lys Gln Gln Arg Gln Ser Pro Ala Gln Val Ile Pro Leu Ala Asp Tyr
 85 90 95
 Tyr Ile Ile Ala Gly Val Ile Tyr Gln Ala Pro Asp Leu Gly Ser Val
 100 105 110
 Ile Asn Ser Arg Val Leu Thr Ala Val His Gly Ile Gln Ser Ala Phe
 115 120 125
 Asp Glu Ala Met Ser Tyr Cys Arg Tyr His Pro Ser Lys Gly Tyr Trp
 130 135 140
 Trp His Phe Lys Asp His Glu Glu Gln Asp Lys Val Arg Pro Lys Ala
 145 150 155 160
 Lys Arg Lys Glu Glu Pro Ser Ser Ile Phe Gln Arg Gln Arg Val Asp
 165 170 175
 Ala Leu Leu Leu Asp Leu Arg Gln Lys Phe Pro Pro Lys Phe Val Gln
 180 185 190
 Leu Lys Pro Gly Glu Lys Pro Val Pro Val Asp Gln Thr Lys Lys Glu
 195 200 205
 Ala Glu Pro Ile Pro Glu Thr Val Lys Pro Glu Glu Lys Glu Thr Thr
 210 215 220
 Lys Asn Val Gln Gln Thr Val Ser Ala Lys Gly Pro Pro Glu Lys Arg
 225 230 235 240
 Met Arg Leu Gln

<210> 47
 <211> 14
 <212> DNA
 <213> Homo sapien

<400> 47
 tttttttttt ttag 14

<210> 48
 <211> 10
 <212> DNA
 <213> Homo sapien

<400> 48
 cttcaacctc 10

<210> 49
 <211> 496
 <212> DNA
 <213> Homo sapien

<400> 49
 gcaccatgta ccgagcactt cggctcctcg cgcgctcgcg tcccctcgtg cgggetccag 60
 ccgcagcctt agcttcggct cccggcttgg gtggcgcggc cgtgccctcg ttttggcctc 120
 cgaacgcggc tcgaatggca agccaaaatt ccttccggat agaatatgat accttgggtg 180
 aactaaaggt gccaaatgat aagtattatg gcgcccagac cgtgagatct acgatgaact 240
 ttaagattgg aggtgtgaca gaacgcgatgc caaccccagt tattaaagct tttggcatct 300

tgaagcgagc	ggccgctgaa	gtaaaccagg	attatggtct	tgatccaaag	attgctaattg	360
caataatgaa	ggcagcagat	gaggtagctg	aaggtaaatt	aaatgatcat	tttcctctcg	420
tggtatggca	gactggatca	ggaactcaga	caaatatgaa	tgtaaattgaa	gtcattagcc	480
aatagagcaa	ttgaaa					496

<210> 50
 <211> 499
 <212> DNA
 <213> Homo sapien

<400> 50	
agaaaaagtc	tatgtttgca
gaaaaattat	taaatgcaaa
aggaaataga	agttgcccc
gaatctgtcg	cacagatgac
ttgtgggaca	tgaggcaact
aaccagggtga	caaagtcac
gcaaccaga	tggaacctt
atggcaccac	cagatttaca
catttaccga	gtacacagt
	60
	120
	180
	240
	300
	360
	420
	480
	499

<210> 51
 <211> 887
 <212> DNA
 <213> Homo sapien

<400> 51	
gagtctgagc	agaaaggaaa
gtggccagtg	accagataga
aaagtggcag	agctgtattc
ctggagagtg	tcaggctgga
gatctggctc	ataccgaaa
gatgaatacc	gagccttcca
ttagaaaaat	taagatcaga
accatctttg	aacttgaaga
ctcattatit	ctgatctaga
gaaagagaaa	taaagacact
tttcaggctg	atctccagac
gaggagattg	gtgatctaaa
acaaaaaat	tgaggaaaat
attacatgaa	tgccgttgag
gaaggctctc	gacttcctca
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	300
	360
	420
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	660
	720
	780
	840
	887

<210> 52
 <211> 491
 <212> DNA
 <213> Homo sapien

<400> 52	
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aaggaaacctt	tcactcttga
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aaagtgaag	tcaaagttcg
ttagtggagg	ttcacaagtc
aaggaggaag	agaagatgca
cagacaccag	gcagaaaaata
caaggataaa	aagatggacc
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	360
	420
	480
	491

<210> 53
 <211> 787
 <212> DNA
 <213> Homo sapien

<400> 53
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 caggggtagt gatcctggca gtcaccatag ctctacttgt ttacttttta gcttttgatc 180
 aaaaatctta cttttatagg agcagttttc aactcctaaa tgttgaatat aatagtcagt 240
 taaattcacc agctacacag gaatacagga ctttgagtgg aagaattgaa tctctgatta 300
 ctaaaacatt caaagaatca aatttaagaa atcagttcat cagagctcat gttgccaaac 360
 tgaggcaaga tggtagtggg gtgagagcgg atgttgtcat gaaatttcaa ttcactagaa 420
 ataacaatgg agcatcaatg aaaagcagaa ttgagtctgt tttacgacaa atgctgaata 480
 actctggaaa cctggaaata aacccttcaa ctgagataac atcacttact gaccaggctg 540
 cagcaaattg gcttattaat gaatgtgggg ccggtccaga cctaataaca ttgtctgagc 600
 agagaatcct tggaggcact gaggtgagg agggaagctg gccgtggcaa gtcagtctgc 660
 ggctcaataa tgcccaccac tgtggaggca gcctgatcaa taacatgtgg atcctgacag 720
 cagctcactg cttcagaagc aactctaate ctcgtgactg gattgccacg tctggtattt 780
 ccacaac 787

<210> 54
 <211> 386
 <212> DNA
 <213> Homo sapien

<400> 54
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 gaaccacatg ttgaagagca acagcagcag acaccagcag aaaataaggc agagtctgaa 180
 gaaatggaga cctctcaagc tggatccaag gataaaaaga tggaccaacc accccaagcc 240
 aagaaggcaa aagtgaagac cagtactgtg gacctgccaa tgcagaatca gctattatgg 300
 cagatagaca gagagatgct caacttgtag attgaaaatg agggttaagat gatcatgcag 360
 gataaactgg agaaggagcg gaatga 386

<210> 55
 <211> 1462
 <212> DNA
 <213> Homo sapien

<400> 55
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 caggggtagt gatcctggca gtcaccatag ctctacttgt ttacttttta gcttttgatc 180
 aaaaatctta cttttatagg agcagttttc aactcctaaa tgttgaatat aatagtcagt 240
 taaattcacc agctacacag gaatacagga ctttgagtgg aagaattgaa tctctgatta 300
 ctaaaacatt caaagaatca aatttaagaa atcagttcat cagagctcat gttgccaaac 360
 tgaggcaaga tggtagtggg gtgagagcgg atgttgtcat gaaatttcaa ttcactagaa 420
 ataacaatgg agcatcaatg aaaagcagaa ttgagtctgt tttacgacaa atgctgaata 480
 actctggaaa cctggaaata aacccttcaa ctgagataac atcacttact gaccaggctg 540
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 agagaatcct tggaggcact gaggtgagg agggaagctg gccgtggcaa gtcagtctgc 660
 ggctcaataa tgcccaccac tgtggaggca gcctgatcaa taacatgtgg atcctgacag 720
 cagctcactg cttcagaagc aactctaate ctcgtgactg gattgccacg tctggtattt 780
 ccacaacatt tcctaaacta agaattagag taagaaatat tttaattcat aacaattata 840
 aatctgcaac tcatgaaaat gacattgcac ttgtgagact tgagaacagt gtcaccttta 900
 ccaaagatat ccatagtgtg tgtctccag ctgctaccca gaatattcca cctggctcta 960

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ctgcttatgt aacaggatgg ggcgctcaag aatatgctgg ccacacagtt ccagagctaa 1020
ggcaaggaca ggtcagaata ataagtaatg atgtatgtaa tgcaccacat agttataatg 1080
gagccatctt gtctggaatg ctgtgtgctg gagtacctca aggtggagtg gacgcatgtc 1140
agggtgactc tgggtggcca ctagtacaag aagactcacg gcggctttgg tttattgtgg 1200
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ctgttgcaaa gtctgtatgc aggtgtgcct gtcttaaatt ccaaagcttt acatttcaac 1380
tgaaaaagaa actagaaatg tctaatttta acatcttggt acataaatat ggtttaacaa 1440
aaaaaaaaa aaaaaactcg ag 1462

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<210> 56
 <211> 159
 <212> PRT
 <213> Homo sapien

<400> 56

Thr	Met	Tyr	Arg	Ala	Leu	Arg	Leu	Leu	Ala	Arg	Ser	Arg	Pro	Leu	Val
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Arg	Ala	Pro	Ala	Ala	Ala	Leu	Ala	Ser	Ala	Pro	Gly	Leu	Gly	Gly	Ala
			20					25					30		
Ala	Val	Pro	Ser	Phe	Trp	Pro	Pro	Asn	Ala	Ala	Arg	Met	Ala	Ser	Gln
			35				40					45			
Asn	Ser	Phe	Arg	Ile	Glu	Tyr	Asp	Thr	Phe	Gly	Glu	Leu	Lys	Val	Pro
			50			55					60				
Asn	Asp	Lys	Tyr	Tyr	Gly	Ala	Gln	Thr	Val	Arg	Ser	Thr	Met	Asn	Phe
65					70					75				80	
Lys	Ile	Gly	Gly	Val	Thr	Glu	Arg	Met	Pro	Thr	Pro	Val	Ile	Lys	Ala
				85					90					95	
Phe	Gly	Ile	Leu	Lys	Arg	Ala	Ala	Ala	Glu	Val	Asn	Gln	Asp	Tyr	Gly
			100					105					110		
Leu	Asp	Pro	Lys	Ile	Ala	Asn	Ala	Ile	Met	Lys	Ala	Ala	Asp	Glu	Val
			115				120						125		
Ala	Glu	Gly	Lys	Leu	Asn	Asp	His	Phe	Pro	Leu	Val	Val	Trp	Gln	Thr
			130				135					140			
Gly	Ser	Gly	Thr	Gln	Thr	Asn	Met	Asn	Val	Asn	Glu	Val	Ile	Ser	
145					150					155					

<210> 57
 <211> 165
 <212> PRT
 <213> Homo sapien

<400> 57

Lys	Lys	Ser	Met	Phe	Ala	Glu	Ile	Gln	Ile	Gln	Asp	Lys	Asp	Arg	Met
1				5					10					15	
Gly	Thr	Ala	Gly	Lys	Val	Ile	Lys	Cys	Lys	Ala	Ala	Val	Leu	Trp	Glu
			20					25					30		
Gln	Lys	Gln	Pro	Phe	Ser	Ile	Glu	Glu	Ile	Glu	Val	Ala	Pro	Pro	Lys
			35				40					45			
Thr	Lys	Glu	Val	Arg	Ile	Lys	Ile	Leu	Ala	Thr	Gly	Ile	Cys	Arg	Thr
			50			55					60				
Asp	Asp	His	Val	Ile	Lys	Gly	Thr	Met	Val	Ser	Lys	Phe	Pro	Val	Ile
65					70					75				80	
Val	Gly	His	Glu	Ala	Thr	Gly	Ile	Val	Glu	Ser	Ile	Gly	Glu	Gly	Val
			85					90					95		
Thr	Thr	Val	Lys	Pro	Gly	Asp	Lys	Val	Ile	Pro	Leu	Phe	Leu	Pro	Gln
			100					105					110		
Cys	Arg	Glu	Cys	Asn	Ala	Cys	Arg	Asn	Pro	Asp	Gly	Asn	Leu	Cys	Ile

115 120 125
 Arg Ser Asp Ile Thr Gly Arg Gly Val Leu Ala Asp Gly Thr Thr Arg
 130 135 140
 Phe Thr Cys Lys Gly Glu Pro Val His His Phe Met Asn Thr Ser Thr
 145 150 155 160
 Phe Thr Glu Tyr Thr
 165

<210> 58
 <211> 259
 <212> PRT
 <213> Homo sapien

<400> 58
 Glu Ser Glu Gln Lys Gly Lys Ala Ala Leu Ala Ala Thr Leu Glu Glu
 1 5 10 15
 Tyr Lys Ala Thr Val Ala Ser Asp Gln Ile Glu Met Asn Arg Leu Lys
 20 25 30
 Ala Gln Leu Glu Asn Glu Lys Gln Lys Val Ala Glu Leu Tyr Ser Ile
 35 40 45
 His Asn Ser Gly Asp Lys Ser Asp Ile Gln Asp Leu Leu Glu Ser Val
 50 55 60
 Arg Leu Asp Lys Glu Lys Ala Glu Thr Leu Ala Ser Ser Leu Gln Glu
 65 70 75 80
 Asp Leu Ala His Thr Arg Asn Asp Ala Asn Arg Leu Gln Asp Ala Ile
 85 90 95
 Ala Lys Val Glu Asp Glu Tyr Arg Ala Phe Gln Glu Glu Ala Lys Lys
 100 105 110
 Gln Ile Glu Asp Leu Asn Met Thr Leu Glu Lys Leu Arg Ser Asp Leu
 115 120 125
 Asp Glu Lys Glu Thr Glu Arg Ser Asp Met Lys Glu Thr Ile Phe Glu
 130 135 140
 Leu Glu Asp Glu Val Glu Gln His Arg Ala Val Lys Leu His Asp Asn
 145 150 155 160
 Leu Ile Ile Ser Asp Leu Glu Asn Thr Val Lys Lys Leu Gln Asp Gln
 165 170 175
 Lys His Asp Met Glu Arg Glu Ile Lys Thr Leu His Arg Arg Leu Arg
 180 185 190
 Glu Glu Ser Ala Glu Trp Arg Gln Phe Gln Ala Asp Leu Gln Thr Ala
 195 200 205
 Val Val Ile Ala Asn Asp Ile Lys Ser Glu Ala Gln Glu Glu Ile Gly
 210 215 220
 Asp Leu Lys Arg Arg Leu His Glu Ala Gln Glu Lys Asn Glu Lys Leu
 225 230 235 240
 Thr Lys Glu Leu Glu Glu Ile Lys Ser Arg Lys Gln Glu Glu Glu Arg
 245 250 255
 Gly Gly Tyr

<210> 59
 <211> 125
 <212> PRT
 <213> Homo sapien

<400> 59
 Gly Thr Ser Phe Ser Lys Asn His Ala Ala Pro Phe Ser Lys Val Leu
 1 5 10 15
 Thr Phe Tyr Arg Lys Glu Pro Phe Thr Leu Glu Ala Tyr Tyr Ser Ser

20				25				30							
Pro	Gln	Asp	Leu	Pro	Tyr	Pro	Asp	Pro	Ala	Ile	Ala	Gln	Phe	Ser	Val
35				40				45							
Gln	Lys	Val	Thr	Pro	Gln	Ser	Asp	Gly	Ser	Ser	Ser	Lys	Val	Lys	Val
50				55				60							
Lys	Val	Arg	Val	Asn	Val	His	Gly	Ile	Phe	Ser	Val	Ser	Ser	Ala	Ser
65				70				75				80			
Leu	Val	Glu	Val	His	Lys	Ser	Glu	Glu	Asn	Glu	Glu	Pro	Met	Glu	Thr
85				90				95				100			
Asp	Gln	Asn	Ala	Lys	Glu	Glu	Glu	Lys	Met	Gln	Val	Asp	Gln	Glu	Glu
100				105				110							
Pro	His	Val	Glu	Glu	Gln	Gln	Gln	Thr	Pro	Gly	Arg				
115				120				125							

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<210> 60
<211> 246
<212> PRT
<213> Homo sapien
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[illegible]

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<210> 61
<211> 128
<212> PRT
<213> Homo sapien
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<400> 61

Gly Ile Phe Ser Val Ser Ser Ala Ser Leu Val Glu Val His Lys Ser
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 Glu Glu Asn Glu Glu Pro Met Glu Thr Asp Gln Asn Ala Lys Glu Glu
 20 25 30
 Glu Lys Met Gln Val Asp Gln Glu Glu Pro His Val Glu Glu Gln Gln
 35 40 45
 Gln Gln Thr Pro Ala Glu Asn Lys Ala Glu Ser Glu Glu Met Glu Thr
 50 55 60
 Ser Gln Ala Gly Ser Lys Asp Lys Lys Met Asp Gln Pro Pro Gln Ala
 65 70 75 80
 Lys Lys Ala Lys Val Lys Thr Ser Thr Val Asp Leu Pro Ile Glu Asn
 85 90 95
 Gln Leu Leu Trp Gln Ile Asp Arg Glu Met Leu Asn Leu Tyr Ile Glu
 100 105 110
 Asn Glu Gly Lys Met Ile Met Gln Asp Lys Leu Glu Lys Glu Arg Asn
 115 120 125

<210> 62

<211> 418

<212> PRT

<213> Homo sapien

<400> 62

Met Tyr Arg Pro Ala Arg Val Thr Ser Thr Ser Arg Phe Leu Asn Pro
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 Tyr Val Val Cys Phe Ile Val Val Ala Gly Val Val Ile Leu Ala Val
 20 25 30
 Thr Ile Ala Leu Leu Val Tyr Phe Leu Ala Phe Asp Gln Lys Ser Tyr
 35 40 45
 Phe Tyr Arg Ser Ser Phe Gln Leu Leu Asn Val Glu Tyr Asn Ser Gln
 50 55 60
 Leu Asn Ser Pro Ala Thr Gln Glu Tyr Arg Thr Leu Ser Gly Arg Ile
 65 70 75 80
 Glu Ser Leu Ile Thr Lys Thr Phe Lys Glu Ser Asn Leu Arg Asn Gln
 85 90 95
 Phe Ile Arg Ala His Val Ala Lys Leu Arg Gln Asp Gly Ser Gly Val
 100 105 110
 Arg Ala Asp Val Val Met Lys Phe Gln Phe Thr Arg Asn Asn Asn Gly
 115 120 125
 Ala Ser Met Lys Ser Arg Ile Glu Ser Val Leu Arg Gln Met Leu Asn
 130 135 140
 Asn Ser Gly Asn Leu Glu Ile Asn Pro Ser Thr Glu Ile Thr Ser Leu
 145 150 155 160
 Thr Asp Gln Ala Ala Ala Asn Trp Leu Ile Asn Glu Cys Gly Ala Gly
 165 170 175
 Pro Asp Leu Ile Thr Leu Ser Glu Gln Arg Ile Leu Gly Gly Thr Glu
 180 185 190
 Ala Glu Glu Gly Ser Trp Pro Trp Gln Val Ser Leu Arg Leu Asn Asn
 195 200 205
 Ala His His Cys Gly Gly Ser Leu Ile Asn Asn Met Trp Ile Leu Thr
 210 215 220
 Ala Ala His Cys Phe Arg Ser Asn Ser Asn Pro Arg Asp Trp Ile Ala
 225 230 235 240
 Thr Ser Gly Ile Ser Thr Thr Phe Pro Lys Leu Arg Met Arg Val Arg
 245 250 255
 Asn Ile Leu Ile His Asn Asn Tyr Lys Ser Ala Thr His Glu Asn Asp
 260 265 270

Ile Ala Leu Val Arg Leu Glu Asn Ser Val Thr Phe Thr Lys Asp Ile
 275 280 285
 His Ser Val Cys Leu Pro Ala Ala Thr Gln Asn Ile Pro Pro Gly Ser
 290 295 300
 Thr Ala Tyr Val Thr Gly Trp Gly Ala Gln Glu Tyr Ala Gly His Thr
 305 310 315 320
 Val Pro Glu Leu Arg Gln Gly Gln Val Arg Ile Ile Ser Asn Asp Val
 325 330 335
 Cys Asn Ala Pro His Ser Tyr Asn Gly Ala Ile Leu Ser Gly Met Leu
 340 345 350
 Cys Ala Gly Val Pro Gln Gly Gly Val Asp Ala Cys Gln Gly Asp Ser
 355 360 365
 Gly Gly Pro Leu Val Gln Glu Asp Ser Arg Arg Leu Trp Phe Ile Val
 370 375 380
 Gly Ile Val Ser Trp Gly Asp Gln Cys Gly Leu Pro Asp Lys Pro Gly
 385 390 395 400
 Val Tyr Thr Arg Val Thr Ala Tyr Ile Asp Trp Ile Arg Gln Gln Thr
 405 410 415
 Gly Ile

<210> 63
 <211> 776
 <212> DNA
 <213> Homo sapien

<400> 63
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 aggcagtagc agtggatcgg gccagaagg aggcagctga gaaggaacag gaacttttaa 120
 aacagaaatt acaggagcag ccagcaacag atggaggctc aagataagag tcgcaaggaa 180
 aactagccaa ctgaaggaga agctgcagat ggagagagaa cacctactga gagagcagat 240
 tatgatgttg gagcacacgc agaagggtcca aaatgatttg cttcatgaag gatttaagaa 300
 gaagtatgag gagatgaatg cagagataag tcaattttaa cgtatgattg atactacaaa 360
 aaatgatgat actccctgga ttgcacgaac cttggacaac cttgccgatg agctaactgc 420
 aatattgtct gctcctgcta aattaatttg tcatggtgtc aaagggtgtga gctcactctt 480
 taaaaagcat aagctcccct tttaaggata ttatagattg tacatatatg ctttggacta 540
 tttttgatct gtatgttttt cattttcatt cagcaagttt tttttttttt tcagagtctt 600
 actctgttgc ccaggctgga gtacagtggt gcaatctcag ctcactgcaa cctctgcctc 660
 ctgggttcaa gagattcacc tgcctcagcc ccctagtagc tgggattata ggtgtacacc 720
 accacacca gctaattttt gtatttttag tagagatggg gtttcactat gttggc 776

<210> 64
 <211> 160
 <212> DNA
 <213> Homo sapien

<400> 64
 gcagcgctct cggttgcagt acccactgga aggacttagg cgctcgcgtg gacaccgcaa 60
 gccctcagt agcctcggcc caagaggcct gctttccact cgctagcccc gccgggggtc 120
 cgtgtcctgt ctcggtggcc ggacccgggc ccgagccga 160

<210> 65
 <211> 72
 <212> PRT
 <213> Homo sapien

<400> 65
 Leu Ser Ala Met Gly Phe Thr Ala Ala Gly Ile Ala Ser Ser Ser Ile

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<210> 66
<211> 2581
<212> DNA
<213> Homo sapien
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<400> 66

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gctggacagc	tggaggatga	acggagaagc	cgactgcccc	acagacctgg	aaatggcccg	180
ccccaaaggc	caagaccgtt	ggtcccagga	agacatgctg	acttttgc	aatgcatgaa	240
gaacaacctt	ccatccaatg	acagctccaa	gttcaaaacc	accgaatcac	acatggactg	300
ggaaaaagta	gcattttaaag	acttttctgg	agacatgtgc	aagctcaa	gggtggagat	360
ttctaagt	gtgaggaagt	tccgtacact	gacagaattg	atcctcgatg	ctcaggaaca	420
tgttaaaaat	ccttacaagg	gcaaaaacc	caagaacac	ccagacttcc	caaagaagcc	480
cctgaccctt	tatttccgct	tcttcatgga	gaagcgccc	aagtatcgga	aactccaccc	540
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gaagaagaag	atgaaatata	ttcaggactt	ccagagagag	aaacaggagt	tcgagcgaaa	660
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cgaggaacgg	ggcaagctgc	ccgagtcctc	caaaagagct	gaggagatct	ggcaacagag	1620
cgttatcggc	gactacctgg	cccgttcaa	gaatgaccgg	gtgaaggcct	tgaagccat	1680
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agaagaccaa	aagcgatatg	agagagagct	gagtggatg	cgggcaacctc	cagctgctac	1800
caaattcttcc	aagaagatga	aattccaggg	agaacccaag	aagcctccca	tgaacggtta	1860
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caaaaagctg	gccgaggagc	agcaaaagca	gtacaagggtg	cacctggacc	tctgggttaa	2040
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catgaccaag	ctgcgaggcc	caaaccccaa	atccagccgg	actactctgc	agtccaagtc	2160
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aggggactcc	tcagactttg	actccaactg	aggcttagcc	ccacccaggg	ggagccaggg	2460
agagcccagg	agctcccctc	cccaactgac	cacctttgtt	tcttccccat	gttctgtccc	2520

ttgccccctt ggcctcccc actttctttt tttctttaaa aaaaaaaaaa aaaaactcga 2580
g 2581

<210> 67
<211> 764
<212> PRT
<213> Homo sapien

<400> 67
Met Asn Gly Glu Ala Asp Cys Pro Thr Asp Leu Glu Met Ala Ala Pro
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Lys Gly Gln Asp Arg Trp Ser Gln Glu Asp Met Leu Thr Leu Leu Glu
20 25 30
Cys Met Lys Asn Asn Leu Pro Ser Asn Asp Ser Ser Lys Phe Lys Thr
35 40 45
Thr Glu Ser His Met Asp Trp Glu Lys Val Ala Phe Lys Asp Phe Ser
50 55 60
Gly Asp Met Cys Lys Leu Lys Trp Val Glu Ile Ser Asn Glu Val Arg
65 70 75 80
Lys Phe Arg Thr Leu Thr Glu Leu Ile Leu Asp Ala Gln Glu His Val
85 90 95
Lys Asn Pro Tyr Lys Gly Lys Lys Leu Lys Lys His Pro Asp Phe Pro
100 105 110
Lys Lys Pro Leu Thr Pro Tyr Phe Arg Phe Phe Met Glu Lys Arg Ala
115 120 125
Lys Tyr Ala Lys Leu His Pro Glu Met Ser Asn Leu Asp Leu Thr Lys
130 135 140
Ile Leu Ser Lys Lys Tyr Lys Glu Leu Pro Glu Lys Lys Lys Met Lys
145 150 155 160
Tyr Ile Gln Asp Phe Gln Arg Glu Lys Gln Glu Phe Glu Arg Asn Leu
165 170 175
Ala Arg Phe Arg Glu Asp His Pro Asp Leu Ile Gln Asn Ala Lys Lys
180 185 190
Ser Asp Ile Pro Glu Lys Pro Lys Thr Pro Gln Gln Leu Trp Tyr Thr
195 200 205
His Glu Lys Lys Val Tyr Leu Lys Val Arg Pro Asp Ala Thr Thr Lys
210 215 220
Glu Val Lys Asp Ser Leu Gly Lys Gln Trp Ser Gln Leu Ser Asp Lys
225 230 235 240
Lys Arg Leu Lys Trp Ile His Lys Ala Leu Glu Gln Arg Lys Glu Tyr
245 250 255
Glu Glu Ile Met Arg Asp Tyr Ile Gln Lys His Pro Glu Leu Asn Ile
260 265 270
Ser Glu Glu Gly Ile Thr Lys Ser Thr Leu Thr Lys Ala Glu Arg Gln
275 280 285
Leu Lys Asp Lys Phe Asp Gly Arg Pro Thr Lys Pro Pro Pro Asn Ser
290 295 300
Tyr Ser Leu Tyr Cys Ala Glu Leu Met Ala Asn Met Lys Asp Val Pro
305 310 315 320
Ser Thr Glu Arg Met Val Leu Cys Ser Gln Gln Trp Lys Leu Leu Ser
325 330 335
Gln Lys Glu Lys Asp Ala Tyr His Lys Lys Cys Asp Gln Lys Lys Lys
340 345 350
Asp Tyr Glu Val Glu Leu Leu Arg Phe Leu Glu Ser Leu Pro Glu Glu
355 360 365
Glu Gln Arg Val Leu Gly Glu Glu Lys Met Leu Asn Ile Asn Lys
370 375 380
Lys Gln Ala Thr Ser Pro Ala Ser Lys Lys Pro Ala Gln Glu Gly Gly

385 390 395 400
 Lys Gly Gly Ser Glu Lys Pro Lys Arg Pro Val Ser Ala Met Phe Ile
 405 410 415
 Phe Ser Glu Glu Lys Arg Arg Gln Leu Gln Glu Glu Arg Pro Glu Leu
 420 425 430
 Ser Glu Ser Glu Leu Thr Arg Leu Leu Ala Arg Met Trp Asn Asp Leu
 435 440 445
 Ser Glu Lys Lys Lys Ala Lys Tyr Lys Ala Arg Glu Ala Ala Leu Lys
 450 455 460
 Ala Gln Ser Glu Arg Lys Pro Gly Gly Glu Arg Glu Glu Arg Gly Lys
 465 470 475 480
 Leu Pro Glu Ser Pro Lys Arg Ala Glu Glu Ile Trp Gln Gln Ser Val
 485 490 495
 Ile Gly Asp Tyr Leu Ala Arg Phe Lys Asn Asp Arg Val Lys Ala Leu
 500 505 510
 Lys Ala Met Glu Met Thr Trp Asn Asn Met Glu Lys Lys Glu Lys Leu
 515 520 525
 Met Trp Ile Lys Lys Ala Ala Glu Asp Gln Lys Arg Tyr Glu Arg Glu
 530 535 540
 Leu Ser Glu Met Arg Ala Pro Pro Ala Ala Thr Asn Ser Ser Lys Lys
 545 550 555 560
 Met Lys Phe Gln Gly Glu Pro Lys Lys Pro Pro Met Asn Gly Tyr Gln
 565 570 575
 Lys Phe Ser Gln Glu Leu Leu Ser Asn Gly Glu Leu Asn His Leu Pro
 580 585 590
 Leu Lys Glu Arg Met Val Glu Ile Gly Ser Arg Trp Gln Arg Ile Ser
 595 600 605
 Gln Ser Gln Lys Glu His Tyr Lys Lys Leu Ala Glu Glu Gln Gln Lys
 610 615 620
 Gln Tyr Lys Val His Leu Asp Leu Trp Val Lys Ser Leu Ser Pro Gln
 625 630 635 640
 Asp Arg Ala Ala Tyr Lys Glu Tyr Ile Ser Asn Lys Arg Lys Ser Met
 645 650 655
 Thr Lys Leu Arg Gly Pro Asn Pro Lys Ser Ser Arg Thr Thr Leu Gln
 660 665 670
 Ser Lys Ser Glu Ser Glu Glu Asp Asp Glu Glu Asp Glu Asp Asp Glu
 675 680 685
 Asp Glu Asp Glu Glu Glu Glu Asp Asp Glu Asn Gly Asp Ser Ser Glu
 690 695 700
 Asp Gly Gly Asp Ser Ser Glu Ser Ser Ser Glu Asp Glu Ser Glu Asp
 705 710 715 720
 Gly Asp Glu Asn Glu Glu Asp Asp Glu Asp Glu Asp Asp Asp Glu Asp
 725 730 735
 Asp Asp Glu Asp Glu Asp Asn Glu Ser Glu Gly Ser Ser Ser Ser Ser
 740 745 750
 Ser Ser Leu Gly Asp Ser Ser Asp Phe Asp Ser Asn
 755 760

<210> 68
 <211> 434
 <212> DNA
 <213> Homo sapien

<400> 68
 ctaagatgct ggatgctgaa gacatcgctc gaactgcccg gccagatgag aaagccatta 60
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 ccaatcgcat ctgcaaagtg ttggcggtca atcaagagaa cgagcagctt atggaagact 180
 atgagaagct ggccagtgat ctgttgagtg ggatccgccg caccatccca tggctggaga 240

atcgggtgcc	tgagaacacc	atgcatgcca	tgcagcagaa	gctggaggac	ttccgagact	300
atagacgcct	gcacaagccg	cccaagggtg	aggagaaatg	ccagctggag	atcaacttta	360
acacgctgca	gaccaaactg	cggtcagca	accggcctgc	cttcattgcc	tccgagggca	420
ggatggtctc	ggat					434

<210> 69

<211> 244

<212> DNA

<213> Homo sapien

<400> 69

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acactgcgga	aggccgcagg	gtcctctgcc	taggaaaaac	agagaccttt	gttcaactgt	120
ttatgtgtg	accttccctc	cactattgtc	ctgtgacct	gccaaatccc	cctttgtgag	180
aaacacccaa	gaatgatcaa	taaaaataa	attaatttag	gaaaaaaaaa	aaaaaaaact	240
cgag						244

<210> 70

<211> 437

<212> DNA

<213> Homo sapien

<400> 70

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cttggtcctt	ggatccagcg	tccggccagcc	cagagcccgt	gccgcacatc	cttgcgtcct	120
ccaggcagtg	ggaccccgcg	agctgcacgt	ccctgggcac	ggacaagtgt	gaggcactgt	180
tggggctgtg	ccaggtgcgg	ggtgggctgc	cccctttctc	agaaccttcc	agcctggtgc	240
cgtggccccc	aggccggagt	cttcctaagg	ctgtgaggcc	acctctgtcc	tggcctccgt	300
tctgcagca	gcagaccttg	cccgtgatga	gcggggaggc	ccttggtctg	ctggggccagg	360
ctggttcctt	ggccatgggg	gctgcacctc	tgggggagcc	agccaaggag	gaccccatgc	420
tggcgaggga	agccggg					437

<210> 71

<211> 271

<212> DNA

<213> Homo sapien

<400> 71

gcgcagagtt	ctgtcgtcca	ccatcgagtg	aggaagagag	cattggttcc	cctgagatag	60
aagagatggc	tctcttcagt	gcccagtcct	catacattaa	cccgatcatc	ccctttactg	120
gaccaatcca	aggagggtcg	caggaggagc	ttcaggtgac	cctccagggg	actaccgaga	180
gttttgca	aaagtgtgtg	gtgaactttt	cagaacagct	tcaatggaga	tgacttggcc	240
ttccacttca	accccgttta	tgaggaagga	g			271

<210> 72

<211> 290

<212> DNA

<213> Homo sapien

<400> 72

ccgagcccta	cccggaggtc	tccagaatcc	ccaccgtcag	gggatgcaac	ggctccctgt	60
ctggtgccct	ctcctgtctg	gaggactcgg	cccagggctc	gggcccggcc	aaggccccta	120
cggtggccga	gggtcccagc	tctgccttc	ggcggaacgt	gatcagcgag	agggagcgca	180
ggaagcggat	gtcgttgagc	tgtgagcgtc	tgcgggccct	gctgccccag	ttcgatggcc	240
ggcgggagga	catggcctcg	gtcctggaga	tgtctgttgc	aattcctgcg		290

<210> 73

<211> 144

<212> PRT

<213> Homo sapien

<400> 73

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Lys Met Leu Asp Ala Glu Asp Ile Val Gly Thr Ala Arg Pro Asp Glu
 1           5           10           15
Lys Ala Ile Met Thr Tyr Val Ser Ser Phe Tyr His Ala Phe Ser Gly
           20           25           30
Ala Gln Lys Ala Glu Thr Ala Ala Asn Arg Ile Cys Lys Val Leu Ala
           35           40           45
Val Asn Gln Glu Asn Glu Gln Leu Met Glu Asp Tyr Glu Lys Leu Ala
           50           55           60
Ser Asp Leu Leu Glu Trp Ile Arg Arg Thr Ile Pro Trp Leu Glu Asn
65           70           75           80
Arg Val Pro Glu Asn Thr Met His Ala Met Gln Gln Lys Leu Glu Asp
           85           90           95
Phe Arg Asp Tyr Arg Arg Leu His Lys Pro Pro Lys Val Gln Glu Lys
           100          105          110
Cys Gln Leu Glu Ile Asn Phe Asn Thr Leu Gln Thr Lys Leu Arg Leu
           115          120          125
Ser Asn Arg Pro Ala Phe Met Pro Ser Glu Gly Arg Met Val Ser Asp
130          135          140

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<210> 74

<211> 64

<212> PRT

<213> Homo sapien

<400> 74

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Gly Ser Met Leu Val Glu Ser His His His Ser Leu Ile Ser Ser Thr
 1           5           10           15
Gln Gly His Lys His Cys Gly Arg Pro Gln Gly Pro Leu Pro Arg Lys
           20           25           30
Thr Arg Asp Leu Cys Ser Leu Val Tyr Val Leu Thr Phe Pro Pro Leu
           35           40           45
Leu Ser Cys Asp Pro Ala Lys Ser Pro Phe Val Arg Asn Thr Gln Glu
50           55           60

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<210> 75

<211> 145

<212> PRT

<213> Homo sapien

<400> 75

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Gly Thr Gly Ala Ser Ser Gly Thr Arg Thr Pro Asp Val Lys Ala Phe
 1           5           10           15
Leu Glu Ser Pro Trp Ser Leu Asp Pro Ala Ser Ala Ser Pro Glu Pro
           20           25           30
Val Pro His Ile Leu Ala Ser Ser Arg Gln Trp Asp Pro Ala Ser Cys
           35           40           45
Thr Ser Leu Gly Thr Asp Lys Cys Glu Ala Leu Leu Gly Leu Cys Gln
50           55           60
Val Arg Gly Gly Leu Pro Pro Phe Ser Glu Pro Ser Ser Leu Val Pro
65           70           75           80
Trp Pro Pro Gly Arg Ser Leu Pro Lys Ala Val Arg Pro Pro Leu Ser
           85           90           95
Trp Pro Pro Phe Ser Gln Gln Gln Thr Leu Pro Val Met Ser Gly Glu
100          105          110

```

Ala Leu Gly Trp Leu Gly Gln Ala Gly Ser Leu Ala Met Gly Ala Ala
 115 120 125
 Pro Leu Gly Glu Pro Ala Lys Glu Asp Pro Met Leu Ala Gln Glu Ala
 130 135 140
 Gly
 145

<210> 76
 <211> 69
 <212> PRT
 <213> Homo sapien

<400> 76
 Ala Glu Phe Cys Arg Pro Pro Ser Ser Glu Glu Glu Ser Ile Gly Ser
 1 5 10 15
 Pro Glu Ile Glu Glu Met Ala Leu Phe Ser Ala Gln Ser Pro Tyr Ile
 20 25 30
 Asn Pro Ile Ile Pro Phe Thr Gly Pro Ile Gln Gly Gly Leu Gln Glu
 35 40 45
 Gly Leu Gln Val Thr Leu Gln Gly Thr Thr Glu Ser Phe Ala Gln Lys
 50 55 60
 Phe Val Val Asn Phe
 65

<210> 77
 <211> 96
 <212> PRT
 <213> Homo sapien

<400> 77
 Glu Pro Tyr Pro Glu Val Ser Arg Ile Pro Thr Val Arg Gly Cys Asn
 1 5 10 15
 Gly Ser Leu Ser Gly Ala Leu Ser Cys Glu Asp Ser Ala Gln Gly
 20 25 30
 Ser Gly Pro Pro Lys Ala Pro Thr Val Ala Glu Gly Pro Ser Ser Cys
 35 40 45
 Leu Arg Arg Asn Val Ile Ser Glu Arg Glu Arg Arg Lys Arg Met Ser
 50 55 60
 Leu Ser Cys Glu Arg Leu Arg Ala Leu Leu Pro Gln Phe Asp Gly Arg
 65 70 75 80
 Arg Glu Asp Met Ala Ser Val Leu Glu Met Ser Val Ala Ile Pro Ala
 85 90 95

<210> 78
 <211> 2076
 <212> DNA
 <213> Homo sapien

<400> 78
 agaaaaagtc tatgtttgca gaaatacaga tccaagacaa agacaggatg ggcactgctg 60
 gaaaagtatt taaatgcaaa gcagctgtgc. tttgggagca gaagcaaccc ttctccattg 120
 aggaaataga agttgcccc ccaaagacta aagaagttcg cattaagatt ttggccacag 180
 gaatctgtcg cacagatgac catgtgataa aaggaacaat ggtgtccaag tttccagtga 240
 ttgtgggaca tgaggcaact gggattgtag agagcatttg agaaggagtg actacagtga 300
 aaccagggtga caaagtcac cctctctttc tgccacaatg tagagaatgc aatgcttgctc 360
 gcaaccaga tggcaacctt tgcattagga gcgatattac tggtcgtgga gtactggctg 420
 atggcaccac cagatttaca tgcaaggga aaccagtcca ccacttcattg aacaccagta 480
 catttaccga gtacacagtg gtggatgaat cttctgttgc taagattgat gatgcagctc 540

ctcctgagaa	agtctgttta	attggctgtg	ggttttccac	tggatatggc	gctgctgtta	600
aaactggcaa	gggtcaaacc	ggttccactt	gcgtcgtctt	tggcctgaga	ggagttggcc	660
tgtcagtcac	catgggctgt	aagtcagctg	gtgcatctag	gatcattggg	attgaacctca	720
acaaagacaa	atttgagaag	gccatggctg	taggtgccac	tgagtgtatc	agtcaccaagg	780
actctaccac	acccatcagt	gaggtgctgt	cagaaatgac	aggcaacaac	gtgggataca	840
cctttgaagt	tattgggcat	cttgaaacca	tgattgatgc	cctggcatcc	tgccacatga	900
actatgggac	cagcgtgggt	gtaggagtgc	ctccatcagc	caagatgctc	acctatgacc	960
cgatgttgct	cttcaactgga	cgacatgga	agggatgtgt	ctttggaggt	ttgaaaagca	1020
gagatgatgt	cccaaaacta	gtgactgagt	tcttggtgaga	gaaatttgac	ctggaccagt	1080
tgataactca	tgtcttacca	tttaaaaaaa	tcaagtgaagg	atttgagctg	ctcaattcag	1140
gacaaagcat	tcgaacgggc	ctgacgtttt	gagatccaaa	gtggcaggag	gtctgtgttg	1200
tcattggtgaa	ctggagtttc	tcttgtgaga	gttccctcat	ctgaaatcat	gtatctgtct	1260
cacaaataga	agcataagta	gaagatttgt	tgaagacata	gaacccttat	aaagaattat	1320
taacctttat	aaacatttaa	agtcttgtga	gcacctggga	attagtataa	taacaatgtt	1380
aatttttttg	atttacattt	tgttaaggcta	taattgtatc	ttttaagaaa	acatacactt	1440
ggattttctat	gttgaaatgg	agatttttaa	gagttttaac	cagctgctgc	agatatatat	1500
ctcaaaacag	atatagcgta	taaagatata	gtaaatgcat	ctcctagagt	aattattcact	1560
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tagattaaga	aagacagaaa	agattaaggg	acgggcacat	ttttcaacga	ttagaatca	1740
tcattacata	acttgggtgaa	actgaaaaag	tatatcatat	gggtacacaa	ggctatttgc	1800
cagcatatat	taatatttta	gaaaatatct	cttttghtat	actgaatata	aacatagagc	1860
tagaatcata	ttatcatact	tatcataatg	ttcaatttga	tacagtagaa	ttgcaagtcc	1920
tttaagtccct	attcactgtg	cttagtagtg	actccattta	ataaaaagtg	tttttagttt	1980
ttacaacta	cactgatgta	tttatatata	tttataacat	gttaaaaatt	tttaaggaaa	2040
ttaaaaatta	tataaaaaaa	aaaaaaaaaa	ctcggag			2076

<210> 79

<211> 2790

<212> DNA

<213> Homo sapien

<400> 79

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cacgtgtaac	ttcgacttca	agattttctga	atccatatgt	agtatgtttc	attgtcgtcg	120
caggggtagt	gatcctggca	gtcaccatag	ctctacttgt	ttacttttta	gcttttgatc	180
aaaaatctta	cttttatagg	agcagttttc	aactcctaaa	tgttgaatat	aatagtcagt	240
taaattcacc	agctacacag	gaatacagga	ctttgagtg	aagaattgaa	tctctgatta	300
ctaaaacatt	caaagaatca	aatttaagaa	atcagttcat	cagagctcat	gttgccaaac	360
tgaggcaaga	tggtagtgg	gtgagagcgg	atgttgtcat	gaaatttcaa	ttcactagaa	420
ataacaatgg	agcatcaatg	aaaagcagaa	ttgagtctgt	ttacgcacaa	atgctgaata	480
actctggaac	cctggaaata	aacccttcaa	ctgagataac	atcacttact	gaccaggctg	540
cagcaaattg	gcttattaat	gaatgtgggg	ccgggtccaga	cctaataaca	ttgtctgagc	600
agagaatcct	tggaggcact	gaggctgagg	agggaagctg	gccgtggcaa	gtcagtcctgc	660
ggctcaataa	tgcccaccac	tgtggaggca	gcctgatcaa	taacatgtgg	atcctgacag	720
cagctcactg	cttcagaagc	aactctaate	ctcgtgactg	gattgccacg	tctggtattt	780
ccacaacatt	tcctaaacta	agaatgagag	taagaaatat	tttaattcat	aacaattata	840
aactgtcaac	tcattgaaaat	gacattgcac	ttgtgagact	tgagaacagt	gtcaccttta	900
ccaaagatat	ccatagtgtg	tgtctcccag	ctgctaccca	gaatattcca	cctggctcta	960
ctgcttatgt	aacaggatgg	ggcgctcaag	aatatgctgg	ccacacagtt	ccagagctaa	1020
ggcaaggaca	ggtcagaata	ataagtaatg	atgtatgtaa	tgaccacat	agttataatg	1080
gagccatctt	gtctggaatg	ctgtgtgctg	gagtacctca	aggtggagtg	gacgcatgtc	1140
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ggatagtaag	ctggggagat	cagtggtggc	tgccggataa	gccaggagtg	tatactcgag	1260
tgacagccta	ccttgactgg	attaggcaac	aaactgggat	ctagtgcaac	aagtgcaccc	1320
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acactgttta	acctttcttt	attattaaag	gttttctatt	ttctccagag	aactatatga	1500

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acatagtact	ttttaacaac	aaaataataa	ttttaagaat	gaaaaattta	atcatcgagg	2160
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gcactcaggac	tgctccatac	atttgctgaa	aacttcttgt	atttctctgat	gtaaaattgt	2640
gcaaacacct	acaataaaagc	catctacttt	tagggaaagg	gagttgaaaa	tgcaaccaac	2700
tcttgcgcaa	ctgtacaaac	aaatctttgc	tatactttat	ttcaaataaa	ttctttttga	2760
aatgaaaaaa	aaaaaaaaaa	aaaactcgag				2790

<210> 80
 <211> 1460
 <212> DNA
 <213> Homo sapien

ctcaaagcag	ttgagtaggc	agaaaaaaga	acctcttcat	taaggattaa	aatgtatagg	60
ccagcacgtg	taacttcgac	ttcaagattt	ctgaatccat	atgtagtatg	tttcattgtc	120
gtcgcagggg	tagtgatcct	ggcagtcacc	atagctctac	ttgtttactt	tttagctttt	180
gatcaaaaat	cttactttta	taggagcagt	tttcaactcc	taaatgttga	atataatagt	240
cagtttaaatt	caccagctac	acaggaatat	aggactttga	gtggaagaat	tgaatctctg	300
attactaaaa	cattcaaaag	atcaaattta	agaaatcagt	tcatcagagc	tcatgttgcc	360
aaactgaggc	aagatggtag	tgggtgtgaga	gcggatgttg	tcatgaaatt	tcaattcact	420
agaaataaca	atggagcatc	aatgaaaagc	agaattgagt	ctgtttttacg	acaaatgctg	480
aataactctg	gaaacctgga	aataaaccct	tcaactgaga	taacatcact	tactgaccag	540
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gagcagagaa	tccttgaggg	cactgaggct	gaggagggaa	gctggccgtg	gcaagtccag	660
ctgcggctca	ataatgccca	ccactgtgga	ggcagcctga	tcaataacat	gtggatcctg	720
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atttccacaa	catttcttaa	actaagaatg	agagtaagaa	atattttaat	tcataacaat	840
tataaatctg	caactcatga	aaatgacatt	gcacttgtga	gacttgagaa	cagtgtcacc	900
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tctactgctt	atgtaacagg	atggggcgct	caagaatatg	ctggccacac	agttccagag	1020
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cgagtgcagc	cctaccttga	ctggattagg	caacaaactg	ggatctagtg	caacaagtgc	1320
atccctgttg	caaagtctgt	atgcaggtgt	gcctgtctta	aattccaaag	ctttacattt	1380
caactgaaaa	agaaactaga	aatgtcctaa	tttaacatct	tgttacataa	atatggttta	1440
acaaaaaa	aaaaaaaa					1460

<210> 81
 <211> 386
 <212> PRT

<213> Homo sapien

<400> 81

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Met Phe Ala Glu Ile Gln Ile Gln Asp Lys Asp Arg Met Gly Thr Ala
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Gly Lys Val Ile Lys Cys Lys Ala Ala Val Leu Trp Glu Gln Lys Gln
      20           25           30
Pro Phe Ser Ile Glu Glu Ile Glu Val Ala Pro Pro Lys Thr Lys Glu
      35           40           45
Val Arg Ile Lys Ile Leu Ala Thr Gly Ile Cys Arg Thr Asp Asp His
 50           55           60
Val Ile Lys Gly Thr Met Val Ser Lys Phe Pro Val Ile Val Gly His
 65           70           75           80
Glu Ala Thr Gly Ile Val Glu Ser Ile Gly Glu Gly Val Thr Thr Val
      85           90           95
Lys Pro Gly Asp Lys Val Ile Pro Leu Phe Leu Pro Gln Cys Arg Glu
      100          105          110
Cys Asn Ala Cys Arg Asn Pro Asp Gly Asn Leu Cys Ile Arg Ser Asp
      115          120          125
Ile Thr Gly Arg Gly Val Leu Ala Asp Gly Thr Thr Arg Phe Thr Cys
 130          135          140
Lys Gly Lys Pro Val His His Phe Met Asn Thr Ser Thr Phe Thr Glu
 145          150          155          160
Tyr Thr Val Val Asp Glu Ser Ser Val Ala Lys Ile Asp Asp Ala Ala
      165          170          175
Pro Pro Glu Lys Val Cys Leu Ile Gly Cys Gly Phe Ser Thr Gly Tyr
      180          185          190
Gly Ala Ala Val Lys Thr Gly Lys Val Lys Pro Gly Ser Thr Cys Val
      195          200          205
Val Phe Gly Leu Arg Gly Val Gly Leu Ser Val Ile Met Gly Cys Lys
 210          215          220
Ser Ala Gly Ala Ser Arg Ile Ile Gly Ile Asp Leu Asn Lys Asp Lys
 225          230          235          240
Phe Glu Lys Ala Met Ala Val Gly Ala Thr Glu Cys Ile Ser Pro Lys
      245          250          255
Asp Ser Thr Lys Pro Ile Ser Glu Val Leu Ser Glu Met Thr Gly Asn
 260          265          270
Asn Val Gly Tyr Thr Phe Glu Val Ile Gly His Leu Glu Thr Met Ile
 275          280          285
Asp Ala Leu Ala Ser Cys His Met Asn Tyr Gly Thr Ser Val Val Val
 290          295          300
Gly Val Pro Pro Ser Ala Lys Met Leu Thr Tyr Asp Pro Met Leu Leu
 305          310          315          320
Phe Thr Gly Arg Thr Trp Lys Gly Cys Val Phe Gly Gly Leu Lys Ser
      325          330          335
Arg Asp Asp Val Pro Lys Leu Val Thr Glu Phe Leu Ala Lys Lys Phe
      340          345          350
Asp Leu Asp Gln Leu Ile Thr His Val Leu Pro Phe Lys Lys Ile Ser
      355          360          365
Glu Gly Phe Glu Leu Leu Asn Ser Gly Gln Ser Ile Arg Thr Val Leu
 370          375          380
Thr Phe
385

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<210> 82

<211> 418

<212> PRT

<213> Homo sapien

<400> 82

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Tyr	Val	Val	Cys	Phe	Ile	Val	Val	Ala	Gly	Val	Val	Ile	Leu	Ala	Val
			20					25					30		
Thr	Ile	Ala	Leu	Leu	Val	Tyr	Phe	Leu	Ala	Phe	Asp	Gln	Lys	Ser	Tyr
		35					40					45			
Phe	Tyr	Arg	Ser	Ser	Phe	Gln	Leu	Leu	Asn	Val	Glu	Tyr	Asn	Ser	Gln
	50					55				60					
Leu	Asn	Ser	Pro	Ala	Thr	Gln	Glu	Tyr	Arg	Thr	Leu	Ser	Gly	Arg	Ile
65					70					75					80
Glu	Ser	Leu	Ile	Thr	Lys	Thr	Phe	Lys	Glu	Ser	Asn	Leu	Arg	Asn	Gln
				85					90					95	
Phe	Ile	Arg	Ala	His	Val	Ala	Lys	Leu	Arg	Gln	Asp	Gly	Ser	Gly	Val
			100					105					110		
Arg	Ala	Asp	Val	Val	Met	Lys	Phe	Gln	Phe	Thr	Arg	Asn	Asn	Asn	Gly
		115					120					125			
Ala	Ser	Met	Lys	Ser	Arg	Ile	Glu	Ser	Val	Leu	Arg	Gln	Met	Leu	Asn
		130				135				140					
Asn	Ser	Gly	Asn	Leu	Glu	Ile	Asn	Pro	Ser	Thr	Glu	Ile	Thr	Ser	Leu
145					150					155					160
Thr	Asp	Gln	Ala	Ala	Ala	Asn	Trp	Leu	Ile	Asn	Glu	Cys	Gly	Ala	Gly
			165					170						175	
Pro	Asp	Leu	Ile	Thr	Leu	Ser	Glu	Gln	Arg	Ile	Leu	Gly	Gly	Thr	Glu
			180					185					190		
Ala	Glu	Glu	Gly	Ser	Trp	Pro	Trp	Gln	Val	Ser	Leu	Arg	Leu	Asn	Asn
		195					200					205			
Ala	His	His	Cys	Gly	Gly	Ser	Leu	Ile	Asn	Asn	Met	Trp	Ile	Leu	Thr
	210					215					220				
Ala	Ala	His	Cys	Phe	Arg	Ser	Asn	Ser	Asn	Pro	Arg	Asp	Trp	Ile	Ala
225				230						235					240
Thr	Ser	Gly	Ile	Ser	Thr	Thr	Phe	Pro	Lys	Leu	Arg	Met	Arg	Val	Arg
			245						250					255	
Asn	Ile	Leu	Ile	His	Asn	Asn	Tyr	Lys	Ser	Ala	Thr	His	Glu	Asn	Asp
		260						265					270		
Ile	Ala	Leu	Val	Arg	Leu	Glu	Asn	Ser	Val	Thr	Phe	Thr	Lys	Asp	Ile
	275						280					285			
His	Ser	Val	Cys	Leu	Pro	Ala	Ala	Thr	Gln	Asn	Ile	Pro	Pro	Gly	Ser
	290				295						300				
Thr	Ala	Tyr	Val	Thr	Gly	Trp	Gly	Ala	Gln	Glu	Tyr	Ala	Gly	His	Thr
305				310						315					320
Val	Pro	Glu	Leu	Arg	Gln	Gly	Gln	Val	Arg	Ile	Ile	Ser	Asn	Asp	Val
			325					330						335	
Cys	Asn	Ala	Pro	His	Ser	Tyr	Asn	Gly	Ala	Ile	Leu	Ser	Gly	Met	Leu
		340						345					350		
Cys	Ala	Gly	Val	Pro	Gln	Gly	Gly	Val	Asp	Ala	Cys	Gln	Gly	Asp	Ser
		355					360					365			
Gly	Gly	Pro	Leu	Val	Gln	Glu	Asp	Ser	Arg	Arg	Leu	Trp	Phe	Ile	Val
	370					375					380				
Gly	Ile	Val	Ser	Trp	Gly	Asp	Gln	Cys	Gly	Leu	Pro	Asp	Lys	Pro	Gly
385					390					395					400
Val	Tyr	Thr	Arg	Val	Thr	Ala	Tyr	Leu	Asp	Trp	Ile	Arg	Gln	Gln	Thr
				405					410					415	

Gly Ile

<210> 83

Met	Tyr	Arg	Pro	Ala	Arg	Val	Thr	Ser	Thr	Ser	Arg	Phe	Leu	Asn	Pro
1				5					10					15	
Tyr	Val	Val	Cys	Phe	Ile	Val	Val	Ala	Gly	Val	Val	Ile	Leu	Ala	Val
			20					25					30		
Thr	Ile	Ala	Leu	Leu	Val	Tyr	Phe	Leu	Ala	Phe	Asp	Gln	Lys	Ser	Tyr
		35					40					45			
Phe	Tyr	Arg	Ser	Ser	Phe	Gln	Leu	Leu	Asn	Val	Glu	Tyr	Asn	Ser	Gln
	50					55					60				
Leu	Asn	Ser	Pro	Ala	Thr	Gln	Glu	Tyr	Arg	Thr	Leu	Ser	Gly	Arg	Ile
65					70					75					80
Glu	Ser	Leu	Ile	Thr	Lys	Thr	Phe	Lys	Glu	Ser	Asn	Leu	Arg	Asn	Gln
				85					90					95	
Phe	Ile	Arg	Ala	His	Val	Ala	Lys	Leu	Arg	Gln	Asp	Gly	Ser	Gly	Val
			100				105						110		
Arg	Ala	Asp	Val	Val	Met	Lys	Phe	Gln	Phe	Thr	Arg	Asn	Asn	Asn	Gly
		115					120					125			
Ala	Ser	Met	Lys	Ser	Arg	Ile	Glu	Ser	Val	Leu	Arg	Gln	Met	Leu	Asn
		130				135					140				
Asn	Ser	Gly	Asn	Leu	Glu	Ile	Asn	Pro	Ser	Thr	Glu	Ile	Thr	Ser	Leu
145					150					155					160
Thr	Asp	Gln	Ala	Ala	Asn	Trp	Leu	Ile	Asn	Glu	Cys	Gly	Ala	Gly	
			165					170					175		
Pro	Asp	Leu	Ile	Thr	Leu	Ser	Glu	Gln	Arg	Ile	Leu	Gly	Gly	Thr	Glu
			180					185					190		
Ala	Glu	Glu	Gly	Ser	Trp	Pro	Trp	Gln	Val	Ser	Leu	Arg	Leu	Asn	Asn
			195				200					205			
Ala	His	His	Cys	Gly	Gly	Ser	Leu	Ile	Asn	Asn	Met	Trp	Ile	Leu	Thr
	210					215					220				
Ala	Ala	His	Cys	Phe	Arg	Ser	Asn	Ser	Asn	Pro	Arg	Asp	Trp	Ile	Ala
225					230					235					240
Thr	Ser	Gly	Ile	Ser	Thr	Thr	Phe	Pro	Lys	Leu	Arg	Met	Arg	Val	Arg
			245						250					255	
Asn	Ile	Leu	Ile	His	Asn	Asn	Tyr	Lys	Ser	Ala	Thr	His	Glu	Asn	Asp
			260					265					270		
Ile	Ala	Leu	Val	Arg	Leu	Glu	Asn	Ser	Val	Thr	Phe	Thr	Lys	Asp	Ile
		275					280					285			
His	Ser	Val	Cys	Leu	Pro	Ala	Ala	Thr	Gln	Asn	Ile	Pro	Pro	Gly	Ser
	290					295					300				
Thr	Ala	Tyr	Val	Thr	Gly	Trp	Gly	Ala	Gln	Glu	Tyr	Ala	Gly	His	Thr
305					310					315					320
Val	Pro	Glu	Leu	Arg	Gln	Gly	Gln	Val	Arg	Ile	Ile	Ser	Asn	Asp	Val
			325						330					335	
Cys	Asn	Ala	Pro	His	Ser	Tyr	Asn	Gly	Ala	Ile	Leu	Ser	Gly	Met	Leu
			340					345					350		
Cys	Ala	Gly	Val	Pro											

<210> 84
 <211> 489
 <212> DNA
 <213> Homo sapien

<400> 84
 aaaagggtaa gcttgatgat taccaggaac gaatgaacaa aggggaaagg cttaatcaag 60
 atcagctgga tgccgtttct aagtaccagg aagtcacaaa taatttggag ttgcaaaaag 120
 aattacagag gagtttcatg gcactaagtc aagatattca gaaaacaata aagaagacag 180
 cacgtcggga gcagcttatg agagaagaag ctgaacagaa acgtttaaaa actgtacttg 240
 agctacagta tgttttggac aaattgggag atgatgaagt gcggactgac ctgaaacaag 300
 gtttgaatgg agtgccaata ttgtccgaag aggagttgtc attgttggat gaattctata 360
 agctagtaga ccctgaacgg gacatgagct tgaggttgaa tgaacagtat gaacatgcct 420
 ccattcacct gtgggacctg ctggaaggga aggaaaaacc tgtatgtgga accacctata 480
 aagttctaa 489

<210> 85
 <211> 304
 <212> DNA
 <213> Homo sapien

<400> 85
 gggacctgga ggaggccacg ctgcagcatg aagccacagc agccaccctg aggaagaagc 60
 acgcgagacag cgtggccgag ctcggggagc agatcgacaa cctgcagcgg gtgaagcaga 120
 agctggagaa ggagaagagc gagatgaaga tggagatcga tgacctcgct tgtaacatgg 180
 aggtcatctc caaatctaag ggaacacctg agaagatgtg ccgcacactg gaggaccaag 240
 tgagtgaact gaagaccacg gaggaggaac agcagcggct gatcaatgaa ctgactgcgc 300
 agag 304

<210> 86
 <211> 296
 <212> DNA
 <213> Homo sapien

<400> 86
 gaaaatcctt cctttgaatg ggaatctcca agcagttgaa ttgggcgaaa aaagaacctc 60
 ttcccttaagg attaaaatgt ttagggcaac acgtgttact tccacttcca gatttctgaa 120
 tccatattgt gtatgtttcc ttgtcctccc aggggttgtg atcctggcag tccccatagc 180
 tctacttggt tactttttag cttttgatca aaaatcttac ttttattgga gcaattttcc 240
 actcccaaat gttgaatata atagtccgtt taattccccc gcttcaccgg gaattc 296

<210> 87
 <211> 904
 <212> DNA
 <213> Homo sapien

<400> 87
 gtgtccagga aacgattcat gaacataaca agcttgctgc aaattcagat catctcatgc 60
 agattcaaaa atgtgagttg gtcttgatcc acacctaccc agttggtgaa gacagccttg 120
 tatctgatcg ttctaaaaaa gagttgtccc cggttttaac cagtgaagtt catagtgttc 180
 gtgcaggacg gcactttgct accaaattga atattttagt acagcaacat ttgacttgg 240
 ctccaactac tattacaaat attccaatga aggaagaaca gcatgctaac acatctgcca 300
 attatgatgt ggagctactt catcacaagg atgcacatgt agatttcctg aaaagtgggtg 360
 attcgcatct aggtggcggc agtcgagaag gctcgtttaa agaaacaata acattaaagt 420
 ggtgtacacc aaggacaaat aacattgaat tacactattg tactggagct tatcggattt 480
 cacctgtaga tgtaaatagt agaccttctt cctgccttac taattttctt ctaaatgggtc 540

gttctgtttt attggaacaa ccacgaaagt cagggttctaa agtcattagt catatgctta	600
gtagccatgg aggagagatt tttttgcacg tccttagcag ttctcgatcc attctagaag	660
atccaccttc aattagtga g gatgtggag gaagagttac agactaccgg attacagatt	720
ttggtgaatt tatgagggga aaacagatta actccttttc tacaccccag atataaaatc	780
gatggaagtc ttgagggtccc tttggaaccg agccaaaaga tcagttaaaa aaacataccc	840
gttactggcc tatgatttca aaaaccacac atttttaaca tgcaagcggg agttccgtta	900
acca	904

<210> 88
 <211> 387
 <212> DNA
 <213> Homo sapien

<400> 88	
cgtctctccc ccagtttgcc gttcaccogg agcgcctcggg acttgccgat agtgggtgacg	60
gcggcaacat gtctgtggct ttcgcggccc cgaggcagcg aggcaagggg gagatcactc	120
ccgctgcgat tcagaagatg ttggatgaca ataaccatct tattcagtggt ataattggact	180
ctcagaataa aggaaagacc tcagagtgtt ctgagtatca gcagatgttg cacacaaact	240
tggtatacct tgctacaata gcagattcta atcaaaatat gcagtctctt ttaccagcac	300
caccacacaca gaatatgcct atgggtcctg gagggatgaa tcagagcggg cctccccac	360
ctccacgctc tcacaacatg ccttcaa	387

<210> 89
 <211> 481
 <212> DNA
 <213> Homo sapien

<400> 89	
tggtcttgga cctgcgggtgc tatagagcag gctcttctag gttggcagtt gccatggaat	60
ctggacccaa aatggttgcc cccgtttgcc tggtggaaaa taacaatgag cagctattgg	120
tgaaccagca agctatacag attcttgaaa agatttctca gccagtgggtg gtggtggcca	180
ttgtaggact gtaccgtaca gggaaatcct acttgatgaa ccactctggca ggacagaatc	240
atggcttccc tctgggtccc acgggtgcagt ctgaaaccaa gggcatctgg atgtgggtgcg	300
tgccccaccc atccaagcca aaccacaccc tggtccttct ggacaccgaa ggtctgggcy	360
atgtggaaaa gggtagacct aagaatgact cctggatctt tgccctggct gtgctcctgt	420
gcagcacctt tgtctacaac agcatgagca ccatcaacca ccaggccctg gagcagctgc	480
a	481

<210> 90
 <211> 491
 <212> DNA
 <213> Homo sapien

<400> 90	
tgaaaactgt tcttggaacct gcggtgctat agagcagggtt ggcagttgcc atggaatctg	60
gacccaaaat gttggccccc gtttgccctgg tggaaaataa caatgagcag ctattggtga	120
accagcaagc tatacagatt cttgaaaaga tttctcagcc agtgggtgggtg gtggccattg	180
taggactgta ccgtacaggg aaatcctact tgatgaacca tctggcagga cagaatcatg	240
gcttccctct gggctccacg gtgcagtcgt aaaccaaggg catctggatg tgggtgcgtgc	300
cccacccatc caagccaaac cacaccctgg tccttctgga caccgaagggt ctgggcatg	360
tggaaaaggg tgaccctaag aatgactcct ggatctttgc cctggctgtg ctctgtgca	420
gcaccttgt ctacaacagc atgagcacca tcaaccacca agccctggag cagctgcatt	480
atgtgacgga c	491

<210> 91
 <211> 488
 <212> DNA
 <213> Homo sapien

<400> 91

```

ttcgacagtc agccgcatct tcttttgcgt cgccagccga gccacatcgc tcagacacca    60
tggggaaggt gaaggtcggg gtcaacggat ttggtcgat tgggcgcctg gtcaccaggg    120
ctgcttttaa ctctggtaaa gtggatattg ttgccatcaa tgaccccttc attgacctca    180
actacatggt ttacatgttc caatatgatt ccacccatgg caaattccat ggcaccgtcg    240
aggctgagaa cgggaagctt gtcatcaatg gaaatcccat caccatcttc caggagcgag    300
atccctccaa aatcaagtgg ggcgatgctg gcgctgagta cgtcgtggag tccactggcg    360
tcttcaccac catggagaag gctggggctc atttgagggg gggagccaaa aggggtcatca    420
tctctgcccc tctgctgatg ccccatgttc gtcatgggtg tgaacatga gaagtatgac    480
acagcctc                                     488

```

<210> 92

<211> 384

<212> DNA

<213> Homo sapien

<400> 92

```

gacagtcagc cgcattcttct tttgcgtcgc cagccgagcc acatcgctca gacaccatgg    60
ggaagggtgaa ggtcggagtc aacggatttg gtcgtattgg gcgcctggtc accagggctg    120
cttttaactc tggtaaagtg gatattgttg ccatcaatga ccccttcatt gacctcaact    180
acatgggttta catgttccaa tatgattcca cccatggcaa attccatggc accgtcgagg    240
ctgagaacgg gaagcttgtc atcaatggaa atcccatcac catcttccag gagcgagatc    300
cctccaaaat caagtggggc gatactggcg ctgagtacgt cgtggagtcc actggcgctct    360
tcaccaccat ggagaaggct gggg                                     384

```

<210> 93

<211> 162

<212> PRT

<213> Homo sapien

<400> 93

```

Lys Gly Lys Leu Asp Asp Tyr Gln Glu Arg Met Asn Lys Gly Glu Arg
 1          5          10          15
Leu Asn Gln Asp Gln Leu Asp Ala Val Ser Lys Tyr Gln Glu Val Thr
 20          25          30
Asn Asn Leu Glu Phe Ala Lys Glu Leu Gln Arg Ser Phe Met Ala Leu
 35          40          45
Ser Gln Asp Ile Gln Lys Thr Ile Lys Lys Thr Ala Arg Arg Glu Gln
 50          55          60
Leu Met Arg Glu Glu Ala Glu Gln Lys Arg Leu Lys Thr Val Leu Glu
 65          70          75          80
Leu Gln Tyr Val Leu Asp Lys Leu Gly Asp Asp Glu Val Arg Thr Asp
 85          90          95
Leu Lys Gln Gly Leu Asn Gly Val Pro Ile Leu Ser Glu Glu Glu Leu
100          105          110
Ser Leu Leu Asp Glu Phe Tyr Lys Leu Val Asp Pro Glu Arg Asp Met
115          120          125
Ser Leu Arg Leu Asn Glu Gln Tyr Glu His Ala Ser Ile His Leu Trp
130          135          140
Asp Leu Leu Glu Gly Lys Glu Lys Pro Val Cys Gly Thr Thr Tyr Lys
145          150          155          160
Val Leu

```

<210> 94

<211> 100

<212> PRT

<213> Homo sapien

<400> 94

```

Asp Leu Glu Glu Ala Thr Leu Gln His Glu Ala Thr Ala Ala Thr Leu
 1          5          10          15
Arg Lys Lys His Ala Asp Ser Val Ala Glu Leu Gly Glu Gln Ile Asp
          20          25          30
Asn Leu Gln Arg Val Lys Gln Lys Leu Glu Lys Glu Lys Ser Glu Met
          35          40          45
Lys Met Glu Ile Asp Asp Leu Ala Cys Asn Met Glu Val Ile Ser Lys
 50          55          60
Ser Lys Gly Asn Leu Glu Lys Met Cys Arg Thr Leu Glu Asp Gln Val
65          70          75          80
Ser Glu Leu Lys Thr Gln Glu Glu Glu Gln Gln Arg Leu Ile Asn Glu
          85          90          95
Leu Thr Ala Gln
          100

```

<210> 95

<211> 99

<212> PRT

<213> Homo sapien

<400> 95

```

Lys Ile Leu Pro Leu Asn Gly Asn Leu Gln Ala Val Glu Leu Gly Glu
 1          5          10          15
Lys Arg Thr Ser Ser Leu Arg Ile Lys Met Phe Arg Ala Thr Arg Val
          20          25          30
Thr Ser Thr Ser Arg Phe Leu Asn Pro Tyr Val Val Cys Phe Leu Val
          35          40          45
Leu Pro Gly Val Val Ile Leu Ala Val Pro Ile Ala Leu Leu Val Tyr
 50          55          60
Phe Leu Ala Phe Asp Gln Lys Ser Tyr Phe Tyr Trp Ser Asn Phe Pro
65          70          75          80
Leu Pro Asn Val Glu Tyr Asn Ser Pro Phe Asn Ser Pro Ala Ser Pro
          85          90          95
Gly Ile Pro

```

<210> 96

<211> 257

<212> PRT

<213> Homo sapien

<400> 96

```

Val Gln Glu Thr Ile His Glu His Asn Lys Leu Ala Ala Asn Ser Asp
 1          5          10          15
His Leu Met Gln Ile Gln Lys Cys Glu Leu Val Leu Ile His Thr Tyr
          20          25          30
Pro Val Gly Glu Asp Ser Leu Val Ser Asp Arg Ser Lys Lys Glu Leu
          35          40          45
Ser Pro Val Leu Thr Ser Glu Val His Ser Val Arg Ala Gly Arg His
 50          55          60
Leu Ala Thr Lys Leu Asn Ile Leu Val Gln Gln His Phe Asp Leu Ala
65          70          75          80
Ser Thr Thr Ile Thr Asn Ile Pro Met Lys Glu Glu Gln His Ala Asn
          85          90          95
Thr Ser Ala Asn Tyr Asp Val Glu Leu Leu His His Lys Asp Ala His

```

```

      100      105      110
Val Asp Phe Leu Lys Ser Gly Asp Ser His Leu Gly Gly Gly Ser Arg
      115      120      125
Glu Gly Ser Phe Lys Glu Thr Ile Thr Leu Lys Trp Cys Thr Pro Arg
      130      135      140
Thr Asn Asn Ile Glu Leu His Tyr Cys Thr Gly Ala Tyr Arg Ile Ser
145      150      155      160
Pro Val Asp Val Asn Ser Arg Pro Ser Ser Cys Leu Thr Asn Phe Leu
      165      170      175
Leu Asn Gly Arg Ser Val Leu Leu Glu Gln Pro Arg Lys Ser Gly Ser
      180      185      190
Lys Val Ile Ser His Met Leu Ser Ser His Gly Gly Glu Ile Phe Leu
      195      200      205
His Val Leu Ser Ser Ser Arg Ser Ile Leu Glu Asp Pro Pro Ser Ile
      210      215      220
Ser Glu Gly Cys Gly Gly Arg Val Thr Asp Tyr Arg Ile Thr Asp Phe
225      230      235      240
Gly Glu Phe Met Arg Gly Lys Gln Ile Asn Ser Phe Ser Thr Pro Gln
      245      250      255
Ile

```

```

<210> 97
<211> 128
<212> PRT
<213> Homo sapien

```

```

<400> 97
Ser Leu Pro Gln Phe Ala Val His Pro Glu Arg Ser Gly Leu Ala Asp
 1      5      10      15
Ser Gly Asp Gly Gly Asn Met Ser Val Ala Phe Ala Ala Pro Arg Gln
      20      25      30
Arg Gly Lys Gly Glu Ile Thr Pro Ala Ala Ile Gln Lys Met Leu Asp
      35      40      45
Asp Asn Asn His Leu Ile Gln Cys Ile Met Asp Ser Gln Asn Lys Gly
50      55      60
Lys Thr Ser Glu Cys Ser Gln Tyr Gln Gln Met Leu His Thr Asn Leu
65      70      75      80
Val Tyr Leu Ala Thr Ile Ala Asp Ser Asn Gln Asn Met Gln Ser Leu
      85      90      95
Leu Pro Ala Pro Pro Thr Gln Asn Met Pro Met Gly Pro Gly Gly Met
      100      105      110
Asn Gln Ser Gly Pro Pro Pro Pro Arg Ser His Asn Met Pro Ser
      115      120      125

```

```

<210> 98
<211> 159
<212> PRT
<213> Homo sapien

```

```

<400> 98
Phe Leu Asp Leu Arg Cys Tyr Arg Ala Gly Ser Ser Arg Leu Ala Val
 1      5      10      15
Ala Met Glu Ser Gly Pro Lys Met Leu Ala Pro Val Cys Leu Val Glu
      20      25      30
Asn Asn Asn Glu Gln Leu Leu Val Asn Gln Gln Ala Ile Gln Ile Leu
      35      40      45
Glu Lys Ile Ser Gln Pro Val Val Val Ala Ile Val Gly Leu Tyr

```

```

      50              55              60
Arg Thr Gly Lys Ser Tyr Leu Met Asn His Leu Ala Gly Gln Asn His
65              70              75              80
Gly Phe Pro Leu Gly Ser Thr Val Gln Ser Glu Thr Lys Gly Ile Trp
      85              90              95
Met Trp Cys Val Pro His Pro Ser Lys Pro Asn His Thr Leu Val Leu
      100             105             110
Leu Asp Thr Glu Gly Leu Gly Asp Val Glu Lys Gly Asp Pro Lys Asn
      115             120             125
Asp Ser Trp Ile Phe Ala Leu Ala Val Leu Leu Cys Ser Thr Phe Val
      130             135             140
Tyr Asn Ser Met Ser Thr Ile Asn His Gln Ala Leu Glu Gln Leu
145              150              155

```

<210> 99
 <211> 147
 <212> PRT
 <213> Homo sapien

```

      <400> 99
Met Glu Ser Gly Pro Lys Met Leu Ala Pro Val Cys Leu Val Glu Asn
1              5              10              15
Asn Asn Glu Gln Leu Leu Val Asn Gln Gln Ala Ile Gln Ile Leu Glu
      20              25              30
Lys Ile Ser Gln Pro Val Val Val Ala Ile Val Gly Leu Tyr Arg
      35              40              45
Thr Gly Lys Ser Tyr Leu Met Asn His Leu Ala Gly Gln Asn His Gly
50              55              60
Phe Pro Leu Gly Ser Thr Val Gln Ser Glu Thr Lys Gly Ile Trp Met
65              70              75              80
Trp Cys Val Pro His Pro Ser Lys Pro Asn His Thr Leu Val Leu Leu
      85              90              95
Asp Thr Glu Gly Leu Gly Asp Val Glu Lys Gly Asp Pro Lys Asn Asp
      100             105             110
Ser Trp Ile Phe Ala Leu Ala Val Leu Leu Cys Ser Thr Phe Val Tyr
      115             120             125
Asn Ser Met Ser Thr Ile Asn His Gln Ala Leu Glu Gln Leu His Tyr
      130             135             140
Val Thr Asp
145

```

<210> 100
 <211> 124
 <212> PRT
 <213> Homo sapien

```

      <400> 100
Met Gly Lys Val Lys Val Gly Val Asn Gly Phe Gly Arg Ile Gly Arg
1              5              10              15
Leu Val Thr Arg Ala Ala Phe Asn Ser Gly Lys Val Asp Ile Val Ala
      20              25              30
Ile Asn Asp Pro Phe Ile Asp Leu Asn Tyr Met Val Tyr Met Phe Gln
      35              40              45
Tyr Asp Ser Thr His Gly Lys Phe His Gly Thr Val Glu Ala Glu Asn
50              55              60
Gly Lys Leu Val Ile Asn Gly Asn Pro Ile Thr Ile Phe Gln Glu Arg
65              70              75              80
Asp Pro Ser Lys Ile Lys Trp Gly Asp Ala Gly Ala Glu Tyr Val Val

```


			85					90				95			
Glu	Ser	Thr	Gly	Val	Phe	Thr	Thr	Met	Glu	Lys	Ala	Gly	Ala	His	Leu
			100					105				110			
Gln	Gly	Gly	Ala	Lys	Arg	Val	Ile	Ile	Ser	Ala	Pro				
			115				120								

<210> 101
 <211> 127
 <212> PRT
 <213> Homo sapien

Gln	Ser	Ala	Ala	Ser	Ser	Phe	Ala	Ser	Pro	Ala	Glu	Pro	His	Arg	Ser
1				5					10					15	
Asp	Thr	Met	Gly	Lys	Val	Lys	Val	Gly	Val	Asn	Gly	Phe	Gly	Arg	Ile
			20					25					30		
Gly	Arg	Leu	Val	Thr	Arg	Ala	Ala	Phe	Asn	Ser	Gly	Lys	Val	Asp	Ile
			35				40					45			
Val	Ala	Ile	Asn	Asp	Pro	Phe	Ile	Asp	Leu	Asn	Tyr	Met	Val	Tyr	Met
	50					55					60				
Phe	Gln	Tyr	Asp	Ser	Thr	His	Gly	Lys	Phe	His	Gly	Thr	Val	Glu	Ala
	65				70					75				80	
Glu	Asn	Gly	Lys	Leu	Val	Ile	Asn	Gly	Asn	Pro	Ile	Thr	Ile	Phe	Gln
				85				90						95	
Glu	Arg	Asp	Pro	Ser	Lys	Ile	Lys	Trp	Gly	Asp	Thr	Gly	Ala	Glu	Tyr
			100					105					110		
Val	Val	Glu	Ser	Thr	Gly	Val	Phe	Thr	Thr	Met	Glu	Lys	Ala	Gly	
			115				120						125		

<210> 102
 <211> 1225
 <212> DNA
 <213> Homo sapien

atggcgggcg	gggtcgctgc	gggggtggcg	gcggcgagag	gggcggcggc	cctggcgcca											60
gcggagacgg	cagccgtgac	gggtggcagc	gcggcgcggg	acctgggcct	gggggaatga											120
ggcgggccgc	gcggggccagc	ggcgagccg	tgtagcggag	aagctcccc	tccctgcttc											180
ccttgccga	gccggggcg	cgcgcgca	cgccgtcca	gagcgggctc	cccacccctc											240
gactcctgcg	accgcaccg	cacccccacc	cgggcccggg	ggatgatgaa	gctcaagtcg											300
aaccagaccc	gcacctacga	cggcgacggc	tacaagaagc	gggccgcgatg	cctgtgtttc											360
cgcagcgaga	gcgaggagga	ggtgctactc	gtgagcagta	gtcgccatcc	agacagatgg											420
attgtccctg	gaggaggcat	ggagcccag	gaggagccaa	gtgtggcagc	agttcgtgaa											480
gtctgtgagg	aggctggagt	aaaagggaca	ttgggaagat	tagttggaat	ttttgagaac											540
caggagagga	agcacaggac	gtatgtctat	gtgctcattg	tcactgaagt	gctggaagac											600
tgggaagatt	cagttaacat	tgggaaggaag	agggaatggt	ttaaaataga	agacgccata											660
aaagtgtctg	agtatcacaa	accgtgcag	gcacatatt	ttgaaacatt	gaggcaaggc											720
tactcagcca	acaatggcac	cccagtcgtg	gccaccacat	actcggtttc	tgctcagagc											780
tcgatgtcag	gcacagatg	actgaagact	tcctgtaaga	gaaatggaaa	ttggaaacta											840
gactgaagtg	caaatcttcc	ctctcaccct	ggctctttcc	acttctcaca	ggcctcctct											900
ttcaaataag	gcattggtgg	cagcaaagaa	agggtgtatt	gataatgttg	ctgtttggtg											960
ttaagtgtatg	gggctttttc	ttctgttttt	attgagggtg	ggggttgggt	gtgtaatttg											1020
taagtacttt	tgtgcatgat	ctgtccctcc	ctcttccac	ccctgcagtc	ctctgaagag											1080
aggccaacag	ccttcccctg	ccttggattc	tgaagtgttc	ctgtttgtct	tatcctggcc											1140
ctggccagac	gttttctttg	atttttaatt	tttttttttt	attaaaagat	accagtatga											1200
gaaaaaaaa	aaaaaaaaaac	tcgag														1225

<210> 103

<211> 741
<212> DNA
<213> Homo sapien

<400> 103
agaaacctca atcggattca gcaaaggaat ggtgttatta tcactacata ccaaagtta 60
atcaataact ggcagcaact ttcaagcttt aggggccaag agtttgtgtg ggactatgtc 120
atcctcgatg aagcacataa aataaaaacc tcactacta agtcagcaat atgtgctcgt 180
gctattcctg caagtaatcg cctcctcctc acaggaaccc caatccagaa taattttacaa 240
gaactatggt ccctatttga ttttgcttgt caagggtccc tgctgggaac attaaaaact 300
tttaagatgg agtatgaaaa tcctattact agagcaagag agaaggatgc taccgccagga 360
gaaaaagcct tgggatttaa aatatctgaa aacttaatgg caatcataaa accctatttt 420
ctcaggagga ctaaagaaga cgtacagaag aaaaagtcaa gcaaccaga ggccagactt 480
aatgaaaaga atccagatgt tgatgccatt tgtgaaatgc cttccctttc caggagaaat 540
gatttaatta tttggatacg acttgtgcct ttacaagaag aaatatacag gaaatttgtg 600
tctttagatc atatacagga gttgctaag gagacgcgct cacctttggc tgagctaggt 660
gtcttaaaga agctgtgtga tcactcctagg ctgctgtctg cacgggcttg ttgtttgcta 720
aatcttggga cattctctgc t 741

<210> 104
<211> 321
<212> DNA
<213> Homo sapien

<400> 104
ttgctctgcg tcatacaaaga caccaaactg ctgtgtctata aaagttccaa ggaccagcag 60
cctcagatgg aactgccact ccaaggctgt aacattacgt acatcccga agacagcaaa 120
aagaagaagc acgagctgaa gattactcag cagggcacgg acccgcttgt tctcgccgtc 180
cagagcaagg aacaggccga gcagtggctg aaggatgatc aagaagccta cagtggttgt 240
agtggccccc tggattcaga gtgtcctcct ccaccaagct ccccggtgca caaggcagaa 300
ctggagaaga aactgtcttc a 321

<210> 105
<211> 389
<212> DNA
<213> Homo sapien

<400> 105
cagcactggc cacactataa aattcaggtt cagaaaaaca ggtaagtca cagacagcaa 60
cgcttccagc atttattttc tttgcaccca tgggcaattt gagaaaattt acctttagaa 120
cgaactctgt taaaggtaca gacagtacaa tactttttat tcagaagggt tctgcataaa 180
ggtgatagtc ttttgactta atatattatt gtctcctgcc ttgtgtttct ggaatgaatg 240
aaggctatta tttagaagat aatctgggtt gtattttgtg cgtcagattg aattttcatt 300
gcacatgcta cttaatgtct ttaccaaata ataacaaagg gaaagaaaac caaatataga 360
tgtataataa ggaaaagctg gcctataga 389

<210> 106
<211> 446
<212> DNA
<213> Homo sapien

<400> 106
gccacatttg ccttggatcat agtttaaaca ccaggctcctg tgtcacatct ttttgggtgcc 60
acaagtatca ctccattgtt cagagagtaa tgtattagtt ctgcccaatt cattcttcac 120
ttttatttct tccatttcat tagcatttat atcagctcaa gaagttaagg ttagaaaatt 180
ttccacttca aattttcagt acagaaatgt gctgtgatgt ttgacaagac tattttcatag 240
taagtgaagt aatgtttatt ggctctgtct ctccctgtg tcagacctag gaagcctgag 300
gattacttag ttgttctgtc tctgggtcca caggcagaat ttggcccatc caaagactgg 360

ccaagtgcc aaaaaaggcc tgattaggcc ctgaaattca gtgaaattct gcctgaagaa 420
acctcttatt gaatttgaaa accata 446

<210> 107
<211> 467
<212> DNA
<213> Homo sapien

<400> 107
ccgcgcgtgc cgtgcgccttc ctgggattgg agtctcgagc tttcttcggt cgttcgcgcg 60
cgggttcgcg cccttctcgc gcctcggggc tgcgaggctg gggagggggt tggagggggc 120
tgttgatcgc cgcgtttaag ttgcgctcgg ggcggccatg tcggccggcg aggtcgagcg 180
cctagtgtcg gagctgagcg gcgggaccgg aggggatgag gaggaagagt ggctctatgg 240
cgtatgaagat gaagttgaaa ggccagaaga agaaaatgcc agtgctaata ctccatctgg 300
aattgaagat gaaactgctg aaaatgggtg accaaaaccg aaagtgactg agaccgaaga 360
tgatagtgat agtgacagcg atgatgatga agatgatgtg catgtcacta taggagacat 420
taaaacggga gcaccacagt atgggagtta tggtagagca cctgtaa 467

<210> 108
<211> 491
<212> DNA
<213> Homo sapien

<400> 108
gaaagataca acttcccaa cccaaaccgg tttgtggagg acgacatgga taagaatgaa 60
atcgccctctg ttgcgtaccg ttaccgcagg tggaaagctg gagatgatat tgaccttatt 120
gtccgttgtg agcacgatgg cgtcatgact ggagccaacg ggaagtgct cttcatcaac 180
atcaagacac tcaatgagtg ggattccagg cactgtaatg gcgttgactg gcgtcagaag 240
ctggactctc acgagggggc tgtcattgcc acggagctga agaacaacag ctacaagttg 300
gcccggtgga cctgctgtgc tttgtgtggt ggatctgagt acctcaagct tggttatgtg 360
tctcggtacc acgtgaaaga ctccctcagc cacgtcatcc taggcacca gcagttcaag 420
cctaattgagt ttgccagcca gatcaacctg agcgtggaga atgcctgagg cattttacgc 480
tgcgtcattg a 491

<210> 109
<211> 489
<212> DNA
<213> Homo sapien

<400> 109
ctcagatagt actgaaccct ttatcaacta tgttttttca gtctgacaac caaggcggt 60
actaagtgac taaggggcag gtagtataca gtgtggataa gcaggacaaa ggggtgattc 120
acatcccagg caggacagag caggagatca tgagatttca tcaactcagga tggcttgtga 180
tttattttat tttattcttt tttttttttg agatggagtc tcaactcttg ccaggctgga 240
gtgcagtggt gcgatcttgg ctcaactgcaa cctctgcctc ctgggttcaa gcagttctcc 300
tgccctcagcc tcccaagtag ctgggattac aggcgtccgc caccatgcc agccaatttt 360
tgtactttta gtagagatgg ggtttcacca tgttgccag gctggtctcg aactcctgac 420
ctcaggtgat ccaactgcct cggcctccca aagtgtctgg attataggca tgcgccacca 480
tgccccggc 489

<210> 110
<211> 391
<212> DNA
<213> Homo sapien

<400> 110
gcggagtcg cgtggctgacc cgagcgctgg tctccgccgg gaaccctggg gcatggagag 60
gtctgagtac ctccggccgc gcgcacgctg catcgccggag ccaggctgcc gctgtcccag 120

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tggagttcca ggagcaccac ctgagtgagg tgcagaatat ggcactctgag gagaagctgg 180
agcaggtgct gagttccatg aaggagaaca aagtggccat cattggaaag attcataccc 240
cgatggagta taagggggag ctagcctcct atgatatgcg gctgaggcgt aagttggact 300
tatttgccaa cgtaatccat gtgaagtcac ttcctgggta tatgactcgg cacaacaatc 360
tagacctggt gatcattcga gagcagacag a 391

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<210> 111
<211> 172
<212> PRT
<213> Homo sapien

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<400> 111
Met Met Lys Leu Lys Ser Asn Gln Thr Arg Thr Tyr Asp Gly Asp Gly
 1          5          10          15
Tyr Lys Lys Arg Ala Ala Cys Leu Cys Phe Arg Ser Glu Ser Glu Glu
 20          25          30
Glu Val Leu Leu Val Ser Ser Ser Arg His Pro Asp Arg Trp Ile Val
 35          40          45
Pro Gly Gly Gly Met Glu Pro Glu Glu Glu Pro Ser Val Ala Ala Val
 50          55          60
Arg Glu Val Cys Glu Glu Ala Gly Val Lys Gly Thr Leu Gly Arg Leu
 65          70          75          80
Val Gly Ile Phe Glu Asn Gln Glu Arg Lys His Arg Thr Tyr Val Tyr
 85          90          95
Val Leu Ile Val Thr Glu Val Leu Glu Asp Trp Glu Asp Ser Val Asn
100          105          110
Ile Gly Arg Lys Arg Glu Trp Phe Lys Ile Glu Asp Ala Ile Lys Val
115          120          125
Leu Gln Tyr His Lys Pro Val Gln Ala Ser Tyr Phe Glu Thr Leu Arg
130          135          140
Gln Gly Tyr Ser Ala Asn Asn Gly Thr Pro Val Val Ala Thr Thr Tyr
145          150          155          160
Ser Val Ser Ala Gln Ser Ser Met Ser Gly Ile Arg
165          170

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<210> 112
<211> 247
<212> PRT
<213> Homo sapien

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<400> 112
Arg Asn Leu Asn Arg Ile Gln Gln Arg Asn Gly Val Ile Ile Thr Thr
 1          5          10          15
Tyr Gln Met Leu Ile Asn Asn Trp Gln Gln Leu Ser Ser Phe Arg Gly
 20          25          30
Gln Glu Phe Val Trp Asp Tyr Val Ile Leu Asp Glu Ala His Lys Ile
 35          40          45
Lys Thr Ser Ser Thr Lys Ser Ala Ile Cys Ala Arg Ala Ile Pro Ala
 50          55          60
Ser Asn Arg Leu Leu Leu Thr Gly Thr Pro Ile Gln Asn Asn Leu Gln
 65          70          75          80
Glu Leu Trp Ser Leu Phe Asp Phe Ala Cys Gln Gly Ser Leu Leu Gly
 85          90          95
Thr Leu Lys Thr Phe Lys Met Glu Tyr Glu Asn Pro Ile Thr Arg Ala
100          105          110
Arg Glu Lys Asp Ala Thr Pro Gly Glu Lys Ala Leu Gly Phe Lys Ile
115          120          125
Ser Glu Asn Leu Met Ala Ile Ile Lys Pro Tyr Phe Leu Arg Arg Thr

```

130		135		140
Lys Glu Asp Val Gln	Lys Lys Lys Ser Ser	Asn Pro Glu Ala Arg Leu		
145	150	155		160
Asn Glu Lys Asn Pro Asp Val Asp Ala Ile Cys Glu Met Pro Ser Leu				
	165	170		175
Ser Arg Arg Asn Asp Leu Ile Ile Trp Ile Arg Leu Val Pro Leu Gln				
	180	185		190
Glu Glu Ile Tyr Arg Lys Phe Val Ser Leu Asp His Ile Lys Glu Leu				
	195	200		205
Leu Met Glu Thr Arg Ser Pro Leu Ala Glu Leu Gly Val Leu Lys Lys				
	210	215		220
Leu Cys Asp His Pro Arg Leu Leu Ser Ala Arg Ala Cys Cys Leu Leu				
225	230	235		240
Asn Leu Gly Thr Phe Ser Ala				
	245			

<210> 113
 <211> 107
 <212> PRT
 <213> Homo sapien

<400> 113
Leu Leu Cys Val Ile Lys Asp Thr Lys Leu Leu Cys Tyr Lys Ser Ser
1 5 10 15
Lys Asp Gln Gln Pro Gln Met Glu Leu Pro Leu Gln Gly Cys Asn Ile
20 25 30
Thr Tyr Ile Pro Lys Asp Ser Lys Lys Lys His Glu Leu Lys Ile
35 40 45
Thr Gln Gln Gly Thr Asp Pro Leu Val Leu Ala Val Gln Ser Lys Glu
50 55 60
Gln Ala Glu Gln Trp Leu Lys Val Ile Lys Glu Ala Tyr Ser Gly Cys
65 70 75 80
Ser Gly Pro Val Asp Ser Glu Cys Pro Pro Pro Ser Ser Pro Val
85 90 95
His Lys Ala Glu Leu Glu Lys Lys Leu Ser Ser
100 105

<210> 114
 <211> 155
 <212> PRT
 <213> Homo sapien

<400> 114
Glu Arg Tyr Asn Phe Pro Asn Pro Asn Pro Phe Val Glu Asp Asp Met
1 5 10 15
Asp Lys Asn Glu Ile Ala Ser Val Ala Tyr Arg Tyr Arg Arg Trp Lys
20 25 30
Leu Gly Asp Asp Ile Asp Leu Ile Val Arg Cys Glu His Asp Gly Val
35 40 45
Met Thr Gly Ala Asn Gly Glu Val Ser Phe Ile Asn Ile Lys Thr Leu
50 55 60
Asn Glu Trp Asp Ser Arg His Cys Asn Gly Val Asp Trp Arg Gln Lys
65 70 75 80
Leu Asp Ser Gln Arg Gly Ala Val Ile Ala Thr Glu Leu Lys Asn Asn
85 90 95
Ser Tyr Lys Leu Ala Arg Trp Thr Cys Cys Ala Leu Leu Ala Gly Ser
100 105 110
Glu Tyr Leu Lys Leu Gly Tyr Val Ser Arg Tyr His Val Lys Asp Ser

115 120 125
 Ser Arg His Val Ile Leu Gly Thr Gln Gln Phe Lys Pro Asn Glu Phe
 130 135 140
 Ala Ser Gln Ile Asn Leu Ser Val Glu Asn Ala
 145 150 155

<210> 115
 <211> 129
 <212> PRT
 <213> Homo sapien

<400> 115
 Gly Val Arg Trp Leu Thr Arg Ala Leu Val Ser Ala Gly Asn Pro Gly
 1 5 10 15
 Ala Trp Arg Gly Leu Ser Thr Ser Ala Ala Ala His Ala Ala Ser Arg
 20 25 30
 Ser Gln Ala Ala Val Pro Val Glu Phe Gln Glu His His Leu Ser
 35 40 45
 Glu Val Gln Asn Met Ala Ser Glu Glu Lys Leu Glu Gln Val Leu Ser
 50 55 60
 Ser Met Lys Glu Asn Lys Val Ala Ile Ile Gly Lys Ile His Thr Pro
 65 70 75 80
 Met Glu Tyr Lys Gly Glu Leu Ala Ser Tyr Asp Met Arg Leu Arg Arg
 85 90 95
 Lys Leu Asp Leu Phe Ala Asn Val Ile His Val Lys Ser Leu Pro Gly
 100 105 110
 Tyr Met Thr Arg His Asn Asn Leu Asp Leu Val Ile Ile Arg Glu Gln
 115 120 125
 Thr

<210> 116
 <211> 550
 <212> DNA
 <213> Homo sapien

<400> 116
 gaattcggca ccagcctcag agccccccag cccggctacc accccctgcg gaaagggtacc 60
 catctgcatt cctgcccgtc gggacctggt ggacagtcca gcctccttgg cctctagcct 120
 tggctcaccg ctgcctagag ccaaggagct catcctgaat gaccttcccg ccagcactcc 180
 tgcttccaaa tctgtgact cctccccgcc ccaggacgct tccaccccca ggcccagctc 240
 ggccagtcac ctctgccagc ttgtgtccaa gccagcacct tccacggaca gcgtcgccct 300
 gaggagcccc ctgactctgt ccagtccctt caccacgtcc ttcagcctgg gctcccacag 360
 cactctcaac ggagacctct ccgtgccag ctcttacgtc agcctccacc tgtcccccca 420
 ggtcagcagc tctgtggtgt acggacgctc ccccgatgat gcatttgagt ctcatcccca 480
 tctccgaggg tcatccgtct cttcctccct acccagcatc cctgggggaa agccggccta 540
 ctcttccac 550

<210> 117
 <211> 154
 <212> DNA
 <213> Homo sapien

<400> 117
 ttctgagggg aagccgagtg gagtggggcg cccggcgggc gtagacaatga gttttcttgg 60
 aggttttttt ggtccatttt gtgagattga tgttgccctt aatgatgggg aaaccaggaa 120
 aatggcagaa atgaaaactg aggatggcaa agta 154

<210> 118
 <211> 449
 <212> DNA
 <213> Homo sapien

<400> 118
 gaattcggca ccagggcccc cagcccgagt gtcgcgcgcca tggettgcgc gcagctctgc 60
 cgcgcgctgg tgtcggcgca atgggtggcg gaggcgctgc gggccccgcg cgctgggcag 120
 cctctgcagc tgctggacgc ctccctggtac ctgccgaagc tggggcgcgca cgcgcgacgc 180
 gagttcgagg agcgccacat cccggggcgcc gctttcttcg acatcgacca gtgcagcgac 240
 cgcacctcgc cctacgacca catgctgccc ggggcccagc atttcgcgga gtacgcaggc 300
 cgctggggcg tggggcgggc caccacgctc gtgatctacg acgccagcga ccagggcctc 360
 tactccgccc cgcgcgctg gtggatgttc cgcgcccttc gccaccacgc cgtgtcactg 420
 cttgatggcg gcctccgcca ctggctgctg 449

<210> 119
 <211> 642
 <212> DNA
 <213> Homo sapien

<400> 119
 gaattcggca cgagcagtaa cccgaccgcc gctggtcttc gctggacacc atgaatcaca 60
 ctgtccaaac cttcttctct cctgtcaaca gtggccagcc ccccaactat gagatgctca 120
 aggaggagca cgaggtggct gtgctggggg cgccccacaa ccctgctccc ccgacgtcca 180
 ccgtgatcca catccgcagc gagacctccg tgcccagacca tgctgtcttg tccctgttca 240
 acaccctctt catgaacccc tgctgcctgg gcttcatagc attcgctac tccgtgaagt 300
 ctagggacag gaagatggtt ggcgacgtga ccggggccca ggcctatgcc tccaccgcca 360
 agtgcctgaa catctggggc ctgattctgg gcattcctcat gaccattctg ctcatcgtca 420
 tcccagtgt gatcttcag gcctatggat agatcaggag gcactactga ggccaggagc 480
 tctgcccatg acctgtatcc cagctactcc aacttccatt cctcgccctg ccccgaggc 540
 cgagtccctg atcagccctt tatctcaca cgcttttcta caatggcatt caataaagtg 600
 cacgtgtttc tgggtgaaaa aaaaaaaaaa aaaaaactcg ag 642

<210> 120
 <211> 603
 <212> DNA
 <213> Homo sapien

<400> 120
 gaattcggca cgagccacaa cagccactac gactgcattc actggatcca cggccacccc 60
 gtctccacc ccgggaacag ctccccctcc caaagtgtg accagcccgg ccaccacacc 120
 catgtccacc atgtccacaa tccacacctc ctctactcca gagaccaccc acacctccac 180
 agtgtgacc accacagcca ccatgacaag ggccaccaat tccacggcca caccctctc 240
 cactctgggg acgaccggga tctcactga gctgaccaca acagccacta caactgcagc 300
 cactggatcc acggccaccc tgtctccac cccagggacc acctggatcc tcacagagcc 360
 gagcactata gccaccgtga tgggtgccac cggttccacg gccaccgcct cctccactct 420
 gggaacagct cacaccccca aagtgggtgac caccatggcc actatgccca cagccactgc 480
 ctccacgggt cccagctcgt ccaaccgtgg gaccacccgc acccctgcag tgctccccag 540
 cagcctgccca accttcagcg tgtccactgt gtctctctca gtctccacca ccctgagacc 600
 cac 603

<210> 121
 <211> 178
 <212> PRT
 <213> Homo sapien

<400> 121
 Ser Glu Pro Pro Ser Pro Ala Thr Thr Pro Cys Gly Lys Val Pro Ile

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1           5           10           15
Cys Ile Pro Ala Arg Arg Asp Leu Val Asp Ser Pro Ala Ser Leu Ala
20           25           30
Ser Ser Leu Gly Ser Pro Leu Pro Arg Ala Lys Glu Leu Ile Leu Asn
35           40           45
Asp Leu Pro Ala Ser Thr Pro Ala Ser Lys Ser Cys Asp Ser Ser Pro
50           55           60
Pro Gln Asp Ala Ser Thr Pro Arg Pro Ser Ser Ala Ser His Leu Cys
65           70           75           80
Gln Leu Ala Ala Lys Pro Ala Pro Ser Thr Asp Ser Val Ala Leu Arg
85           90           95
Ser Pro Leu Thr Leu Ser Ser Pro Phe Thr Thr Ser Phe Ser Leu Gly
100          105          110
Ser His Ser Thr Leu Asn Gly Asp Leu Ser Val Pro Ser Ser Tyr Val
115          120          125
Ser Leu His Leu Ser Pro Gln Val Ser Ser Ser Val Val Tyr Gly Arg
130          135          140
Ser Pro Val Met Ala Phe Glu Ser His Pro His Leu Arg Gly Ser Ser
145          150          155          160
Val Ser Ser Ser Leu Pro Ser Ile Pro Gly Gly Lys Pro Ala Tyr Ser
165          170          175
Phe His

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<210> 122
<211> 36
<212> PRT
<213> Homo sapien

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<400> 122
Met Ser Phe Leu Gly Gly Phe Phe Gly Pro Ile Cys Glu Ile Asp Val
1           5           10           15
Ala Leu Asn Asp Gly Glu Thr Arg Lys Met Ala Glu Met Lys Thr Glu
20           25           30
Asp Gly Lys Val
35

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<210> 123
<211> 136
<212> PRT
<213> Homo sapien

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```

<400> 123
Met Ala Ser Pro Gln Leu Cys Arg Ala Leu Val Ser Ala Gln Trp Val
1           5           10           15
Ala Glu Ala Leu Arg Ala Pro Arg Ala Gly Gln Pro Leu Gln Leu Leu
20           25           30
Asp Ala Ser Trp Tyr Leu Pro Lys Leu Gly Arg Asp Ala Arg Arg Glu
35           40           45
Phe Glu Glu Arg His Ile Pro Gly Ala Ala Phe Phe Asp Ile Asp Gln
50           55           60
Cys Ser Asp Arg Thr Ser Pro Tyr Asp His Met Leu Pro Gly Ala Glu
65           70           75           80
His Phe Ala Glu Tyr Ala Gly Arg Leu Gly Val Gly Ala Ala Thr His
85           90           95
Val Val Ile Tyr Asp Ala Ser Asp Gln Gly Leu Tyr Ser Ala Pro Arg
100          105          110
Val Trp Trp Met Phe Arg Ala Phe Gly His His Ala Val Ser Leu Leu

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115 120 125
 Asp Gly Gly Leu Arg His Trp Leu
 130 135

<210> 124
 <211> 133
 <212> PRT
 <213> Homo sapien

<400> 124
 Met Asn His Thr Val Gln Thr Phe Phe Ser Pro Val Asn Ser Gly Gln
 1 5 10 15
 Pro Pro Asn Tyr Glu Met Leu Lys Glu Glu His Glu Val Ala Val Leu
 20 25 30
 Gly Ala Pro His Asn Pro Ala Pro Pro Thr Ser Thr Val Ile His Ile
 35 40 45
 Arg Ser Glu Thr Ser Val Pro Asp His Val Val Trp Ser Leu Phe Asn
 50 55 60
 Thr Leu Phe Met Asn Pro Cys Cys Leu Gly Phe Ile Ala Phe Ala Tyr
 65 70 75 80
 Ser Val Lys Ser Arg Asp Arg Lys Met Val Gly Asp Val Thr Gly Ala
 85 90 95
 Gln Ala Tyr Ala Ser Thr Ala Lys Cys Leu Asn Ile Trp Ala Leu Ile
 100 105 110
 Leu Gly Ile Leu Met Thr Ile Leu Leu Ile Val Ile Pro Val Leu Ile
 115 120 125
 Phe Gln Ala Tyr Gly
 130

<210> 125
 <211> 195
 <212> PRT
 <213> Homo sapien

<400> 125
 Thr Thr Ala Thr Thr Thr Ala Ser Thr Gly Ser Thr Ala Thr Pro Ser
 1 5 10 15
 Ser Thr Pro Gly Thr Ala Pro Pro Pro Lys Val Leu Thr Ser Pro Ala
 20 25 30
 Thr Thr Pro Met Ser Thr Met Ser Thr Ile His Thr Ser Thr Pro
 35 40 45
 Glu Thr Thr His Thr Ser Thr Val Leu Thr Thr Thr Ala Thr Met Thr
 50 55 60
 Arg Ala Thr Asn Ser Thr Ala Thr Pro Ser Ser Thr Leu Gly Thr Thr
 65 70 75 80
 Arg Ile Leu Thr Glu Leu Thr Thr Thr Ala Thr Thr Thr Ala Ala Thr
 85 90 95
 Gly Ser Thr Ala Thr Leu Ser Ser Thr Pro Gly Thr Thr Trp Ile Leu
 100 105 110
 Thr Glu Pro Ser Thr Ile Ala Thr Val Met Val Pro Thr Gly Ser Thr
 115 120 125
 Ala Thr Ala Ser Ser Thr Leu Gly Thr Ala His Thr Pro Lys Val Val
 130 135 140
 Thr Thr Met Ala Thr Met Pro Thr Ala Thr Ala Ser Thr Val Pro Ser
 145 150 155 160
 Ser Ser Thr Val Gly Thr Thr Arg Thr Pro Ala Val Leu Pro Ser Ser
 165 170 175
 Leu Pro Thr Phe Ser Val Ser Thr Val Ser Ser Ser Val Leu Thr Thr

180 185 190

Leu Arg Pro
195

<210> 126
<211> 509
<212> DNA
<213> Homo sapien

<400> 126

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actgcagcct	gggagctcta	ttccacctta	caacaccgag	gtgactgaga	ccaccattgt	180
gatcacatgg	acgcctgctc	caagaattgg	ttttaagctg	gggtgtacgac	caagccaggg	240
aggagaggca	ccacgagaag	tgacttcaga	ctcaggaagc	atcgttgtgt	ccggcttgac	300
tccaggagta	gaatacgtct	acaccatcca	agtcctgaga	gatggacagg	aaagagatgc	360
gccaaattgta	aacaaagtgg	tgacaccatt	gtctccacca	acaaacttgc	atctggaggc	420
aaacctgac	actggagtgc	tcacagtctc	ctggagagga	gcaccacccc	agacattact	480
gggtatagaa	ttaccacaac	ccctacaaa				509

<210> 127
<211> 500
<212> DNA
<213> Homo sapien

<400> 127

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ttgctgagag	gacgcgtcta	gtcctgaagg	ccaagggaat	caggcatgaa	gtcatcaata	180
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agatgatctt	agagttgttt	tctaagggtgc	catccttggg	aggaagcttt	attagaagcc	420
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aggaggttct	gactaataag					500

<210> 128
<211> 500
<212> DNA
<213> Homo sapien

<400> 128

agctttcctc	tgctgccgct	cggtcacgct	tgtgcccgaa	ggaggaaaca	gtgacagacc	60
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cttctcaata	tgttgatcaa	gcagagttgg	aaaaatatga	tggtgtagat	gctggaaagt	240
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ctctttgcat	gactgtgggt	cagaatctta	tggagagaaa	taacctttcc	tatgattgca	360
ttgggcggct	ggaagttgga	acagagacaa	tcacgcacaa	atcaaagtct	gtgaagacta	420
atgtgatgca	gctgtttgaa	gagtctggga	atacagatat	agaaggaatc	gacacaacta	480
atgcatgcta	tggaggcaca					500

<210> 129
<211> 497
<212> DNA
<213> Homo sapien

<400> 129

gaattcggca	cgagcagagg	tctccagagc	cttctctctc	ctgtgcaaaa	tggcaactct	60
taaggaaaaa	ctcattgcac	cagttgcgga	agaagaggca	acagttccaa	acaataagat	120
cactgtagtg	ggtgttgac	aagttggtat	ggcgtgtgct	atcagcattc	tgggaaagtc	180
tctggctgat	gaacttgctc	ttgtggatgt	tttgaagat	aagcttaaag	gagaaatgat	240
ggatctgcag	catgggagct	tatttcttca	gacacctaaa	attgtggcag	ataaagatta	300
ttctgtgacc	gccaatctta	agattgtagt	ggtaactgca	ggagtccgtc	agcaagaagg	360
ggagagtcgg	ctcaatctgg	tgcagagaaa	tgtaaatgtc	ttcaaattca	ttattcctca	420
gatcgtcaag	tacagtcctg	attgcatcat	aattgtggtt	tccaaccag	tggacattct	480
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<210> 130

<211> 383

<212> DNA

<213> Homo. sapien

<400> 130

gaattcggca	cgagggccgc	ggctgccgac	tgggtccct	gcgctgtcg	ccaccatggc	60
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gctgcccgtc	cgcgcggcca	ctgcgtcgcg	gggggcgtcc	caggcggggg	cgccccaggg	180
gcgggtgccc	gaggcgcggc	ccaacagcat	ggtggtggaa	caccccgagt	tcctcaaggc	240
agggaaaggag	cctggcctgc	agatctggcg	tgtggagaaa	gttcgatctg	gtggcccgtg	300
cccaccaacc	tttatggaga	cttcttcacg	ggcgacgcct	acgtcatcct	gaagacagtg	360
cagcttaaga	acggaaaatc	ttg				383

<210> 131

<211> 509

<212> DNA

<213> Homo sapien

<400> 131

gaattcggca	cgagagtcag	cgcgatcttc	ttttgcgtcg	ccagccgagc	cacatcgctc	60
agacaccatg	gggaaggtga	aggtcggagt	caacggattt	ggtcgtattg	ggcgccctggt	120
caccagggct	gcttttaact	ctggtaaagt	ggatattggt	gccatcaatg	accccttcat	180
tgacctcaac	tacatggttt	acatgttcca	atatgattcc	acccatggca	aattccatgg	240
caccgtcaag	gctgagaacg	ggaagcttgt	catcaatgga	aatcccatca	ccatcttcca	300
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cactggccgt	cttcaccacc	atggagaagg	ctggggctca	tttgaggggg	ggagccaaaa	420
gggtcatcat	ctctgcccc	tctgctgacg	cccccatggt	cgtcatgggt	gtgaaccatg	480
agaagtatga	caacagcctc	aagatcatc				509

<210> 132

<211> 357

<212> DNA

<213> Homo sapien

<400> 132

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aatctgggtg	tgagttgaag	aagcctgggg	cctcagtga	ggtttctctg	aaggcttctg	180
gacacatctt	cagtatctat	ggtttgaatt	gggtgcgaca	ggcccctggt	caaggccttg	240
agtggatggg	atggatcaaa	gtcgacactg	cgaacccaac	gtatgccag	ggcttcacag	300
gacgatttgt	cttctccctg	gacacctctg	tcagcacggc	atatctgcag	atcagca	357

<210> 133

<211> 468

<212> DNA

<213> Homo sapien

<400> 133

gaattcggca	cgaggcgccc	cgaaccgtcc	tctgtctgct	ctcggcgggc	ctggccctga	60
ccgagacctg	ggccggctcc	cactccatga	ggtatttcga	caccgccatg	tcccggcccc	120
gccgcgggga	gccccgcttc	atctcagtgg	gctacgtgga	cgacacgcag	ttcgtgaggt	180
tcgacagcga	cgccgcgagt	ccgagagagg	agccgcgggc	gccgtggata	gagcaggagg	240
ggccggagta	ttgggaccgg	aacacacaga	tcttcaagac	caacacacag	actgaccgag	300
agagcctgcg	gaacctgcgc	ggctactaca	accagagcga	ggccgggtct	cacaccctcc	360
agagcatgta	cggctgcgac	gtggggccgg	acgggcgcct	cctccgcggg	cataaccagt	420
acgcctacga	cggcaaggat	tacatcgccc	tgaacgagga	cctgcgct		468

<210> 134

<211> 214

<212> DNA

<213> Homo sapien

<400> 134

gaattcggca	cgagctgcgt	cctgctgagc	tctgttctct	ccagcacctc	ccaacccact	60
agtgcctggt	tctcttgctc	caccaggaac	aagccaccat	gtctcgccag	tcaagtgtgt	120
ccttcgggag	cgggggcagt	cgtagcttca	gcaccgcctc	tgccatcacc	ccgtctgtct	180
cccgcaccag	cttcacctcc	gtgtcccggg	ccgg			214

<210> 135

<211> 355

<212> DNA

<213> Homo sapien

<400> 135

gaattcggca	cgaggtgaac	aggaccgcgtc	gccatggggc	gtgtgatccg	tggacagagg	60
aagggcgccg	ggtctgtgtt	ccgcgcgcac	gtgaagcacc	gtaaaggcgc	tgcgcgcctg	120
cgcgcgctgg	atttcgctga	gcggcacggc	tacatcaagg	gcatcgtaa	ggacatcatc	180
cacgaccgcg	gccgcggcgc	gcccctcgcc	aaggtggtct	tccgggatcc	gtatcggttt	240
aagaagcgga	cggagctgtt	cattgcgcgc	gagggcattc	acacggggca	gtttgtgtat	300
tgcggcaaga	aggcccagct	caacattggc	aatgtgctcc	ctgtgggcac	catgc	355

<210> 136

<211> 242

<212> DNA

<213> Homo sapien

<400> 136

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gcccggattg	cagacggagt	ctccttcact	cagtgtctca	tggtgccag	gctggagtgc	120
agtgggtgta	tctcggtctg	ctacaacatc	cacctcccag	cagcctgcct	tggcctccca	180
aagtgccgag	attgcagctc	tctgcccggc	cgccaccctc	gtctgggaag	tgaggatgct	240
gt						242

<210> 137

<211> 424

<212> DNA

<213> Homo sapien

<400> 137

gaattcggca	cgagcccaga	tcccagagtc	cgacagcgcc	cggcccagat	ccccacgcct	60
gccaggagca	agccgagagc	cagccggccg	gcgcactccg	actccgagca	gtctctgtcc	120
ttcgacccca	gccccgcgcc	ctttccggga	cccttgcccc	gcgggcagcg	ctgccaacct	180
gccggccatg	gagaccccgt	cccagcggcg	cgccacccgc	agcggggcgc	aggccagctc	240
cactccgtcg	tcgcccaccc	gcatcaccgc	gctgcaggag	aaggaggacc	tgcaggagct	300
caatgatcgc	ttggcggtct	acatcgaccg	tgtgcgctcg	ctggaaaacg	agaacgcag	360

gctgcgctt cgcacaccg agtctgaaga ggtggtcagc cgcgaggtgt ccggcatcaa 420
ggcc 424

<210> 138
<211> 448
<212> DNA
<213> Homo sapien

<400> 138
gaattcggca cgagcctgtg ttccaggagc cgaatcagaa atgtcatcct caggcacgcc 60
agacttacct gtcctactca ccgatttgaa gattcaatat actaagatct tcataaacia 120
tgaatggcat gattcagtga gtggcaagaa atttctgtc tttaatcctg caactgagga 180
ggagctctgc caggtagaag aaggagataa ggaggatgtt gacaaggcag tgaaggccgc 240
aagacaggct tttcagattg gatccccgtg gcgtactatg gatgcttccg agagggggcg 300
actattatac aagttggctg atttaatcga aagagatcgt ctgctgctgg ccgacaatgg 360
agtcaatgaa tgggtgaaaa ctctattcca atgcatactc gaatgattta gcaggctgca 420
tcaaaacatt gcgctactgt gcagggtg 448

<210> 139
<211> 510
<212> DNA
<213> Homo sapien

<400> 139
gaattcggca cgagggttccg tgcagctcac ggagaagcga atggacaaag tcggcaagta 60
ccccaaaggag ctgcgcaagt gctgcgagga cggcatgcgg gagaacccca tgaggttctc 120
gtgccagcgc cggaccggtt tcatctccct ggcgaggcgt gcaagaaggt cttcctggac 180
tgctgcaact acatcacaga gctgcgggcg cagcacgcgc gggccagcca cctggcctgc 240
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cccagagagc tggctgtgga acgttgagga cttgaaagag ccaccgaaaa atggaatctc 360
tacgaagctc atgaatatat ttttgaaaga ctccatcacc acgtgggaga ttctggctgt 420
gagcatgtcg gacaagaaag ggatctgtgt ggcagacccc ttcgaggtca cagtaatgca 480
ggactttctc atcgacctgc ggctacccta 510

<210> 140
<211> 360
<212> DNA
<213> Homo sapien

<400> 140
gaattcggca cgagcggtaa ctaccccggc tgcgcacagc tcggcgctcc ttcccgtcc 60
ctcacacacc ggcctcagcc cgcaccggca gtagaagatg gtgaaagaaa caacttacta 120
cgatgttttg ggggtcaaac ccaatgtac ttaggaagaa ttgaaaaagg cttataggaa 180
actggctttg aagtaccatc ctgataagaa cccaaatgaa ggagagaagt ttaaacagat 240
ttctcaagct tacgaagttc tctctgatgc aaagaaaagg gaattatatg acaaaggagg 300
agaacaggca attaaagagg gtggagcagg tggcggtttt ggctccccc tggacatctt 360

<210> 141
<211> 483
<212> DNA
<213> Homo sapien

<400> 141
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ccctgtctga ctacaacatc cagaaagagt ccaccctgca cctggtgctc cgtctcagag 120
gtgggatgca aatcttctgt aagacactca ctggcaagac catcaccctt gaggtggagc 180
ccagtacac catcgagaac gtcaaagcaa agatccagga caagggaagg attcctcctg 240
accagcagag gttgatcttt gccggaaagc agctggaaga tgggcgcacc ctgtctgact 300

acaacatcca	gaaagagtct	accctgcacc	tggtgctccg	tctcagaggt	gggatgcaga	360
tcttcgtgaa	gacctgact	ggtaagacca	tcacctcga	ggtggagccc	agtgacacca	420
tcgagaatgt	caaggcaaag	atccaagata	aggaaggcat	tcctcctgat	cagcagaggt	480
tga						483

<210> 142
 <211> 500
 <212> DNA
 <213> Homo sapien

<400> 142						
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gccggcgagc	ccggtccccg	ccggcaccat	gcttcccttg	tcactgctga	agacggctca	120
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caagttcttg	cggatgcccc	agtgtacat	ccgcggcagc	accatcaagt	acctgcgcat	300
ccccgacgag	atcatcgaca	tggtcaagga	ggaggtggtg	gccaaaggcc	gcggcccgcg	360
aggcctgcag	cagcagaagc	agcagaaaag	ccgcggcatg	ggcggcgctg	gccgaggtgt	420
gtttggtggc	cggggccgag	gtgggatccc	gggcacaggc	agaagccagc	cagagaagaa	480
gcctggcaga	caggcgggca					500

<210> 143
 <211> 400
 <212> DNA
 <213> Homo sapien

<400> 143						
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ctcagaagaa	agcgatcggc	cccgaggcag	gaaggccggc	tccggtgcag	ggcgcgcgcg	120
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gcctgaagga	cccatggaca	cgtgactcca	gtgttctcaa	caacatctta	gatcaagttg	360
gtttgcacaa	catttgcata	tacttgggac	aaagcaagaa			400

<210> 144
 <211> 243
 <212> DNA
 <213> Homo sapien

<400> 144						
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gcccggtattg	cagacggagt	ctccttcact	cagtgtctaa	tggtgcccag	gctggagtgc	120
agtgtgtga	tctcggtcgc	ctacaacata	cacctcccag	cagcctgcct	tggcctccca	180
aagtgccgag	attgcagcct	ctgcccggcc	gtcaccgccg	ctgggaagtg	aggagcgttt	240
ctg						243

<210> 145
 <211> 450
 <212> DNA
 <213> Homo sapien

<400> 145						
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cggcggcggc	ggcggtggtg	gttacaaccg	cagcagtggt	ggctatgaac	ccagaggtcg	120
tgaggtggc	cgtggaggca	gaggtggcat	ggcggaagt	gaccgtggtg	gcttcaataa	180
atttgggtggc	cctcggaac	aaggatcacg	tcatgactcc	gaacaggata	attcagacaa	240
caacaccatac	tttgtgcaag	gcctgggtga	gaatgttaca	attgagtctg	tggtgatta	300

<211> 560
<212> DNA
<213> Homo sapiens

<400> 254
gaattcggca ccagtttggg gggtagaggtt taattggaaa tggctctctgg ggactgaaaa 60
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accaaaggcc gtgggaaaac ccctctccag ctccaggga ttggtcagga ccacccacta 180
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gctaccggct cctccctgat gattctgaaa tacactactg aacgagctct ggctggtcct 480
ttctatcctg gatgtggttc ttctgtgtag caattccttg atgtccagtt tggaaagatg 540
tactcttctc aacaagaaaa 560

<210> 255
<211> 612
<212> DNA
<213> Homo sapiens

<400> 255
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aaggcatgga cc 612

<210> 256
<211> 1132
<212> DNA
<213> Homo sapiens

<400> 256
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ccaaggc'ccc gccgtccagc ttctaagtgc cagatgatgg aggagcgtgc caacctgatg 120
cacatgatga aactcagcat caagg'tgtg ctccag'tcgg ctctgagcct gggccgcagc 180
ctggatg'cgg accatgcccc c'ttgcagcag ttctt'tgtag tgatggagca ctgcctcaaa 240
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gagctggtgg agaaact'ttg tccagaagca tcagatatag cgactagtgt cagaàatctt 360
ccagaattaa agacagctgt ggg'aagaggc cgagcgtggc t'ttatcttgc actcatgcaa 420
aagaaactgg cagattatct gaaagtgc'tt atagacaata aacatctctt aagcgag'ttc 480
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ttgagctgca cag'ttg'g'gga tcttcaaacc aagatagatg gcttggaaaa gactaactca 780
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cagcag'ttaa gagaacaaaa tgaattaatt cgagaaagaa gtgaaaagag tgtagagata 900
acaaaacagg ataccaaagt tgagctggag acttacaagc aaactcggca aggtctggat 960
gaaatgtaca gtgatgtgtg gaagcagcta aaagaggaga agaaagtccg gttggaactg 1020
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acctaaaaca gattctactt tgagttttga tttgacattg cagcagggtg gtcacactaa 240
catccatctc ctggtaacta catacaatct gagggatgcc ccagctgaat ctgttgctta 300
ccatgcccaa aataatcctc cagttcctcc aaagccacag ccaaagggtc aggaaaaggc 360
agatatccct gtaaaaagtt cacctcaagc tgcagtggcc tataaaaaag atgttgggaa 420
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tcacttacga gagaggcacc aagttattca gacggttcat ccagttgaga aaaagctcac 540
ctacaaatgt atccattgcc ttggtgtgta taccagcaac atgaccgcct caactatcac 600
tctgcat 607

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<210> 252

<211> 618

<212> DNA

<213> Homo sapiens

<400> 252

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cgcacggagc tgaacaagct gcccaagtct gtccagaaca aacttgaaaa gttccttgct 180
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gaacaacagt attttgaaat agaaaagagg ttgtcccaca gtcaggagag acttgtgaat 300
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gcactaactg agaaaaacaa agaacttgaa attgctcagg atcgcaatat tgccattcag 420
agccaattta caagaacaaa ggaagaatta gaagctgaga aaagagactt aattagaacc 480
aatgagagac tatctcaaga acttgaatac ttaacagagg atgttaaacg tctgaatgaa 540
aaacttaaaag aaagcaatac aacaaagggt gaacttcagt taaaattgga tgaacttcaa 600
gcttctgatg tttctggt 618

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<210> 253

<211> 1201

<212> DNA

<213> Homo sapiens

<400> 253

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gaattcggca ccaggggtggc gagcggcggt gctgtgctgg ggcgagcagc ggggaccgtg 60
tgtgagtttg gcatgatttg gtcccctggg attctgcctt agcaagaaag aagttggaaa 120
tacttctctg aagaaaacta aaacaataca aaagccacag cttattgatt gcatgtcagc 180
ccccttacaa atatggacac atttccctagc ctatttccac ctggaggaga tagtaggctg 240
aatcctgagc ctgagttcca aaatatgtta attgatgaaa gggtagcgtg tgaacatcat 300
aaacataatt atcaggctct gaaaattgaa cacaaaagggt tgcaggaaga atatgtaaaa 360
tcacaaaatg aacttaaacg tgtattaatt gaaaagcaag caagccagga aaaattccaa 420
ctgctccttg aagacttaag gggagaatta gtagagaaag ctagagacat agaaaaaatg 480
aaactgcagg tactaacacc acaaaaattg gaattggtaa aagcccaact acaacaagaa 540
ttagaagctc caatgcgaga acgttttcgg actcttgatg aagaagtggg aaggtacaga 600
gctgagtata acaagctgcg ctacgagtat acatttctca agtcagagtt tgaacaccag 660
aaagaagagt ttactcgggt ttcagaagaa gagaaaatga aatacaagtc agaggttgca 720
cgactggaga aggacaaaga ggagctacat aaccagctgc ttagtggtga tcccacgaga 780
gacagcaaac gaatggagca acttgttcga gaaaaaaccc atttgcttca gaaattgaaa 840
agtttagagg ctgaagtagc agaattaagg gctgagaaag aaaattctgg tgctcaggta 900
gaaaatgtcc aaagaataca ggtgaggcag ttggctgaga tgcaggctac actcagatcc 960
ttgaggctg aaaagcagtc agctaaacta caagctgagc gtttagaata agaactaca 1020
tcaagcaatg aacagaatac ctgcttaatc agcaaaactgc atagagctga ccgagaaatc 1080
agcacactgg ccagtgaagt gaaagagctt aaacatgcaa acaaactaga aataactgac 1140
atcaaaactg aggcagcaag agctaagagt gagctcgaaa gagaaaggaa taagatccaa 1200
a 1201

```

<210> 254

agaacttagc caaaagaact ctcaaaacca ggaaaaactg caagaactta atcaacgtct 360
aacagaaatg ctatgccaga aggaaaaaga gccaggaaac agtgcattgg aggaacggga 420
acaagagaag tttaatctga aagaagaact ggaacgttgt aaagtgcagt cctccacttt 480
agtgtcttct ctggaggcgg agctctctga agttaaata cagaccata ttgtgcaaca 540
ggaaaaccac cttctcaaag atga 564

<210> 248

<211> 434

<212> DNA

<213> Homo sapiens

<400> 248

gttcttgttt gtggatcgct gtgatcgta cttgacaatg cagatcttgg tgaagactct 60
gactggtaag accatcacc tgcagggtga gccagtgac accatcgaga atgtcaaggc 120
aaagatccaa gataaggaag gcatccctcc tgaccagcag aggctgatct ttgtctggaa 180
acagctggaa gatgggcgca ccctgtctga ctacaacatc cagaaagagt ccaccctgca 240
cctgggtgctc cgtctcagag gtgggatgca aatcttcgtg aagacactca ctggcaagac 300
catcaccctt gaggtggagc ccagtgcac catcgagaac gtcaaagcaa agatccagga 360
caagggaaggc attcctcctg accagcagag gttgatcttt gccggaaagc cagcctggga 420
agatggggcc gcc 434

<210> 249

<211> 416

<212> DNA

<213> Homo sapiens

<400> 249

gcgggcccag gagggcgagg cgggcggggc ggacggggcc cccgcggcag acggcgagga 60
cggacaggac cgcacagca agcacctgta cacggccgac atgttcacgc acgggatcca 120
gagcgccgag cacttcgtca tgttcttcgc gccctggtgt ggacactgcc agcggctgca 180
gccgacttgg aatgacctgg gagacaaata caacagcatg gaagatgcca aagtctatgt 240
ggctaaagtg gactgcacgg cccactccga cgtgtgctcc gccagggggg tgcgaggata 300
ccccaccta aagcttttca agccaggcca agaagctgtg aagtaccagg gtcctcggga 360
cttcagaca ctggaaaact ggatgctgca gacactgaac gaggagccag tgacac 416

<210> 250

<211> 504

<212> DNA

<213> Homo sapiens

<400> 250

gaattcgcca cgaggcgggt aacgttatag tatttgtcag aagtgggggt ctccgtgggc 60
atttgtatcc gtccaggca gtggattagg aggcagaag gagatccctt ccacggtgct 120
aggctgagat ggatcctctc agggcccaac agctggctgc ggagctggag gtggagatga 180
tggccgatat gtacaacaga atgaccagtg cctgccaccg gaagtgtgtg cctcctcact 240
acaaggaagc agagctctcc aagggcgagt ctgtgtgcct ggaccgatgt gtctctaagt 300
acctggacat ccatgagcgg atgggcaaaa agttgacaga gttgtctatg caggatgaag 360
agctgatgaa gaggggtgcag cagagctctg ggccctgcag aggtccctgt cagtatacac 420
ctgggggtgt accccacccc ttcccacttt aataaacgtg ctccctgttg ggtgtcatct 480
gtgaagactg ccaggcctag ctct 504

<210> 251

<211> 607

<212> DNA

<213> Homo sapiens

<400> 251

gatgaaaata cacaatttta ctagcaaatg cctctactgt aatcgctatt taccacaga 60

```

tgtgataaaa ggaacaatgg tgtccaagtt tccagtgtatt gtgggacatg aggcaactgg 300
gattgttagag agcattggag aaggagtgtac tacagtgtgaaa ccaggtgtgaca aagtcattccc 360
tctctttctg ccacaatgta gagaatgcaa tgcttgtctgc aaccagatg gcaacctttg 420
cattaggagc gatattactg gtcgtggagt actggctgat ggcaccacca gatttacatg 480
caagggcaaa ccagtcacc acttcatgaa caccagtaca tttaccgagt acacagtggg 540
ggatgaatct tctgttgcta agattgatga tgcagctcct cctgagaaag tctg 594

```

<210> 245

<211> 615

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (105)

<223> n=A,T,C or G

<400> 245

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gtccctttcc tctgctgccg ctcggtcacg cttgtgcccg aaggaggaaa cagtgtacaga 60
cctggagact gcagttctct atccttccac agctctttca ccatnctgga tcacttctct 120
tgaatgcaga agcttgctgg ccaaaagatg tgggaattgt tgcccttgag atctattttc 180
cttctcaata tgttgatcaa gcagagttgg aaaaatatga tgggtgtgat gctggaaagt 240
ataccattgg ctggggccag gccaaagatg gcttctgcac agatagagaa gatattaact 300
ctctttgcat gactgtggtt cagaatctta tggagagaaa taacctttcc tatgattgca 360
ttgggcggtt ggaagttgga acagagacaa tcatcgacaa atcaaagtct gtgaagacta 420
atttgatgca gctgtttgaa gactctggga atacagatat agaaggaatc gacacaacta 480
atgcatgcta tggaggcaca gctgctgtct tcaatgcttg ttaactggat tgagtcacag 540
tcttggtgatg gacggtatgc cctggttaagt tgcaggagat attgctgtat atgccacagg 600
aatgctaga cctac 615

```

<210> 246

<211> 546

<212> DNA

<213> Homo sapiens

<400> 246

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gaattcggca ccaggtgcc tcccgctgc cctgaaccca gtgcctgcag ccatggctcc 60
cgccagctc gccttattta gtgtctctgc aaaaccggcc ttgtgaattt gcaagaaacc 120
tgaccgctct tggtttgaat ctggtcgctt ccggaggac tgcaaaagct ctgaggatg 180
ctggtctggc agtcagagat gtctctgagt tgacgggatt tcttgaatg ttggggggag 240
gtgtgaaaac tttgcattct gcagtcattg ctggaatcct agctcgtaat attccagaag 300
ataatgctga catggccaga cttgatttca atcttataag agttgttgcc tgcaatctct 360
atccctttgt aaagacagtg gcttctccag gtgtaactgt tgaggaggct gtggagcaaa 420
ttgacattgg tggagtaacc ttactgagag ctgcagccaa aaaccacgct cgagtgacag 480
tgggtgtgta accagaggac tatgtgggtg ggtgtccacg gagatgcaga gctccgagag 540
taagga 546

```

<210> 247

<211> 564

<212> DNA

<213> Homo sapiens

<400> 247

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gaattcggca ccagagatca cgtgcagtga gatgcagcaa aaagtgaac ttctgagata 60
tgaatctgaa aagcttcaac aggaaaattc tattttgaga aatgaaatta ctactttaaa 120
tgaagaagat agcatttcta acctgaaatt agggacatta aatggatctc aggaagaaat 180
gtggcaaaaa acggaaactg taaaacaaga aaatgctgca gttcagaaga tgggtgaaaa 240
tttaaagaaa cagatttcag aattaaaaat caaaaaccaa caattggatt tggaaaatac 300

```

<213> Homo sapiens

<400> 241

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gaattcggca ccaggcgagc tgcacctcga ggtgaaggcc tcaatgatga acgatgactt 60
cgagaagatc aagaactggc agaaggaagc ctttcacaag cagatgatgg gcggcttcaa 120
ggagaccaag gaagctgagg acggctttcg gaaggcacag aagccctggg ccaagaagct 180
gaaagaggta gaagcagcaa agaaagccca ccatgcagcg tgcaaagagg agaagctggc 240
tatctcacga gaagccaaca gcaaggcaga cccatccctc aaccctgaac agctcaagaa 300
attgcaagac aaaatagaaa agtgcaagca agatgttctt aagaccaaag agaagtatga 360
gaagtccctg aaggaactcg accagggcac accccagtac atggagaaca tggagcaggt 420
gtttgagcag tgccagcagt tcgaggagaa acgccttcgc ttcttcggg aggttctgct 480
ggaggttcag aagcacctag acctgtccaa tgtggctggc tacaagcca tttacatga 540
cctggagcag agcatcagag cagctg
```

<210> 242

<211> 556

<212> DNA

<213> Homo sapiens

<400> 242

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gaattcggca cgagcaaagg tgaagcagga catgcctccg cccgggggct atgggcccat 60
cgactacaaa cggaacttgc cgcgtcgagg actgtcgggc tacagcatgc tggccatagg 120
gattggaacc ctgatctacg ggcactggag cataatgaag tggaaccgtg agcgaggcg 180
cctacaaatc gaggacttcg aggtcgcgat cgcgtgttg ccaactgttac aggcagaaac 240
cgaccggagg acctgcaga tgcttcggga gaacctggag gaggaggcca tcatcatgaa 300
ggacgtgccc gactggaagg tgggggagtc tgtgttcac acaaccgct ggggtgcccc 360
cttgatcggg gagctgtacg ggctgcgcac cacagaggag gctctccatg ccagccacgg 420
cttcattgtg tacacgtagg cctgtgccc tccggccacc tggatccctg cccctcccca 480
ctgggacgga ataatgctc tgcagacctg gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 540
aaaaaaaaaa ctcgag
```

<210> 243

<211> 591

<212> DNA

<213> Homo sapiens

<400> 243

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gtctatgttt gcagaaatac agatccaaga caaagacagg atgggcactg ctggaaaagt 60
tattaaatgc aaagcagctg tgctttggga gcagaagcaa cccttctcca ttgaggaaat 120
agaagtgtgc ccaccaaaaga ctaaagaagt tcgcattaag attttgcca caggaatctg 180
tcgcacagat gacctgtga taaaaggaa aatgggtgtc aagtttccag tgattgtggg 240
acatgaggga actgggattg tagagagcat tggagaagga gtgactacag tgaaccagg 300
tgacaaaagtc atccctctct ttctgccaca atgtagagaa tgcaatgctt gtcgcaacc 360
agatggcaac ctttgcatga ggagcgatat tactggtcgt ggagtactgg ctgatggcac 420
caccagattt acatgcaagg gcaaaccagt ccaccacttc atgaacacca gtacatttac 480
cgagtacaca gtggtggatg aatcttctgt tgctaagatt gatgatgcag ctctctctga 540
gaaagtctgt ttaattggct gtgggttttc cactggatat ggcgctgctg t 591
```

<210> 244

<211> 594

<212> DNA

<213> Homo sapiens

<400> 244

```
gaattcggca cgagaacaga gtgaactgag catcagtcag aaaaagtcta tgtttgcaga 60
aatacagatc caagacaaag acaggatggg cactgctgga aaagtattta aatgcaaagc 120
agctgtgctt tgggagcaga agcaaccctt ctccattgag gaaatagaag ttgccccacc 180
aaagactaaa gaagtgcga ttaagatttt ggccacagga atctgtcgca cagatgacca 240
```

<213> Homo sapiens

<220>

<221> misc_feature

<222> (399)

<223> n=A,T,C or G

<400> 238

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gaattcggca ccagccttct tggatcagga ccagtctcca ccccgtttct acagtggaga 60
tcagcctcct tcttatcttg gtgcaagtgt ggataaactc catcaccctt tagaatttgc 120
agacaaatct cccacacctc ctaatttacc tagcgataaa atctaccctc cttctgggtc 180
ccccgaagag aataccagca cagccaccat gacttacatg acaactactc cagcaacagc 240
ccaaatgagc accaaggaag ccagctggga tgtggctgaa caaccacca ctgctgattt 300
tgctgctgcc aacttccagc gcacgcacag aactaatcgt ccccttcccc ctccgccttc 360
ccagagatct gcagagcagc caccagttgt ggggcaggna caagcagcaa ccaatatagg 420
attaaataat tcccacaagg ttcaaggagt agttccagtt ccagagaggc cacctgaacc 480
tcgagccatg gatgaccctg cgtctgcctt catcagtgac agtggtgctg ctgctgctca 540
gtgtcccatg gctacagctg tccagccagg cctgcctgag aaagtgcggg acggtgcccc 600
ggtcccgtg ctg 613
```

<210> 239

<211> 613

<212> DNA

<213> Homo sapiens

<400> 239

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gaattcggca ccaggggaca ctgggtgctga gctggatgat gatcagcact ggtctgacag 60
cccgctggat gctgacagag agctgcgttt gccgtgcccc gctgaggggg aagcagagct 120
ggagctgagg gtgtcggaag atgaggagaa gctgcccggc tcaccgaagc accaagagag 180
aggtccctcc caagccacca gcccatccg gtctccccag gaatcagctc ttctgttcat 240
tccagtcacac agcccctcaa cagaggggccc ccaactccca cctgtccctg ccgccacca 300
ggagaaatca cctgaggagc gccttttccc tgagcctttg ctccccaaag agaagcccaa 360
agctgatgcc ccctcggatc tgaaagctgt gcactctccc atccgatcac agccagtgc 420
cctgccagaa gctaggactc ctgtctcacc agggagcccg cagccccagc caccctgtgc 480
ggctccacg cccccaccda gcgaggtctc cagagccttc tctctcctgt gcaaaatggc 540
aactcttaag gaaaaactca ttgcaccagt tgcggaagaa gaggcaacag ttccaaacaa 600
taagatcact gta 613
```

<210> 240

<211> 585

<212> DNA

<213> Homo sapiens

<400> 240

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gaattcggca cgaggtgaga tctacgatga actttaagat tggaggtgtg acagaacgca 60
tgccaacccc agttattaaa gcttttgcca tcttgaagcg agcgccgct gaagtaaacc 120
aggattatgg tcttgatcca aagattgcta atgcaataat gaaggcagca gatgaggtag 180
ctgaaggtaa attaaatgat cattttcctc tcgtggtatg gcagactgga tcaggaaactc 240
agacaaatat gaatgtaat gaagtcatta gcaatagagc aattgaaatg ttaggaggtg 300
aacttggcag caagatacct gtgcatccca acgatcatgt taataaaagc cagagctcaa 360
atgatacttt tcccacagca atgcacattg ctgctgcaat agaagttcat gaagtactgt 420
taccaggact acagaagtta catgatgctc ttgatgcaa atccaaagag tttgcacaga 480
tcataaagat tggacgtact catactcagg atgctgttcc acttactctt gggcaggaat 540
ttagtggtta tgttcaacaa gtaaaatatg caatgacaag aataa 585
```

<210> 241

<211> 566

<212> DNA

<210> 234
 <211> 379
 <212> DNA
 <213> Homo sapien

<400> 234
 gagggcagcc ctctacctg cgcacgtggt gccgcgcgtg ctgcctcccg ctgcgccctga 60
 acccagtgcc tgcagccatg gctcccggcc agctcgcctt atttagtgct tctgacaaaa 120
 ccggccttgt ggaatttgca agaaacctga ccgctcttgg ttggaatctg gtcgcttccg 180
 gagggactgc aaaagctctc agggatgctg gtctggcagt cacagatgct tctgagttga 240
 cgggatttct gaaatgttgg ggggacgtgt gaaaactttg catcctgcac gatcccatgc 300
 tggaatccta gctcctaata ttcagaagat aatgcttgac atgcgccaca cttgattcaa 360
 tcttataaca attgttgcc 379

<210> 235
 <211> 406
 <212> DNA
 <213> Homo sapien

<400> 235
 caggctgcac catgtacccc accttcagtt taaaagaaaa aaaaaatccc cttcactcct 60
 actgggaggt gggacccctt tcattttcag ttttgctcat ctagggaaaa taaggctttg 120
 gtttccagtt taattgtttt tgaccttcta aaatgttttt atgttagcac tgatagttgg 180
 cattactgtt gttaagcact gtgttccaga ccgtgtctga cttagtgtaa cctaggagat 240
 tttatagttt tattttaatg aaaccctgat tgacgcacag cagtggggag aacagcgtct 300
 tttacctgtc accgaagcca ggaagcccg tttgtaagcg tgtgttggtg tgctttattg 360
 tacatcctcc agtggcggtt tttttactct aatgttcttt tggttt 406

<210> 236
 <211> 278
 <212> DNA
 <213> Homo sapien

<400> 236
 gagattagca cctgtgaaca atgcgttctc tgatgacact ctgagcatgg accaacgcct 60
 tcttaagcta attctgcaaa atcacatatt gaaagtaaaa gttggcctta gcgacctcta 120
 caatggacag atactggaaa ccattggagg caaacaactc cgagtctttg tgtatcggac 180
 ggctatctgc atagaaaact catgcatggt gagaggaagc aagcaggga ggaacggtgc 240
 cattcacata ttccgagaga tcatccaacc agcagaat 278

<210> 237
 <211> 322
 <212> DNA
 <213> Homo sapien

<400> 237
 cagggccgtg gcggaggagg agcgtgcac ggtggagcgt cgggccgacc tcacctacgc 60
 ggagttcgtg cagcagtacg tgcgccctg atcgcggagg tcgcgtcctg ttcaccggcc 120
 cgtctgcccc gaccgccc aa ggcgccttc ccctgacctc gcgcgcacgc gtggggctgg 180
 ggccggcagg ctggcggtcc ggccctggcc cgactctgct cttctttcca gaggttccgg 240
 gccctgtgct cccgcgacag gttgctggct tcgtttgggg acagagtggc ccggtgagca 300
 ccgccaacac ctactcctac ct 322

<210> 238
 <211> 613
 <212> DNA

tggtgaatat	ctccctgcga	gtgttgcttc	gacccaatgc	tcaggagctt	cctagcatgt	120
accagcgctt	agggctggac	tacgaggaac	gagtgttgcc	gtccattgtc	aacgagggtgc	180
tcaagagtgt	ggtggccaag	ttcaatgcct	cacagctgat	cacccagcgg	gcccagggtat	240
ccctgttgat	ccgccgggag	ctgacagaaa	gggccaaagg	acttcagcct	catcctggat	300
gatgtggcca	tcacagactt	gagctttagc	cgagaagtac	acaagctgcc	tgtaaagaaac	360
ccaaccaagt	ggggtgaatt	ccaaaaaccc	gtgggggtga	agggcttctt	aagaatgcaa	420
ggaaggagga	aaagaattcc	atgggggggg	ggttccttaa	cccaggaaca	ggggtttccc	480
ttgaattttt	ttcca					495

<210> 231

<211> 498

<212> DNA

<213> Homo sapien

<400> 231

ggcagcttct	gagaccaggg	ttgctccgtc	cgtgctccgc	ctcgccatga	cttcctacag	60
ctatcgccag	tcgtcggcca	cgctcgtcct	cggaggcctg	ggcggcggct	ccgtgcgttt	120
tgggcggggg	gtcgtttttc	gcgcgccccag	cattcacggg	ggctccggcg	gccgcggcgt	180
atccgtgtcc	tcgcgccgct	ttgtgtcctc	gtcctcctcg	gggggctacg	gcggcggcta	240
cggcggcgct	ctgaccgcgt	ccgacgggct	gctggcgggc	aacgagaagc	taaccatgca	300
gaacctcaac	gaccgcctgc	ctcctacctg	gacaaagtgc	gcgccctgga	agcgggcaac	360
ggcgaaactta	gaggtgaaag	aatcccgcca	actggtacca	aaaacaaggg	gcctggggcc	420
ttccgcgact	tacagccaac	ttactacacc	gaacattcaa	gaacttgccg	gaacaaaaat	480
ttttggtgcc	acccattt					498

<210> 232

<211> 465

<212> DNA

<213> Homo sapien

<400> 232

caggccggcc	gagtaggaaa	gctggaggcg	cgggtgggga	acatgtctga	gtcggagctc	60
ggcaggaagt	gggaccggtg	tctggcggat	gcggctcgtga	agataggtac	tggttttgga	120
ttaggaattg	ttttctcact	taccttcttt	aaaagaagaa	tgtggccatt	agccttcggt	180
tctggcatgg	gattaggaat	ggcttattcc	aactgtcagc	atgatttcca	ggctccatat	240
cttctacatg	gaaaatatgt	caaagagcag	gagcagtgac	ttcacctgag	aacatcccag	300
cgggaggaca	agagaaaaatc	atgtttattc	ctcaggaata	cttgaagtgc	cctggagtaa	360
actgccattc	ttctgtaaca	atggtatcag	taatgcttta	aactccagca	cctggttatg	420
catttgaaac	ccaagtctgg	ttcttggttt	ggattttctc	tctgg		465

<210> 233

<211> 366

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(366)

<223> n = A,T,C or G

<400> 233

cagtaaaaaa	ggttatgttt	tattaattgc	tggacaaccg	tgggaaaaca	aataagcaat	60
tgacaccacc	aaattcttat	tacattcaan	ataaaanatt	tattcacacc	acaaaaagat	120
aatcacacaa	aaatatacac	taacttaaaa	aacaaaagat	tatagtgaac	taaaatgtta	180
tattctcttt	ttaagtgggt	aaaagtattt	tgtttgcttc	tacataaatt	tctattcatg	240
ananaataac	aaatattaaa	atacagtgat	agtttgcat	tcttctatag	aatgaacata	300
gacataaccc	tgaagctttt	agtttacagg	gagtttccat	gaagccacaa	actaaactaa	360
ttatca						366

ttgaagtttg aaaggtgttt agattcagaa gttgtcacct ttgaaatttt gtctgatgac 420
tactcaaaga ttgtcttctt acataatgat agatacattg aatttcattc gcaatcaggt 480
ttt 483

<210> 227
<211> 486
<212> DNA
<213> Homo sapien

<400> 227
gagcctcgct aagctccgac tctgggcggc accgggcgct ccacgatgcc gaagaacaag 60
aagcgggaaca ctccccaccg cggtagcagt gctggcggcg gcgggtcagg agcagccgca 120
gcgacggcgg cgacagcagg tggccagcat cgaatgttc agccttttag tgatgaagat 180
gcatcaattg aaacagtgag ccattgcagt ggttatagcg atccttcag ttttgctgaa 240
gatggaccag aagtccctga tgaggaagga actcaagaag acctagagta caagttgaag 300
ggattaattg acctaacctt ggataagagt gcgaagacaa ggcaagcagc tcttgaaggt 360
attaaaaatg cactggcttc aaaaatgctg tatgaattta ttctggaaag gagaatgact 420
ttaactgata gcattgaacg ctgcctgaaa aaaggttaaga gtgatgagca acgtgcagct 480
gcagcg 486

<210> 228
<211> 494
<212> DNA
<213> Homo sapien

<400> 228
gaggccagga ctccgggaat gcgagcaggc cccttattct ccagtggcc tcggtctgtc 60
cccacagcgg ccgggtcagg gttgccgag cccaaggcg gggggcggca ccggggtgct 120
gaaagggaca gaatgctttg acctccaagc tgttttaaat ctagtagata agccagatcc 180
tgtgttgcca taagcccttg gccacattt aagtgggaat gcagctagct tggatgtctg 240
aaactttgta agcgcttct gtctgaatcc tgaacacagg caccaagact actgaagaag 300
ctcgtcattc ttgtgcaggg atagccacac aagcaaacat gtttgcaaaa cttgaaagaa 360
agaaaattgc agaaagaaga cttgctgttc ttaagaggcc caggaaggtg ctacttagga 420
atcccaccgg cttgtgaagc aagggaatca agtttgctt caatggggaa cttgacttca 480
ggaaaatgaa cttt 494

<210> 229
<211> 465
<212> DNA
<213> Homo sapien

<400> 229
gtcagagagc tgggtataacc tctgttggc catgcagAAC cgactcaata aggtcatcaa 60
aagcgtgggc aagattgagc actccttctg gagatccttt cactatgagc gaaagacaga 120
accagccaca ggcttcacg atggtgatct gattgaaagt ttcctagata tcagccgccc 180
taagatgcag gaggttgttg caaacttgca gtatgatgat ggacgtggtg tgaagcggga 240
ggcaactgca gatgacctca tcaaagtcgt ggaggaacta actcgatcc attagccaag 300
gacaggatct cttttcctga ccctcctaaa ggcgttgccc tcctatcctc ctttccttgc 360
ccacccttgg tttctttggc atgggaagggt tttccttaac cacttgcctt agagccacca 420
gtgaccttgt gtggaaacag ggtttttttt acttaaaaca gttca 465

<210> 230
<211> 495
<212> DNA
<213> Homo sapien

<400> 230
caggggaaag ggtgtttggc cttgaccagc cactgctgac ctcaatctca gacctacaga 60

<400> 224

cagaccacgt	ctgccctcgc	cgctctagcc	ctgcgcccc	gcccggccgc	ggcacctccg	60
cctcgccgcc	gctaggtcgg	ccggctccgc	ccggctgccg	cctaggatga	atatcatgga	120
cttcaacgtg	aagaagctgg	cgggccgacgc	aggcaccttc	ctcagtcgcg	ccgtgcagtt	180
cacagaagaa	aagcttgcc	aggctgagaa	gacagaattg	gatgctcact	tagagaaact	240
ccttagcaaa	gctgaatgta	ccaaaatatg	gacagaaaaa	ataatgaaac	aaactgaagt	300
gttattgcag	ccaaatccaa	atgccaggat	agaagaattt	gtttatgaga	aactggatag	360
aaaagctcca	agtcgtataa	acaaccagaa	acttttgga	caatatatga	ttgatgcagg	420
gactgagttt	ggcccaggaa	cagcttatgg	taatgccctt	attaaatgtg	gagaaaccca	480
aaaaagaatt	ggaacagcag	acagagaact	gattcaaacg	tcagccttaa	attttcttac	540
tcctttaaga	aactttatag	aaggagatta	caaaacaatt	gctaaagaaa	ggaactattt	600
gcaaaataag	agactggatt	tggatgctgc	aaaaacgaga	ctaaaaaagg	caaaagctgc	660
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agcagagatt	accagacttc	tgctagaggg	aatcagcagt	acacatgccc	atcaccttcg	780
ctgtctgaat	gactttgtag	aagcccagat	gacttactat	gcacagtgtt	accagtatat	840
gttggaacctc	cagaaacaac	tgggaagttt	tccatccaat	tatcttagta	acaacaatca	900
gacttctgtg	acacctgtac	catcagtttt	accaaatgcg	attggttctt	ctgccatggc	960
ttcaacaagt	ggcctagtaa	tcacctctcc	ttccaacctc	agtgaacctt	aggagtgtag	1020
tggcagcaga	aaggccaggg	ttctctatga	ttatgatgca	gcaaacagta	ctgaattatc	1080
acttctggga	gatgaggtga	tcactgtgtt	cagtgttgtt	ggaatggatt	cagactggct	1140
aatgggggaa	aggggaaacc	agaagggcaa	ggtgccaat	acctacttag	aactgctcaa	1200
ttaagtaggt	ggactatgga	aagggtgccc	atcatgactt	tgtatttata	tacaattaac	1260
tctaaataaa	gcagggttaag	tatcttccat	gttaatgtgt	taagagactg	aaaataccag	1320
ccatcagaaa	ctggcctttt	tgccaataaa	gttgcatggt	aaatatattca	ttacagaatt	1380
tatgttagag	ctttcatgcc	aagaatgttt	tcttacaaaa	ttctcttttt	attgaggttt	1440
cactaataag	cagcttctac	ttttgagcct	caacttaag	cagaactgtt	ttttactgga	1500
tttttcatta	acagcaagct	tttttttta	tgtaaaataa	atctattgtg	aattgaaaaa	1560
aaaaaaaaaa	aaaaaaactc	gag				1583

<210> 225

<211> 491

<212> DNA

<213> Homo sapien

<400> 225

gaacaacatc	atcttgaatc	actagataga	ctcttgacgg	aaagcaaagg	ggaaatgaaa	60
aaggaaaata	tgaagaaaga	tgaagcttta	aaagcattac	agaaccaagt	atctgaagaa	120
acaatcaagg	ttaggcaact	agattcagca	ttggaaattt	gtaaggaaga	acttgtcttg	180
catttgaatc	aattggaagg	aaataaggaa	aagtttgaaa	aacagttaaa	gaagaaatct	240
gaagaggtat	attgtttaca	gaaagagcta	aagataaaaa	atcacagtct	tcaagagact	300
tctgagcaaa	acgttattct	acagcatact	cttcagcaac	agcagcaaat	gttacacaaa	360
gagacaatta	gaaatggaga	gctagaagat	actcaacta	aacttgaaaa	acaggtgtca	420
aaactggaac	aagaacttca	aaaacaaagg	gaaagttcag	ctgaaaagtt	gagaaaaatg	480
gaggagaaat	g					491

<210> 226

<211> 483

<212> DNA

<213> Homo sapien

<400> 226

cagccgcacg	ccgcggagca	ggggctcgga	ggtcccggga	ttacggtgct	cgagcacgct	60
ggtgggaaag	gacccgggac	ttgaacagtg	ttgtgcggcg	ccatgcaggt	ctccagcctc	120
aatgaggtga	agatttacag	cctcagctgc	ggcaagtccc	ttcctgagtg	gctttctgat	180
aggaagaaga	gagcgctaca	gaagaaaagt	gtagatgtcc	gtaggagaat	tgaacttatt	240
caggactttg	aaatgcctac	tgtgtgtacc	actattaagg	tgtcaaaaaga	tggacagtac	300
attttagcaa	ctggaaacata	taaacctcgg	gttcgatgtt	atgacaccta	tcaattatcc	360

catgcctctt	gggacgagat	cacaggactt	gacccatcat	caaataggac	caggtgacct	540
acagagacat	cacaatgatg	gcttcctaca	gtcaagtcca	tttccaataa	tgctctcatc	600
taagagaacc	catgaacctt	atttgaatcc	tggttcaaac	aaaaacctta	aattatttat	660
gagacaatta	taaacttgat	agattttgat	gtgtgaaggt	atttatgaat	atttttagtc	720
agtgatggta	tactgttaag	gaaaagggtc	atattttagg	gacaaaggct	gaaacattta	780
tggaacagagt	gatatgatat	ctgggatttg	ttttaggatg	aagtgggagg	gaggaaatga	840
atggaaatag	tggtgaaaca	gtattggcca	cgagtcagct	attgtgtgct	aagacgctcc	900
tcacaccagt	ctactctgta	tgtgtttgaa	tatctctgta	ataaacttaa	caaggaaaaa	960
aaaaaaaaaa	aaaaaaactc	gag				983

<210> 221

<211> 373

<212> DNA

<213> Homo sapien

<400> 221

cattttatgg	gttaattttt	tattaaatag	caataagata	cttttataac	tcaataaaat	60
tattcaatga	tacattcgga	aaataaatgt	ataaaatatg	aaaaagtact	aaaaagcatt	120
tttcagtact	tttaggtaag	attaatccaa	ctaaacacta	gcataatgta	tacagtaata	180
ataaggggaa	aatacaataa	tggtgagaaa	gcaaaactca	agcatagatc	aatgaaaaaa	240
ttgagaaatg	gacataaatg	atttagtatt	tttaaagaga	gtgaaaaatc	attattttat	300
gcittttgtg	agcgtagat	gaattaaata	acatatgcac	atatagcttt	gcgatacaaa	360
ttccagacc	ata					373

<210> 222

<211> 544

<212> DNA

<213> Homo sapien

<400> 222

cagagatgct	gctgctacaa	aggatcggtg	taagcagtta	accagggaaa	tgatgacaga	60
gaaagaaaga	agcaatgtgg	ttataacaag	gatgaaagat	cgaattggaa	cattagaaaa	120
ggaacataat	gtatttcaaa	acaaaataca	tgtagttat	caagagactc	aacagatgca	180
gatgaagttt	cagcaagttc	gtgagcagat	ggaggcagag	atagctcact	tgaagcagga	240
aaatggtata	ctgagagatg	cagtcagcaa	cactacaaat	caactggaaa	gcaagcagtc	300
tgacagaacta	aataaaactac	gccaggatta	tgctaggttg	gtgaatgagc	tgactgagaa	360
aacaggaaaag	ctacagcaag	aggaagtcca	aaagaagaat	gctgagcaag	cagctactca	420
gttgaagggt	caactacaag	aagctgagag	aagggtggaa	gaagttcaga	gctacatcag	480
gaagagaaca	gcggaacatg	aggcagcaca	gctagattta	cagagtaaat	ttgtggccaa	540
agaa						544

<210> 223

<211> 316

<212> DNA

<213> Homo sapien

<400> 223

gaggcaaggg	atatgcttta	gtgcctatta	tagttaattc	ttcaactcca	aagtctaaaa	60
cagttgaatc	tgctgaagga	aaatctgaag	aagtaaatga	aacattagtt	ataccactg	120
aggaagcaga	aatggaagaa	agtggaacga	gtgcaactcc	tggttaactgt	gaacagcctg	180
atatcttggt	ttcttctaca	ccaataaatg	aaggacagac	tgtgttagac	aagggtggctg	240
agcagtgtga	acctgctgaa	agtcagccag	aagcacttct	gagaggaaga	tgtttgcaag	300
gtaactctaa	cagttg					316

<210> 224

<211> 1583

<212> DNA

<213> Homo sapien

<210> 218
 <211> 381
 <212> DNA
 <213> Homo sapien

<400> 218
 gagtttcctt cgcaagttca tgtggggtac cttcccaggc tgcctggctg accagctggt 60
 tttaaagcgc cggggttaacc agttggagat ctgtgccgtg gtcctgaggc agttgtctcc 120
 acacaagtac tacttcctcg tgggctacag tgaaactttg ctgtcctact tttaaaaatg 180
 tcctgtgcga ctccacctcc aaactgtgcc ctcaaagggt gtgtataagt acctctagaa 240
 caatccccctt ttttccatca agctgtagcc tgcagagaat ggaaacgtgg gaaaggaatg 300
 gtatgtgggg gaaatgcatc ccctcagagg actgaggcat agtctctcat ctgctattga 360
 ataaagacct tctatcttgt a 381

<210> 219
 <211> 1293
 <212> DNA
 <213> Homo sapien

<400> 219
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 tactaccagt acctgctggt cagggcgctc tacatgctgg agccctggga gcggacgggtg 120
 ttcaattcca tgctggtttc cattgtgggg atggcactat acacaggata cgtcttcatg 180
 cccagcacca tcatggcgat attgcactac tttgaaatcg tacaatgacc aagatgagac 240
 caggatcaga ggttccttgg ggaagaccca ccctacgaag ttggaatgag accatcagat 300
 gtgataagaa actcttctag atgtcaacat aaccaacctt ataaagacta aaattcatga 360
 gtagaacagg aaaatcatcc tgactcatgt gttgtgttct ttatttttaa ttttcaaaga 420
 ggctcttgta tagcagtttt tgtctatttt aacattgtag tcatattgtac tttgatataca 480
 gtatttttctt aacctttgtg actgtttcaa tattaccccc gtgaaagctt ttcttaaatgt 540
 aactttgagt acatttttaat tgccttctat ttttaaaaact caaaatcatt agttgggctt 600
 tactgttctt gctattgtat ggcataataca tctgcctgga tatatttcta ctcttgacca 660
 aagttttgta aagaacaata taagattttcg ggtaggggta tggggaggga agatatttta 720
 ttgagaacta ctttaacaaaa gatttatctg taagcttgaa ctacaggagta cagtttttagc 780
 tatctagact ctaacagctt ttgcttttaa attattaaag tgtttcttaa tgaaaaagaa 840
 aagatcttgc taaagttaaa ataaggaaca tttcaccttt taaatattta attcttatgt 900
 ggacttattt ccagaaaaact ttggtgataa ttcttgagac aaaagggtgt taagtagcat 960
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 gggtcactat taacaatgta ctctcttaaa tttagtttaa tgattgtaat ggggtgctgca 1080
 tttgcacatt gcattaagtt atgatgagac gaattgttgt taaaaattat agcaaaaaaga 1140
 aatgtaaaact tgggttaaaat cctttcactc tttgtattgt tttttttaag gtttttatc 1200
 cttaaatgta aaatgactac ctaatttttt gatgtaaata cattaaattc aaagagaaaa 1260
 aaaatcaaaa aaaaaaaaaa aaaaaaaactc gag 1293

<210> 220
 <211> 983
 <212> DNA
 <213> Homo sapien

<400> 220
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 taaagtgacc ggaatgttag agatgcaatt tgcagagctg gggcaaggaa gggctccttg 120
 tcaactgtagt tactttcctt gcagtggcca aatgcccaat aagaaggaa acatgaccac 180
 tgctgtgggg agtcagcagg tgcgtgatgc agctggccac actccatcca cggccatgac 240
 ataaaaacaga caagaagtaa ggcctggactg taacacctca aggctgctc cagtgaacca 300
 cttttcttcag agaggctcta ccacacacac aaccaccttc caaatttaca ctacagatcac 360
 tacaccatgt ctcccaagtt aaaacatgta tccacctaga ctttaaatgt gctttgtaac 420
 tgttgatggc actgtacaga gggccaaagt atttcccatc agatagcatt tttctgaacc 480

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<210> 217
<211> 466
<212> DNA
<213> Homo sapien
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<400> 217							
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accaagatgg	tcgttactct	ctgacctata	tctacactgg	gctgtccaag	catgttgaag		120
acgtccccgc	gtttcaggcc	cttggctcac	tcaatgacct	ccagttcttt	agatacaaca		180
gtaaagacag	gaagtctcag	cccatgggac	tctggagaca	ggtggaagga	atggaggatt		240
ggaagcagga	cagccaactt	cagaaggcca	gggaggacat	ctttatggag	accctgaaag		300
acatcgtgga	gtattacaac	gacagtaacg	ggtctcacgt	attgcaggga	aggtttggtt		360
gtgagatcga	.gaataacaga	agcagcggag	cattctggaa	atattactat	gatggaaaag		420
actacattga	attcaacaaa	gaaatcccaq	cctgggtccc	cttcga			466

<210> 215
 <211> 148
 <212> PRT
 <213> Homo sapien

<400> 215
 Met Ala Thr Leu Lys Glu Lys Leu Ile Ala Pro Val Ala Glu Glu Glu
 1 5 10 15
 Ala Thr Val Pro Asn Asn Lys Ile Thr Val Val Gly Val Gly Gln Val
 20 25 30
 Gly Met Ala Cys Ala Ile Ser Ile Leu Gly Lys Ser Leu Ala Asp Glu
 35 40 45
 Leu Ala Leu Val Asp Val Leu Glu Asp Lys Leu Lys Gly Glu Met Met
 50 55 60
 Asp Leu Gln His Gly Ser Leu Phe Leu Gln Thr Pro Lys Ile Val Ala
 65 70 75 80
 Asp Lys Asp Tyr Ser Val Thr Ala Asn Ser Lys Ile Val Val Val Thr
 85 90 95
 Ala Gly Val Arg Gln Gln Glu Gly Glu Ser Arg Leu Asn Leu Val Gln
 100 105 110
 Arg Asn Val Asn Val Phe Lys Phe Ile Ile Pro Gln Ile Val Lys Tyr
 115 120 125
 Ser Pro Asp Cys Ile Ile Ile Val Val Ser Asn Pro Val Asp Ile Leu
 130 135 140
 Thr Tyr Val Thr
 145

<210> 216
 <211> 527
 <212> PRT
 <213> Homo sapien

<400> 216
 Gln Arg Ala Pro Gly Ile Glu Glu Lys Ala Ala Glu Asn Gly Ala Leu
 1 5 10 15
 Gly Ser Pro Glu Arg Glu Glu Lys Val Leu Glu Asn Gly Glu Leu Thr
 20 25 30
 Pro Pro Arg Arg Glu Glu Lys Ala Leu Glu Asn Gly Glu Leu Arg Ser
 35 40 45
 Pro Glu Ala Gly Glu Lys Val Leu Val Asn Gly Gly Leu Thr Pro Pro
 50 55 60
 Lys Ser Glu Asp Lys Val Ser Glu Asn Gly Gly Leu Arg Phe Pro Arg
 65 70 75 80
 Asn Thr Glu Arg Pro Pro Glu Thr Gly Pro Trp Arg Ala Pro Gly Pro
 85 90 95
 Trp Glu Lys Thr Pro Glu Ser Trp Gly Pro Ala Pro Thr Ile Gly Glu
 100 105 110
 Pro Ala Pro Glu Thr Ser Leu Glu Arg Ala Pro Ala Pro Ser Ala Val
 115 120 125
 Val Ser Ser Arg Asn Gly Gly Glu Thr Ala Pro Gly Pro Leu Gly Pro
 130 135 140
 Ala Pro Lys Asn Gly Thr Leu Glu Pro Gly Thr Glu Arg Arg Ala Pro
 145 150 155 160
 Glu Thr Gly Gly Ala Pro Arg Ala Pro Gly Ala Gly Arg Leu Asp Leu
 165 170 175
 Gly Ser Gly Gly Arg Ala Pro Val Gly Thr Gly Thr Ala Pro Gly Gly

65				70				75				80			
Gly	Ser	Ile	Gly	Asn	Tyr	Cys	Gln	Asp	Val	Thr	Asp	Ala	Gln	Ile	Lys
				85				90					95		
Asn	Glu	Leu	Leu	Glu	Ser	Glu	Met	Lys	Asn	Leu	Lys	Lys	Cys	Val	Ser
			100					105					110		
Glu	Leu	Glu	Glu	Glu	Lys	Gln	Gln	Leu	Val	Lys	Glu	Lys	Thr	Lys	Val
		115					120					125			
Glu	Ser	Glu	Ile	Arg	Lys	Glu	Tyr	Leu	Glu	Lys	Ile	Gln	Gly		
	130					135					140				

<210> 213

<211> 142

<212> PRT

<213> Homo sapien

<400> 213

Gly	Gly	Tyr	Gly	Gly	Gly	Tyr	Gly	Gly	Val	Leu	Thr	Ala	Ser	Asp	Gly
1			5					10						15	
Leu	Leu	Ala	Gly	Asn	Glu	Lys	Leu	Thr	Met	Gln	Asn	Leu	Asn	Asp	Arg
		20					25					30			
Leu	Ala	Ser	Tyr	Leu	Asp	Lys	Val	Arg	Ala	Leu	Glu	Ala	Ala	Asn	Gly
	35					40					45				
Glu	Leu	Glu	Val	Lys	Ile	Arg	Asp	Trp	Tyr	Gln	Lys	Gln	Gly	Pro	Gly
	50				55					60					
Pro	Ser	Arg	Asp	Tyr	Ser	His	Tyr	Tyr	Thr	Thr	Ile	Gln	Asp	Leu	Arg
65				70					75					80	
Asp	Lys	Ile	Leu	Gly	Ala	Thr	Ile	Glu	Asn	Ser	Arg	Ile	Val	Leu	Gln
			85					90					95		
Ile	Asp	Asn	Ala	Arg	Leu	Ala	Ala	Asp	Asp	Phe	Arg	Thr	Lys	Phe	Glu
		100					105					110			
Thr	Glu	Gln	Ala	Leu	Arg	Met	Ser	Val	Glu	Ala	Asp	Ile	Asn	Gly	Leu
	115					120					125				
Arg	Arg	Val	Leu	Asp	Glu	Leu	Thr	Leu	Ala	Arg	Thr	Asp	Leu		
	130					135					140				

<210> 214

<211> 129

<212> PRT

<213> Homo sapien

<400> 214

Val	Met	Arg	Val	Asp	Phe	Asn	Val	Pro	Met	Lys	Asn	Asn	Gln	Ile	Thr
1			5					10					15		
Asn	Asn	Gln	Arg	Ile	Lys	Ala	Ala	Val	Pro	Ser	Ile	Lys	Phe	Cys	Leu
		20					25					30			
Asp	Asn	Gly	Ala	Lys	Ser	Val	Val	Leu	Met	Ser	His	Leu	Gly	Arg	Pro
	35					40					45				
Asp	Gly	Val	Pro	Met	Pro	Asp	Lys	Tyr	Ser	Leu	Glu	Pro	Val	Ala	Val
	50				55					60					
Glu	Leu	Arg	Ser	Leu	Leu	Gly	Lys	Asp	Val	Leu	Phe	Leu	Lys	Asp	Cys
65				70					75					80	
Val	Gly	Pro	Glu	Val	Glu	Lys	Ala	Cys	Ala	Asn	Pro	Ala	Ala	Gly	Ser
			85				90					95			
Val	Ile	Leu	Leu	Glu	Asn	Leu	Arg	Phe	His	Val	Glu	Glu	Glu	Gly	Lys
		100					105					110			
Gly	Lys	Asp	Ala	Ser	Gly	Asn	Lys	Val	Lys	Ala	Glu	Pro	Ala	Lys	Ile
	115					120					125				

Glu

<213> Homo sapien

<400> 210

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Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly Lys Glu
1      5      10      15
Val Leu Leu Leu Ala His Asn Leu Pro Gln Asn Arg Ile Gly Tyr Ser
      20      25      30
Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Ser Leu Ile Val Gly Tyr
      35      40      45
Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser Gly Arg
      50      55      60
Glu Thr Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Val Thr Gln
65      70      75      80
Asn Asp Thr Gly Phe Tyr Thr Leu Gln Val Ile Lys Ser Asp Leu Val
      85      90      95
Asn Glu Glu Ala Thr Gly Gln Phe His Val Tyr Pro Glu Leu Pro Lys
      100      105      110
Pro Ser Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys Asp Ala
      115      120      125
Val Ala Phe Thr Cys Glu Pro Glu Val Gln Asn Thr Thr Tyr Leu Trp
130      135      140
Trp Val Asn Gly Gln Ser Leu Pro Val Ser Pro Lys
145      150      155

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<210> 211

<211> 92

<212> PRT

<213> Homo sapien

<400> 211

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Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln
1      5      10      15
Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
      20      25      30
Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
      35      40      45
Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
      50      55      60
Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
65      70      75      80
Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly
      85      90

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<210> 212

<211> 142

<212> PRT

<213> Homo sapien

<400> 212

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Glu Lys Gln Lys Asn Lys Glu Phe Ser Gln Thr Leu Glu Asn Glu Lys
1      5      10      15
Asn Thr Leu Leu Ser Gln Ile Ser Thr Lys Asp Gly Glu Leu Lys Met
      20      25      30
Leu Gln Glu Glu Val Thr Lys Met Asn Leu Leu Asn Gln Gln Ile Gln
      35      40      45
Glu Glu Leu Ser Arg Val Thr Lys Leu Lys Glu Thr Ala Glu Glu Glu
      50      55      60
Lys Asp Asp Leu Glu Glu Arg Leu Met Asn Gln Leu Ala Glu Leu Asn

```

20 25 30
 Ala Pro Gly Pro Lys Gly Glu Gly Glu Arg Pro Ala Gln Asn Glu Lys
 35 40 45
 Arg Lys Glu Lys Asn Ile Lys Arg Gly Gly Asn Arg Phe Glu Pro Tyr
 50 55 60
 Ala Asn Pro Thr Lys Arg Tyr Arg Ala Phe Ile Thr Asn Ile Pro Phe
 65 70 75 80
 Asp Val Lys Trp Gln Ser Leu Lys Asp Leu Val Lys Glu Lys Val Gly
 85 90 95
 Glu Val Thr Tyr Val Glu Leu Leu Met Asp Ala Glu Gly Lys Ser Arg
 100 105 110
 Gly Cys Ala Val Val Glu Phe Lys Met Glu Glu Ser Met Lys Lys Ala
 115 120 125
 Ala Glu Val Leu Asn Lys His Ser Leu Ser Gly Arg Pro Leu Lys Val
 130 135 140
 Lys Glu Asp Pro Asp Gly Glu His Ala Arg Arg Ala Met Gln Lys Val
 145 150 155 160
 Met Ala Thr Thr Gly Gly Met Gly Met Gly Pro Gly Gly Pro Gly Met
 165 170 175
 Ile

<210> 209
 <211> 196
 <212> PRT
 <213> Homo sapien

<400> 209
 Asp Leu Gln Asp Met Phe Ile Val His Thr Ile Glu Glu Ile Glu Gly
 1 5 10 15
 Leu Ile Ser Ala His Asp Gln Phe Lys Ser Thr Leu Pro Asp Ala Asp
 20 25 30
 Arg Glu Arg Glu Ala Ile Leu Ala Ile His Lys Glu Ala Gln Arg Ile
 35 40 45
 Ala Glu Ser Asn His Ile Lys Leu Ser Gly Ser Asn Pro Tyr Thr Thr
 50 55 60
 Val Thr Pro Gln Ile Ile Asn Ser Lys Trp Glu Lys Val Gln Gln Leu
 65 70 75 80
 Val Pro Lys Arg Asp His Ala Leu Leu Glu Glu Gln Ser Lys Gln Gln
 85 90 95
 Ser Asn Glu His Leu Arg Arg Gln Phe Ala Ser Gln Ala Asn Val Val
 100 105 110
 Gly Pro Trp Ile Gln Thr Lys Met Glu Glu Ile Gly Arg Ile Ser Ile
 115 120 125
 Glu Met Asn Gly Thr Leu Glu Asp Gln Leu Ser His Leu Lys Gln Tyr
 130 135 140
 Glu Arg Ser Ile Val Asp Tyr Lys Pro Asn Leu Asp Leu Leu Glu Gln
 145 150 155 160
 Gln His Gln Leu Ile Gln Glu Ala Leu Ile Phe Asp Asn Lys His Thr
 165 170 175
 Asn Tyr Thr Met Glu His Ile Arg Val Gly Trp Glu Gln Leu Leu Thr
 180 185 190
 Thr Ile Ala Arg
 195

<210> 210
 <211> 156
 <212> PRT

50 55 60
 Phe Gly Pro Thr Gly Cys Gln Gly Ala Cys Leu Gly Cys Arg Asp His
 65 70 75 80
 Thr Gly Gly Glu His Cys Glu Arg Cys Ile Ala Gly Phe His Gly Asp
 85 90 95
 Pro Arg Leu Pro Tyr Gly Gly Gln Cys Arg Pro Cys Pro Cys Pro Glu
 100 105 110
 Gly Pro Gly Ser Gln Arg His Phe Ala Thr Ser Cys His Gln Asp Glu
 115 120 125
 Tyr Ser Gln Gln Ile Val Cys His Cys Arg Ala Gly Tyr Thr Gly Leu
 130 135 140
 Arg Cys Glu Ala Cys Ala Pro Gly His Phe Gly Asp Pro Ser Arg Pro
 145 150 155 160
 Gly Gly Arg Cys Gln Leu Cys Glu Cys Ser Gly Asn Ile Asp Pro Met
 165 170 175
 Asp Pro Asp Ala Cys Asp Pro His Thr Gly Gln Cys Leu Arg Cys Leu
 180 185 190
 His His Thr Glu Gly
 195

<210> 207

<211> 175

<212> PRT

<213> Homo sapien

<400> 207

Ile Ile Arg Gln Gln Gly Leu Ala Ser Tyr Asp Tyr Val Arg Arg Arg
 1 5 10 15
 Leu Thr Ala Glu Asp Leu Phe Glu Ala Arg Ile Ile Ser Leu Glu Thr
 20 25 30
 Tyr Asn Leu Leu Arg Glu Gly Thr Arg Ser Leu Arg Glu Ala Leu Glu
 35 40 45
 Ala Glu Ser Ala Trp Cys Tyr Leu Tyr Gly Thr Gly Ser Val Ala Gly
 50 55 60
 Val Tyr Leu Pro Gly Ser Arg Gln Thr Leu Ser Ile Tyr Gln Ala Leu
 65 70 75 80
 Lys Lys Gly Leu Leu Ser Ala Glu Val Ala Arg Leu Leu Leu Glu Ala
 85 90 95
 Gln Ala Ala Thr Gly Phe Leu Leu Asp Pro Val Lys Gly Glu Arg Leu
 100 105 110
 Thr Val Asp Glu Ala Val Arg Lys Gly Leu Val Gly Pro Glu Leu His
 115 120 125
 Asp Arg Leu Leu Ser Ala Glu Arg Ala Val Thr Gly Tyr Arg Asp Pro
 130 135 140
 Tyr Thr Glu Gln Thr Ile Ser Leu Phe Gln Ala Met Lys Lys Glu Leu
 145 150 155 160
 Ile Pro Thr Glu Glu Ala Leu Arg Leu Trp Met Pro Ser Trp Pro
 165 170 175

<210> 208

<211> 177

<212> PRT

<213> Homo sapien

<400> 208

Met Ala Ala Gly Val Glu Ala Ala Ala Glu Val Ala Ala Thr Glu Ile
 1 5 10 15
 Lys Met Glu Glu Glu Ser Gly Ala Pro Gly Val Pro Ser Gly Asn Gly


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      115      120      125
Ser Phe Ile Arg Ser Gln Asn Lys Glu Asp Tyr Asp Gly Leu Lys Glu
  130      135      140
Glu Phe Arg Lys Glu Phe Thr Lys Leu Glu Glu Val Leu Thr Asn Lys
145      150      155      160
Lys Thr Thr Phe Phe Gly Gly Asn Ser Ile Ser Met Ile Asp Tyr Leu
      165      170      175
Ile Trp Pro Trp Phe Glu Arg Leu Glu Ala Met Lys Leu Asn Glu Cys
      180      185      190
Val Asp His Thr Pro Lys Leu Lys Leu Trp Met Ala Ala Met Lys Glu
      195      200      205
Asp Pro Thr Val Ser Ala Leu Leu Thr Ser Glu Lys Asp Trp Gln Gly
      210      215      220
Phe Leu Glu Leu Tyr Leu Gln Asn Ser Pro Glu Ala Cys Asp Tyr Gly
225      230      235      240
Leu

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<210> 205
<211> 160
<212> PRT
<213> Homo sapien

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      <400> 205
Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu
  1      5      10      15
Val Glu Pro Ser Asp Thr Ile Glu Asn Val Lys Ala Lys Ile Gln Asp
      20      25      30
Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys
      35      40      45
Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu
      50      55      60
Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Met Gln Ile Phe
65      70      75      80
Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Pro Ser
      85      90      95
Asp Thr Ile Glu Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile
      100      105      110
Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp
      115      120      125
Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His
      130      135      140
Leu Val Leu Arg Leu Arg Gly Gly Met Gln Ile Phe Val Lys Thr Leu
145      150      155      160

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<210> 206
<211> 197
<212> PRT
<213> Homo sapien

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      <400> 206
Thr Ser Pro Ser Glu Ala Cys Ala Pro Leu Leu Ile Ser Leu Ser Thr
  1      5      10      15
Leu Ile Tyr Asn Gly Ala Leu Pro Cys Gln Cys Asn Pro Gln Gly Ser
      20      25      30
Leu Ser Ser Glu Cys Asn Pro His Gly Gly Gln Cys Leu Cys Lys Pro
      35      40      45
Gly Val Val Gly Arg Arg Cys Asp Leu Cys Ala Pro Gly Tyr Tyr Gly

```

130 135 140
 Lys Glu Asp Pro Asp Gly Glu His Ala Arg Arg Ala Met Gln Lys Ala
 145 150 155 160
 Gly Arg Leu Gly Ser Thr Val Phe Val Ala Asn Leu Asp Tyr Lys Val
 165 170 175
 Gly

<210> 203
 <211> 164
 <212> PRT
 <213> Homo sapien

<400> 203
 Met Arg Leu Ala Val Gly Ala Leu Leu Val Cys Ala Val Leu Gly Leu
 1 5 10 15
 Cys Leu Ala Val Pro Asp Lys Thr Val Arg Trp Cys Ala Val Ser Glu
 20 25 30
 His Glu Ala Thr Lys Cys Gln Ser Phe Arg Asp His Met Lys Ser Val
 35 40 45
 Ile Pro Ser Asp Gly Pro Ser Val Ala Cys Val Lys Lys Ala Ser Tyr
 50 55 60
 Leu Asp Cys Ile Arg Ala Ile Ala Ala Asn Glu Ala Asp Ala Val Thr
 65 70 75 80
 Leu Asp Ala Gly Leu Val Tyr Asp Ala Tyr Leu Ala Pro Asn Asn Leu
 85 90 95
 Lys Pro Val Val Ala Glu Phe Tyr Gly Ser Lys Glu Asp Pro Gln Thr
 100 105 110
 Phe Tyr Tyr Ala Val Ala Val Val Lys Lys Asp Ser Gly Phe Gln Met
 115 120 125
 Asn Gln Leu Arg Gly Lys Lys Ser Cys His Thr Gly Leu Gly Arg Ser
 130 135 140
 Ala Gly Trp Asn Ile Pro Ile Gly Leu Leu Tyr Cys Asp Leu Pro Glu
 145 150 155 160
 Pro Arg Lys Pro

<210> 204
 <211> 241
 <212> PRT
 <213> Homo sapien

<400> 204
 Met Ser Gly Glu Ser Ala Arg Ser Leu Gly Lys Gly Ser Ala Pro Pro
 1 5 10 15
 Gly Pro Val Pro Glu Gly Ser Ile Arg Ile Tyr Ser Met Arg Phe Cys
 20 25 30
 Pro Phe Ala Glu Arg Thr Arg Leu Val Leu Lys Ala Lys Gly Ile Arg
 35 40 45
 His Glu Val Ile Asn Ile Asn Leu Lys Asn Lys Pro Glu Trp Phe Phe
 50 55 60
 Lys Lys Asn Pro Phe Gly Leu Val Pro Val Leu Glu Asn Ser Gln Gly
 65 70 75 80
 Gln Leu Ile Tyr Glu Ser Ala Ile Thr Cys Glu Tyr Leu Asp Glu Ala
 85 90 95
 Tyr Pro Gly Lys Lys Leu Leu Pro Asp Asp Pro Tyr Glu Lys Ala Cys
 100 105 110
 Gln Lys Met Ile Leu Glu Leu Phe Ser Lys Val Pro Ser Leu Val Gly

```

      1           5           10           15
His Lys Tyr Ser Gly Arg Glu Gly Asp Lys His Thr Leu Ser Lys Lys
      20           25           30
Glu Leu Lys Glu Leu Ile Gln Lys Glu Leu Thr Ile Gly Ser Lys Leu
      35           40           45
Gln Asp Ala Glu Ile Ala Arg Leu Met Glu Asp Leu Asp Arg Asn Lys
      50           55           60
Asp Gln Glu Val Asn Phe Gln Glu Tyr Val Thr Phe Leu Gly Ala Leu
      65           70           75           80
Ala Leu Ile Tyr Asn Glu Ala Leu Lys Gly
      85           90

```

<210> 201
 <211> 120
 <212> PRT
 <213> Homo sapien

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      <400> 201
Met Glu Thr Pro Ser Gln Arg Arg Ala Thr Arg Ser Gly Ala Gln Ala
      1           5           10           15
Ser Ser Thr Pro Leu Ser Pro Thr Arg Ile Thr Arg Leu Gln Glu Lys
      20           25           30
Glu Asp Leu Gln Glu Leu Asn Asp Arg Leu Ala Val Tyr Ile Asp Arg
      35           40           45
Val Arg Ser Leu Glu Thr Glu Asn Ala Gly Leu Arg Leu Arg Ile Thr
      50           55           60
Glu Ser Glu Glu Val Val Ser Arg Glu Val Ser Gly Ile Lys Ala Ala
      65           70           75           80
Tyr Glu Ala Glu Leu Gly Asp Ala Arg Lys Thr Leu Asp Ser Val Ala
      85           90           95
Lys Glu Arg Ala Arg Leu Gln Leu Glu Leu Ser Lys Val Arg Glu Glu
      100          105          110
Phe Lys Glu Leu Lys Ala Arg Asn
      115          120

```

<210> 202
 <211> 177
 <212> PRT
 <213> Homo sapien

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      <400> 202
Met Ala Ala Gly Val Glu Ala Ala Ala Glu Val Ala Ala Thr Glu Ile
      1           5           10           15
Lys Met Glu Glu Glu Ser Gly Ala Pro Gly Val Pro Ser Gly Asn Gly
      20           25           30
Ala Pro Gly Pro Lys Gly Glu Gly Glu Arg Pro Ala Gln Asn Glu Lys
      35           40           45
Arg Lys Glu Lys Asn Ile Lys Arg Gly Gly Asn Arg Phe Glu Pro Tyr
      50           55           60
Ala Asn Pro Thr Lys Arg Tyr Arg Ala Phe Ile Thr Asn Ile Pro Phe
      65           70           75           80
Asp Val Lys Trp Gln Ser Leu Lys Asp Leu Val Lys Glu Lys Val Gly
      85           90           95
Glu Val Thr Tyr Val Glu Leu Leu Met Asp Ala Glu Gly Lys Ser Arg
      100          105          110
Gly Cys Ala Val Val Glu Phe Lys Met Glu Glu Ser Met Lys Lys Ala
      115          120          125
Ala Glu Val Leu Asn Lys His Ser Leu Ser Gly Arg Pro Leu Lys Val

```

Ser Glu Ala Glu Leu Ser Pro Glu Thr Leu Cys Asn Gly Gln Leu Gly
 100 105 110
 Cys Ser Asp Pro Ala Phe Leu Thr Pro Ser Pro Thr Lys Arg Leu Ser
 115 120 125
 Ser Lys Lys Val Ala Arg Tyr Leu His Gln
 130 135

<210> 198
 <211> 100
 <212> PRT
 <213> Homo sapien

<400> 198
 Met Gly Asp Val Lys Asn Phe Leu Tyr Ala Trp Cys Gly Lys Arg Lys
 1 5 10 15
 Met Thr Pro Ser Tyr Glu Ile Arg Ala Val Gly Asn Lys Asn Arg Gln
 20 25 30
 Lys Phe Met Cys Glu Val Gln Val Glu Gly Tyr Asn Tyr Thr Gly Met
 35 40 45
 Gly Asn Ser Thr Asn Lys Lys Asp Ala Gln Ser Asn Ala Ala Arg Asp
 50 55 60
 Phe Val Asn Tyr Leu Val Arg Ile Asn Glu Ile Lys Ser Glu Glu Val
 65 70 75 80
 Pro Ala Phe Gly Val Ala Ser Pro Pro Pro Leu Thr Asp Thr Pro Asp
 85 90 95
 Thr Thr Ala Asn
 100

<210> 199
 <211> 127
 <212> PRT
 <213> Homo sapien

<400> 199
 Met Val Lys Glu Thr Thr Tyr Tyr Asp Val Leu Gly Val Lys Pro Asn
 1 5 10 15
 Ala Thr Gln Glu Glu Leu Lys Lys Ala Tyr Arg Lys Leu Ala Leu Lys
 20 25 30
 Tyr His Pro Asp Lys Asn Pro Asn Glu Gly Glu Lys Phe Lys Gln Ile
 35 40 45
 Ser Gln Ala Tyr Glu Val Leu Ser Asp Ala Lys Lys Arg Glu Leu Tyr
 50 55 60
 Asp Lys Gly Gly Glu Gln Ala Ile Lys Glu Gly Gly Ala Gly Gly Gly
 65 70 75 80
 Phe Gly Ser Pro Met Asp Ile Phe Asp Met Phe Phe Gly Gly Gly Gly
 85 90 95
 Arg Met Gln Arg Glu Arg Arg Gly Lys Asn Val Val His Gln Leu Ser
 100 105 110
 Val Thr Leu Glu Asp Leu Tyr Asn Gly Ala Thr Arg Lys Leu Ala
 115 120 125

<210> 200
 <211> 90
 <212> PRT
 <213> Homo sapien

<400> 200
 Met Ala Cys Pro Leu Asp Gln Ala Ile Gly Leu Leu Val Ala Ile Phe

Gln Thr Lys Ile Leu Glu Glu Asp Leu Glu Gln Ile Lys Leu Ser Leu
 1 5 10 15
 Arg Glu Arg Gly Arg Glu Leu Thr Thr Gln Arg Gln Leu Met Gln Glu
 20 25 30
 Arg Ala Glu Glu Gly Lys Gly Pro Ser Lys Ala Gln Arg Gly Ser Leu
 35 40 45
 Glu His Met Lys Leu Ile Leu Arg Asp Lys Glu Lys Glu Val Glu Cys
 50 55 60
 Gln Gln Glu His Ile His Glu Leu Gln Glu Leu Lys Asp Gln Leu Glu
 65 70 75 80
 Gln Gln Leu Gln Gly Leu His Arg Lys Val Gly Glu Thr Ser Leu Leu
 85 90 95
 Leu Ser Gln Arg Glu Gln Glu Ile Val Val Leu Gln Gln Gln Leu Gln
 100 105 110
 Glu Ala Arg Glu Gln Gly Glu Leu Lys Glu Gln Ser Leu Gln Ser Gln
 115 120 125
 Leu Asp Glu Ala Gln Arg Ala Leu Ala Gln
 130 135

<210> 196
 <211> 102
 <212> PRT
 <213> Homo sapien

<400> 196
 Met Ser Lys Arg Lys Ala Pro Gln Glu Thr Leu Asn Gly Gly Ile Thr
 1 5 10 15
 Asp Met Leu Thr Glu Leu Ala Asn Phe Glu Lys Asn Val Ser Gln Ala
 20 25 30
 Ile His Lys Tyr Asn Ala Tyr Arg Lys Ala Ala Ser Val Ile Ala Lys
 35 40 45
 Tyr Pro His Lys Ile Lys Ser Gly Ala Glu Ala Lys Lys Leu Pro Gly
 50 55 60
 Val Gly Thr Lys Ile Ala Glu Lys Ile Asp Glu Phe Leu Ala Thr Gly
 65 70 75 80
 Lys Leu Arg Lys Leu Glu Lys Ile Arg Gln Asp Asp Thr Ser Ser Ser
 85 90 95
 Ile Asn Phe Leu Thr Arg
 100

<210> 197
 <211> 138
 <212> PRT
 <213> Homo sapien

<400> 197
 Glu Ala Asn Glu Val Thr Asp Ser Ala Tyr Met Gly Ser Glu Ser Thr
 1 5 10 15
 Tyr Ser Glu Cys Glu Thr Phe Thr Asp Glu Asp Thr Ser Thr Leu Val
 20 25 30
 His Pro Glu Leu Gln Pro Glu Gly Asp Ala Asp Ser Ala Gly Gly Ser
 35 40 45
 Ala Val Pro Ser Glu Cys Leu Asp Ala Met Glu Glu Pro Asp His Gly
 50 55 60
 Ala Leu Leu Leu Leu Pro Gly Arg Pro His Pro His Gly Gln Ser Val
 65 70 75 80
 Ile Thr Val Ile Gly Gly Glu Glu His Phe Glu Asp Tyr Gly Glu Gly
 85 90 95

Ser Ser Leu Pro Gln Ile Pro Thr Pro Thr Leu Pro Pro Pro Pro Ser
 385 390 395 400
 Glu Thr Asp Phe Met Leu Gln Val Phe Gln Pro Ser Pro Ser Leu Ala
 405 410 415
 Pro Arg Met Pro Phe Ser Ile Gly Gln Val Thr Met Pro Met Val Met
 420 425 430
 Pro Ser Ala Asp Pro Arg Ser Leu Ser Phe Pro Ile Leu Asn Pro Ala
 435 440 445
 Leu Ser Gln Pro Ser Gln Pro Ser Ser Pro Leu Pro Gly Ser His Gly
 450 455 460
 Arg Asn Ser Pro Gly Leu Gly Ser Leu Val Ser
 465 470 475

<210> 194

<211> 241

<212> PRT

<213> Homo sapien

<400> 194

Met Ser Gly Glu Ser Ala Arg Ser Leu Gly Lys Gly Ser Ala Pro Pro
 1 5 10 15
 Gly Pro Val Pro Glu Gly Ser Ile Arg Ile Tyr Ser Met Arg Phe Cys
 20 25 30
 Pro Phe Ala Glu Arg Thr Arg Leu Val Leu Lys Ala Lys Gly Ile Arg
 35 40 45
 His Glu Val Ile Asn Ile Asn Leu Lys Asn Lys Pro Glu Trp Phe Phe
 50 55 60
 Lys Lys Asn Pro Phe Gly Leu Val Pro Val Leu Glu Asn Ser Gln Gly
 65 70 75 80
 Gln Leu Ile Tyr Glu Ser Ala Ile Thr Cys Glu Tyr Leu Asp Glu Ala
 85 90 95
 Tyr Pro Gly Lys Lys Leu Leu Pro Asp Asp Pro Tyr Glu Lys Ala Cys
 100 105 110
 Gln Lys Met Ile Leu Glu Leu Phe Ser Lys Val Pro Ser Leu Val Gly
 115 120 125
 Ser Phe Ile Arg Ser Gln Asn Lys Glu Asp Tyr Ala Gly Leu Lys Glu
 130 135 140
 Glu Phe Arg Lys Glu Phe Thr Lys Leu Glu Glu Val Leu Thr Asn Lys
 145 150 155 160
 Lys Thr Thr Phe Phe Gly Gly Asn Ser Ile Ser Met Ile Asp Tyr Leu
 165 170 175
 Ile Trp Pro Trp Phe Glu Arg Leu Glu Ala Met Lys Leu Asn Glu Cys
 180 185 190
 Val Asp His Thr Pro Lys Leu Lys Leu Trp Met Ala Ala Met Lys Glu
 195 200 205
 Asp Pro Thr Val Ser Ala Leu Leu Thr Ser Glu Lys Asp Trp Gln Gly
 210 215 220
 Phe Leu Glu Leu Tyr Leu Gln Asn Ser Pro Glu Ala Cys Asp Tyr Gly
 225 230 235 240
 Leu

<210> 195

<211> 138

<212> PRT

<213> Homo sapien

<400> 195

305 310 315 320
Ala Glu Gly Lys Thr Ser Leu His Lys Asp Leu .
 325 330

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<210> 193
<211> 475
<212> PRT
<213> Homo sapien
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	<400>	193														
Lys 1	Asn	Ser	Pro	Leu 5	Leu	Ser	Val	Ser	Ser	Gln	Thr	Ile	Thr	Lys 15	Glu	
Asn	Asn	Arg	Asn 20	Val	His	Leu	Glu	His 25	Ser	Glu	Gln	Asn 30	Pro	Gly	Ser	
Ser	Ala	Gly 35	Asp	Thr	Ser	Ala	Ala 40	His	Gln	Val	Val	Leu 45	Gly	Glu	Asn	
Leu	Ile 50	Ala	Thr	Ala	Leu	Cys 55	Leu	Ser	Gly	Ser	Gly 60	Ser	Gln	Ser	Asp	
Leu 65	Lys	Asp	Val	Ala	Ser 70	Thr	Ala	Gly	Glu	Glu 75	Gly	Asp	Thr	Ser	Leu 80	
Arg	Glu	Ser	Leu 85	His	Pro	Val	Thr	Arg	Ser 90	Leu	Lys	Ala	Gly	Cys 95	His	
Thr	Lys	Gln	Leu 100	Ala	Ser	Arg	Asn	Cys 105	Ser	Glu	Glu	Lys	Ser	Pro	Gln	
Thr	Ser	Ile 115	Leu	Lys	Glu	Gly	Asn 120	Arg	Asp	Thr	Ser	Leu 125	Asp	Phe	Arg	
Pro	Val	Val	Ser	Pro	Ala	Asn 135	Gly	Val	Glu	Gly	Val 140	Arg	Val	Asp	Gln	
Asp 145	Asp	Asp	Gln	Asp 150	Ser	Ser	Ser	Leu	Lys	Leu 155	Ser	Gln	Asn	Ile	Ala 160	
Val	Gln	Thr	Asp	Phe 165	Lys	Thr	Ala	Asp	Ser 170	Glu	Val	Asn	Thr	Asp 175	Gln	
Asp	Ile	Glu	Lys 180	Asn	Leu	Asp	Lys	Met 185	Met	Thr	Glu	Arg	Thr	Leu 190	Leu	
Lys	Glu	Arg 195	Tyr	Gln	Glu	Val	Leu 200	Asp	Lys	Gln	Arg	Gln 205	Val	Glu	Asn	
Gln	Leu 210	Gln	Val	Gln	Leu	Lys 215	Gln	Leu	Gln	Gln	Arg 220	Arg	Glu	Glu	Glu	
Met 225	Lys	Asn	His	Gln 230	Glu	Ile	Leu	Lys	Ala	Ile 235	Gln	Asp	Val	Thr	Ile 240	
Lys	Arg	Glu	Glu	Thr 245	Lys	Lys	Lys	Ile	Glu 250	Lys	Glu	Lys	Lys	Glu 255	Phe	
Leu	Gln	Lys 260	Glu	Gln	Asp	Leu	Lys	Ala 265	Glu	Ile	Glu	Lys	Leu 270	Cys	Glu	
Lys	Gly	Arg 275	Arg	Glu	Val	Trp	Glu 280	Met	Glu	Leu	Asp	Arg 285	Leu	Lys	Asn	
Gln	Asp 290	Gly	Glu	Ile	Asn	Arg 295	Asn	Ile	Met	Glu	Glu 300	Thr	Glu	Arg	Ala	
Trp 305	Lys	Ala	Glu	Ile 310	Leu	Ser	Leu	Glu	Ser	Arg 315	Lys	Glu	Leu	Leu	Val 320	
Leu	Lys	Leu	Glu	Glu 325	Ala	Glu	Lys	Glu	Ala 330	Glu	Leu	His	Leu 335	Thr	Tyr	
Leu	Lys	Ser 340	Thr	Pro	Pro	Thr	Leu	Glu 345	Thr	Val	Arg	Ser	Lys 350	Gln	Glu	
Trp	Glu	Thr 355	Arg	Leu	Asn	Gly	Val 360	Arg	Ile	Met	Lys	Lys 365	Asn	Val	Arg	
Asp	Gln 370	Phe	Asn	Ser	His	Ile 375	Gln	Leu	Val	Arg	Asn 380	Gly	Ala	Lys	Leu	

Met Gly Leu His Leu Ser Gln Ser Lys Leu Lys Met Glu Asp Ile Lys
 610 615 620
 Glu Val Asn Gln Ala Leu Lys Gly His Ala Trp Leu Lys Asp Asp Glu
 625 630 635 640
 Ala Thr His Cys Arg Gln Cys Glu Lys Glu Phe Ser Ile Ser Arg Arg
 645 650 655
 Lys His His Cys Arg Asn Cys Gly His Ile Phe Cys Asn Thr Cys Ser
 660 665 670
 Ser Asn Glu Leu Ala Leu Pro Ser Tyr Pro Lys Pro Val Arg Val Cys
 675 680 685
 Asp Ser Cys His Thr Leu Leu Gln Arg Cys Ser Ser Thr Ala Ser
 690 695 700

<210> 192
 <211> 331
 <212> PRT
 <213> Homo sapien

<400> 192
 Arg Ala Gly Ala Ser Ala Met Ala Leu Arg Lys Glu Leu Leu Lys Ser
 1 5 10 15
 Ile Trp Tyr Ala Phe Thr Ala Leu Asp Val Glu Lys Ser Gly Lys Val
 20 25 30
 Ser Lys Ser Gln Leu Lys Val Leu Ser His Asn Leu Tyr Thr Val Leu
 35 40 45
 His Ile Pro His Asp Pro Val Ala Leu Glu Glu His Phe Arg Asp Asp
 50 55 60
 Asp Asp Gly Pro Val Ser Ser Gln Gly Tyr Met Pro Tyr Leu Asn Lys
 65 70 75 80
 Tyr Ile Leu Asp Lys Val Glu Glu Gly Ala Phe Val Lys Glu His Phe
 85 90 95
 Asp Glu Leu Cys Trp Thr Leu Thr Ala Lys Lys Asn Tyr Arg Ala Asp
 100 105 110
 Ser Asn Gly Asn Ser Met Leu Ser Asn Gln Asp Ala Phe Arg Leu Trp
 115 120 125
 Cys Leu Phe Asn Phe Leu Ser Glu Asp Lys Tyr Pro Leu Ile Met Val
 130 135 140
 Pro Asp Glu Val Glu Tyr Leu Leu Lys Lys Val Leu Ser Ser Met Ser
 145 150 155 160
 Leu Glu Val Ser Leu Gly Glu Leu Glu Glu Leu Leu Ala Gln Glu Ala
 165 170 175
 Gln Val Ala Gln Thr Thr Gly Gly Leu Ser Val Trp Gln Phe Leu Glu
 180 185 190
 Leu Phe Asn Ser Gly Arg Cys Leu Arg Gly Val Gly Arg Asp Thr Leu
 195 200 205
 Ser Met Ala Ile His Glu Val Tyr Gln Glu Leu Ile Gln Asp Val Leu
 210 215 220
 Lys Gln Gly Tyr Leu Trp Lys Arg Gly His Leu Arg Arg Asn Trp Ala
 225 230 235 240
 Glu Arg Trp Phe Gln Leu Gln Pro Ser Cys Leu Cys Tyr Phe Gly Ser
 245 250 255
 Glu Glu Cys Lys Glu Lys Arg Gly Ile Ile Pro Leu Asp Ala His Cys
 260 265 270
 Cys Val Glu Val Leu Pro Asp Arg Asp Gly Lys Arg Cys Met Phe Cys
 275 280 285
 Val Lys Thr Ala Thr Arg Thr Tyr Glu Met Ser Ala Ser Asp Thr Arg
 290 295 300
 Gln Arg Gln Glu Trp Thr Ala Ala Ile Gln Met Ala Ile Arg Leu Gln

Phe Val Val Met Glu His Cys Leu Lys His Gly Leu Lys Val Lys Lys
 145 150 155 160
 Ser Phe Ile Gly Gln Asn Lys Ser Phe Phe Gly Pro Leu Glu Leu Val
 165 170 175
 Glu Lys Leu Cys Pro Glu Ala Ser Asp Ile Ala Thr Ser Val Arg Asn
 180 185 190
 Leu Pro Glu Leu Lys Thr Ala Val Gly Arg Gly Arg Ala Trp Leu Tyr
 195 200 205
 Leu Ala Leu Met Gln Lys Lys Leu Ala Asp Tyr Leu Lys Val Leu Ile
 210 215 220
 Asp Asn Lys His Leu Leu Ser Glu Phe Tyr Glu Pro Glu Ala Leu Met
 225 230 235 240
 Met Glu Glu Glu Gly Met Val Ile Val Gly Leu Leu Val Gly Leu Asn
 245 250 255
 Val Leu Asp Ala Asn Leu Cys Leu Lys Gly Glu Asp Leu Asp Ser Gln
 260 265 270
 Val Gly Val Ile Asp Phe Ser Leu Tyr Leu Lys Asp Val Gln Asp Leu
 275 280 285
 Asp Gly Gly Lys Glu His Glu Arg Ile Thr Asp Val Leu Asp Gln Lys
 290 295 300
 Asn Tyr Val Glu Glu Leu Asn Arg His Leu Ser Cys Thr Val Gly Asp
 305 310 315 320
 Leu Gln Thr Lys Ile Asp Gly Leu Glu Lys Thr Asn Ser Lys Leu Gln
 325 330 335
 Glu Glu Leu Ser Ala Ala Thr Asp Arg Ile Cys Ser Leu Gln Glu Glu
 340 345 350
 Gln Gln Gln Leu Arg Glu Gln Asn Glu Leu Ile Arg Glu Arg Ser Glu
 355 360 365
 Lys Ser Val Glu Ile Thr Lys Gln Asp Thr Lys Val Glu Leu Glu Thr
 370 375 380
 Tyr Lys Gln Thr Arg Gln Gly Leu Asp Glu Met Tyr Ser Asp Val Trp
 385 390 395 400
 Lys Gln Leu Lys Glu Glu Lys Lys Val Arg Leu Glu Leu Glu Lys Glu
 405 410 415
 Leu Glu Leu Gln Ile Gly Met Lys Thr Glu Met Glu Ile Ala Met Lys
 420 425 430
 Leu Leu Glu Lys Asp Thr His Glu Lys Gln Asp Thr Leu Val Ala Leu
 435 440 445
 Arg Gln Gln Leu Glu Glu Val Lys Ala Ile Asn Leu Gln Met Phe His
 450 455 460
 Lys Ala Gln Asn Ala Glu Ser Ser Leu Gln Gln Lys Asn Glu Ala Ile
 465 470 475 480
 Thr Ser Phe Glu Gly Lys Thr Asn Gln Val Met Ser Ser Met Lys Gln
 485 490 495
 Met Glu Glu Arg Leu Gln His Ser Glu Arg Ala Arg Gln Gly Ala Glu
 500 505 510
 Glu Arg Ser His Lys Leu Gln Gln Glu Leu Gly Gly Arg Ile Gly Ala
 515 520 525
 Leu Gln Leu Gln Leu Ser Gln Leu His Glu Gln Cys Ser Ser Leu Glu
 530 535 540
 Lys Glu Leu Lys Ser Glu Lys Glu Gln Arg Gln Ala Leu Gln Arg Glu
 545 550 555 560
 Leu Gln His Glu Lys Asp Thr Ser Ser Leu Leu Arg Met Glu Leu Gln
 565 570 575
 Gln Val Glu Gly Leu Lys Lys Glu Leu Arg Glu Leu Gln Asp Glu Lys
 580 585 590
 Ala Glu Leu Gln Lys Ile Cys Glu Glu Gln Glu Gln Ala Leu Gln Glu
 595 600 605

Val His Leu Thr Asp Gly Ile Trp Ser Gln Ile Lys Ser Ala Gly Ser
 115 120 125
 Ala Leu Tyr Ala Ser Arg Leu Tyr Leu Ser Arg Tyr Gln Asp Thr His
 130 135 140
 Pro Glu Arg Leu Ala Lys His Thr Pro Gly Gly Pro Trp Ile Arg Gly
 145 150 155 160

<210> 190
 <211> 146
 <212> PRT
 <213> Homo sapien

<400> 190
 Met Asp Pro Arg Ala Ser Leu Leu Leu Leu Gly Asn Val Tyr Ile His
 1 5 10 15
 Pro Thr Ala Lys Val Ala Pro Ser Ala Val Leu Gly Pro Asn Val Ser
 20 25 30
 Ile Gly Lys Gly Val Thr Val Gly Glu Gly Val Arg Leu Arg Glu Ser
 35 40 45
 Ile Val Leu His Gly Ala Thr Leu Gln Glu His Thr Cys Val Leu His
 50 55 60
 Ser Ile Val Gly Trp Gly Ser Thr Val Gly Arg Trp Ala Arg Val Glu
 65 70 75 80
 Gly Thr Pro Ser Asp Pro Asn Pro Asn Asp Pro Arg Ala Arg Met Asp
 85 90 95
 Ser Glu Ser Leu Phe Lys Asp Gly Lys Leu Leu Pro Ala Ile Thr Ile
 100 105 110
 Leu Gly Cys Arg Val Arg Ile Pro Ala Glu Val Leu Ile Leu Asn Ser
 115 120 125
 Ile Val Leu Pro His Lys Glu Leu Ser Arg Ser Phe Thr Asn Gln Ile
 130 135 140
 Ile Leu
 145

<210> 191
 <211> 704
 <212> PRT
 <213> Homo sapien

<400> 191
 Glu Gly Gly Cys Ala Ala Gly Arg Gly Arg Glu Leu Glu Pro Glu Leu
 1 5 10 15
 Glu Pro Gly Pro Gly Pro Gly Ser Ala Leu Glu Pro Gly Glu Phe
 20 25 30
 Glu Ile Val Asp Arg Ser Gln Leu Pro Gly Pro Gly Asp Leu Arg Ser
 35 40 45
 Ala Thr Arg Pro Arg Ala Ala Glu Gly Trp Ser Ala Pro Ile Leu Thr
 50 55 60
 Leu Ala Arg Arg Ala Thr Gly Asn Leu Ser Ala Ser Cys Gly Ser Ala
 65 70 75 80
 Leu Arg Ala Ala Ala Gly Leu Gly Gly Gly Asp Ser Gly Asp Gly Thr
 85 90 95
 Ala Arg Ala Ala Ser Lys Cys Gln Met Met Glu Glu Arg Ala Asn Leu
 100 105 110
 Met His Met Met Lys Leu Ser Ile Lys Val Leu Leu Gln Ser Ala Leu
 115 120 125
 Ser Leu Gly Arg Ser Leu Asp Ala Asp His Ala Pro Leu Gln Gln Phe
 130 135 140

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<210> 189
<211> 160
<212> PRT
<213> Homo sapien
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<400> 189															
Met	Leu	Glu	Ala	His	Arg	Arg	Gln	Arg	His	Pro	Phe	Leu	Leu	Leu	Gly
1				5					10					15	
Thr	Thr	Ala	Asn	Arg	Thr	Gln	Ser	Leu	Asn	Tyr	Gly	Cys	Ile	Val	Glu
			20					25					30		
Asn	Pro	Gln	Thr	His	Glu	Val	Leu	His	Tyr	Val	Glu	Lys	Pro	Ser	Thr
		35					40					45			
Phe	Ile	Ser	Asp	Ile	Ile	Asn	Cys	Gly	Ile	Tyr	Leu	Phe	Ser	Pro	Glu
	50					55					60				
Ala	Leu	Lys	Pro	Leu	Arg	Asp	Val	Phe	Gln	Arg	Asn	Gln	Gln	Asp	Gly
65					70					75					80
Gln	Leu	Glu	Asp	Ser	Pro	Gly	Leu	Trp	Pro	Gly	Ala	Gly	Thr	Ile	Arg
				85					90					95	
Leu	Glu	Gln	Asp	Val	Phe	Ser	Ala	Leu	Ala	Gly	Gln	Gly	Gln	Ile	Tyr
			100					105					110		

Ala Asp Gln Ser Gln Ala Leu Pro Ala Leu Ala Gly Ala Ala Ala Ala
 290 295 300
 His Ala His Ala Ile Pro Gly Ala Gly Pro Ala Ala Ala Pro Val Gly
 305 310 315 320
 Gly Arg Gly Arg Arg Gly Gly Trp Arg Gly Gly Arg Arg Gly Gly Ser
 325 330 335
 Ala Gly Ala Gly Gly Gly Gly Arg Gly Gly Arg Gly Arg Gly Arg Gly
 340 345 350
 Gly Gly Arg Gly Gly Gly Gly Ala Gly Arg Gly Gly Gly Ala Ala Gly
 355 360 365
 Pro Arg Glu Gly Ala Ser Ser Pro Gly Ala Arg Arg Gly Glu Gln Arg
 370 375 380
 Arg Arg Gly Arg Gly Pro Pro Ala Ala Gly Ala Ala Gln Val Ser Ala
 385 390 395 400
 Arg Gly Arg Arg Ala Arg Gly Gln Arg Ala Gly Glu Glu Ala Gln Asp
 405 410 415
 Gly Leu Leu Pro Arg Gly Arg Asp Arg Leu Pro Leu Arg Pro Gly Asp
 420 425 430
 Ala Asn Gln Arg Ala Glu Arg Pro Gly Pro Pro Arg Gly Gly His Gly
 435 440 445
 Pro Val Asn Ala Ser Ser Ala Pro Asp Thr Ser Pro Pro Arg His Pro
 450 455 460
 Arg Arg Trp Val Ser Gln Gln Arg Gln Arg Leu Trp Arg Gln Phe Arg
 465 470 475 480
 Val Gly Gly Gly Phe Pro Pro Pro Pro Pro Ser Arg Pro Pro Ala Val
 485 490 495
 Leu Leu Pro Leu Leu Arg Leu Ala Cys Ala Gly Asp Pro Gly Ala Thr
 500 505 510
 Arg Pro Gly Pro Arg Arg Pro Ala Arg Arg Pro Arg Gly Glu Leu Ile
 515 520 525
 Pro Arg Arg Pro Asp Pro Ala Ala Pro Ser Glu Glu Gly Leu Arg Met
 530 535 540
 Glu Ser Ser Val Asp Asp Gly Ala Thr Ala Thr Thr Ala Asp Ala Ala
 545 550 555 560
 Ser Gly Glu Ala Pro Glu Ala Gly Pro Ser Pro Ser His Ser Pro Thr
 565 570 575
 Met Cys Gln Thr Gly Gly Pro Gly Pro Pro Pro Pro Gln Pro Pro Arg
 580 585 590
 Trp Leu Pro
 595

<210> 188

<211> 376

<212> PRT

<213> Homo sapien

<400> 188

Glu Met Arg Lys Phe Asp Val Pro Ser Met Glu Ser Thr Leu Asn Gln
 1 5 10 15
 Pro Ala Met Leu Glu Thr Leu Tyr Ser Asp Pro His Tyr Arg Ala His
 20 25 30
 Phe Pro Asn Pro Arg Pro Asp Thr Asn Lys Asp Val Tyr Lys Val Leu
 35 40 45
 Pro Glu Ser Lys Lys Ala Pro Gly Ser Gly Ala Val Phe Glu Arg Asn
 50 55 60
 Gly Pro His Ala Ser Ser Ser Gly Val Leu Pro Leu Gly Leu Gln Pro
 65 70 75 80
 Ala Pro Gly Leu Ser Lys Ser Leu Ser Ser Gln Val Trp Gln Pro Ser

595 600 605
 Ile Asp Leu Thr Ala Pro Ser Asn Asn Ser Ser Pro Arg Asp Ser Pro
 610 615 620
 Cys Lys Glu Asn Lys Ile Lys Lys Arg Lys Gly Glu Glu Ile Thr Arg
 625 630 635 640
 Glu Ala Lys Lys Ala Arg Lys Val Gly Gly Leu Thr Gly Ser Ser Ser
 645 650 655
 Asp Asp Ser Gly Ser Glu Ser Asp Ala Ser Asp Asn Glu Glu Ser Asp
 660 665 670
 Tyr Glu Ser Ser Lys Asn Met Ser Ser Gly Asp Asp Asp Phe Asn
 675 680 685
 Pro Phe Leu Asp Glu Ser Asn Glu Asp Asp Glu Asn Asp Pro Trp Leu
 690 695 700
 Ile
 705

<210> 187
 <211> 595
 <212> PRT
 <213> Homo sapien

<400> 187
 Glu Ser Pro Arg His Arg Gly Glu Gly Gly Gly Glu Trp Gly Pro Gly
 1 5 10 15
 Val Pro Arg Glu Arg Arg Glu Ser Ala Gly Glu Trp Gly Ala Asp Thr
 20 25 30
 Pro Lys Glu Gly Gly Glu Ser Ala Gly Glu Trp Gly Ala Glu Val Pro
 35 40 45
 Arg Gly Arg Gly Glu Gly Ala Gly Glu Trp Gly Pro Asp Thr Pro Lys
 50 55 60
 Glu Arg Gly Gln Gly Val Arg Glu Trp Gly Pro Glu Ile Pro Gln Glu
 65 70 75 80
 His Gly Glu Ala Thr Arg Asp Trp Ala Leu Glu Ser Pro Arg Ala Leu
 85 90 95
 Gly Glu Asp Ala Arg Glu Leu Gly Ser Ser Pro His Asp Arg Gly Ala
 100 105 110
 Ser Pro Arg Asp Leu Ser Gly Glu Ser Pro Cys Thr Gln Arg Ser Gly
 115 120 125
 Leu Leu Pro Glu Arg Arg Gly Asp Ser Pro Trp Pro Pro Trp Pro Ser
 130 135 140
 Pro Gln Glu Arg Asp Ala Gly Thr Arg Asp Arg Glu Glu Ser Pro Arg
 145 150 155 160
 Asp Trp Gly Gly Ala Glu Ser Pro Arg Gly Trp Glu Ala Gly Pro Arg
 165 170 175
 Glu Trp Gly Pro Ser Pro Ser Gly His Gly Asp Gly Pro Arg Arg Arg
 180 185 190
 Pro Arg Lys Arg Arg Gly Arg Lys Gly Arg Met Gly Arg Gln His Glu
 195 200 205
 Ala Ala Ala Thr Ala Ala Thr Ala Thr Ala Thr Gly Gly Thr Ala
 210 215 220
 Glu Glu Ala Gly Ala Ser Ala Pro Glu Ser Gln Ala Gly Gly Gly Pro
 225 230 235 240
 Arg Gly Arg Ala Arg Gly Pro Arg Gln Gln Gly Arg Arg Arg His Gly
 245 250 255
 Thr Gln Arg Arg Arg Gly Pro Pro Gln Ala Arg Glu Glu Gly Pro Arg
 260 265 270
 Asp Ala Thr Thr Ile Leu Gly Leu Gly Thr Pro Ser Gly Glu Gln Arg
 275 280 285

130						135						140					
Val	Pro	Val	Val	Lys	Glu	Asp	Asp	Glu	Pro	Glu	Glu	Glu	Glu	Asp	Glu	Glu	
145					150					155							160
Glu	Met	Gly	His	Ala	Glu	Thr	Tyr	Ala	Glu	Tyr	Met	Pro	Ile	Lys	Leu		
				165						170							175
Lys	Ile	Gly	Leu	Arg	His	Pro	Asp	Ala	Val	Val	Glu	Thr	Ser	Ser	Leu		
			180							185				190			
Ser	Ser	Val	Thr	Pro	Pro	Asp	Val	Trp	Tyr	Lys	Thr	Ser	Ile	Ser	Glu		
		195					200					205					
Glu	Thr	Ile	Asp	Asn	Gly	Trp	Leu	Ser	Ala	Leu	Gln	Leu	Glu	Ala	Ile		
	210					215					220						
Thr	Tyr	Ala	Ala	Gln	Gln	His	Glu	Thr	Phe	Leu	Pro	Asn	Gly	Asp	Arg		
225					230						235						240
Ala	Gly	Phe	Leu	Ile	Gly	Asp	Gly	Ala	Gly	Val	Gly	Lys	Gly	Arg	Thr		
			245						250								255
Ile	Ala	Gly	Ile	Ile	Tyr	Glu	Asn	Tyr	Leu	Leu	Ser	Arg	Lys	Arg	Ala		
			260					265					270				
Leu	Trp	Phe	Ser	Val	Ser	Asn	Asp	Leu	Lys	Tyr	Asp	Ala	Glu	Arg	Asp		
		275					280					285					
Leu	Arg	Asp	Ile	Gly	Ala	Lys	Asn	Ile	Leu	Val	His	Ser	Leu	Asn	Lys		
	290					295					300						
Phe	Lys	Tyr	Gly	Lys	Ile	Ser	Ser	Lys	His	Asn	Gly	Ser	Val	Lys	Lys		
305					310					315							320
Gly	Val	Ile	Phe	Ala	Thr	Tyr	Ser	Ser	Leu	Ile	Gly	Glu	Ser	Gln	Ser		
			325						330								335
Gly	Gly	Lys	Tyr	Lys	Thr	Arg	Leu	Lys	Gln	Leu	Leu	His	Trp	Cys	Gly		
			340					345					350				
Asp	Asp	Phe	Asp	Gly	Val	Ile	Val	Phe	Asp	Glu	Cys	His	Lys	Ala	Lys		
		355					360					365					
Asn	Leu	Cys	Pro	Val	Gly	Ser	Ser	Lys	Pro	Thr	Lys	Thr	Gly	Leu	Ala		
	370						375					380					
Val	Leu	Glu	Leu	Gln	Asn	Lys	Leu	Pro	Lys	Ala	Arg	Val	Val	Tyr	Ala		
385					390					395							400
Ser	Ala	Thr	Gly	Ala	Ser	Glu	Pro	Arg	Asn	Met	Ala	Tyr	Met	Asn	Arg		
			405						410								415
Leu	Gly	Ile	Trp	Gly	Glu	Gly	Thr	Pro	Phe	Arg	Glu	Phe	Ser	Asp	Phe		
			420					425					430				
Ile	Gln	Ala	Val	Glu	Arg	Arg	Gly	Val	Gly	Ala	Met	Glu	Ile	Val	Ala		
	435						440					445					
Met	Asp	Met	Lys	Leu	Arg	Gly	Met	Tyr	Ile	Ala	Arg	Gln	Leu	Ser	Phe		
	450					455					460						
Thr	Gly	Val	Thr	Phe	Lys	Ile	Glu	Glu	Val	Leu	Leu	Ser	Gln	Ser	Tyr		
465					470					475							480
Val	Lys	Met	Tyr	Asn	Lys	Ala	Val	Lys	Leu	Trp	Val	Ile	Ala	Arg	Glu		
			485						490								495
Arg	Phe	Gln	Gln	Ala	Ala	Asp	Leu	Ile	Asp	Ala	Glu	Gln	Arg	Met	Lys		
			500						505					510			
Lys	Ser	Met	Trp	Gly	Gln	Phe	Trp	Ser	Ala	His	Gln	Arg	Phe	Phe	Lys		
		515					520					525					
Tyr	Leu	Cys	Ile	Ala	Ser	Lys	Val	Lys	Arg	Val	Val	Gln	Leu	Ala	Arg		
	530					535					540						
Glu	Glu	Ile	Lys	Asn	Gly	Lys	Cys	Val	Val	Ile	Gly	Leu	Gln	Ser	Thr		
545					550					555							560
Gly	Glu	Ala	Arg	Thr	Leu	Glu	Ala	Leu	Glu	Glu	Gly	Gly	Gly	Glu	Leu		
			565						570								575
Asn	Asp	Phe	Val	Ser	Thr	Ala	Lys	Gly	Val	Leu	Gln	Ser	Leu	Ile	Glu		
			580					585					590				
Lys	His	Phe	Pro	Ala	Pro	Asp	Arg	Lys	Lys	Leu	Tyr	Ser	Leu	Leu	Gly		

Val Arg Gly Cys Thr Arg Gly Gly Arg Leu Ile Thr Asn Ser Tyr Arg
 485 490 495
 Ser Pro Gly Gly Tyr Lys Gly Phe Asp Thr Tyr Arg Gly Leu Pro Ser
 500 505 510
 Ile Ser Asn Gly Asn Tyr Ser Gln Leu Gln Phe Gln Ala Arg Glu Tyr
 515 520 525
 Ser Gly Ala Pro Tyr Ser Gln Arg Asp Asn Phe Gln Gln Cys Tyr Lys
 530 535 540
 Arg Gly Gly Thr Ser Gly Gly Pro Arg Ala Asn Ser Arg Ala Gly Trp
 545 550 555 560
 Ser Asp Ser Ser Gln Val Ser Ser Pro Glu Arg Asp Asn Glu Thr Phe
 565 570 575
 Asn Ser Gly Asp Ser Gly Gln Gly Asp Ser Arg Ser Met Thr Pro Val
 580 585 590
 Asp Val Pro Val Thr Asn Pro Ala Ala Thr Ile Leu Pro Val His Val
 595 600 605
 Tyr Pro Leu Pro Gln Gln Met Arg Val Ala Phe Ser Ala Ala Arg Thr
 610 615 620
 Ser Asn Leu Ala Pro Gly Thr Leu Asp Gln Pro Ile Val Phe Asp Leu
 625 630 635 640
 Leu Leu Asn Asn Leu Gly Glu Thr Phe Asp Leu Gln Leu Gly Arg Phe
 645 650 655
 Asn Cys Pro Val Asn Gly Thr Tyr Val Phe Ile Phe His Met Leu Lys
 660 665 670
 Leu Ala Val Asn Val Pro Leu Tyr Val Asn Leu Met Lys Asn Glu Glu
 675 680 685
 Val Leu Val Ser Ala Tyr Ala Asn Asp Gly Ala Pro Asp His Glu Thr
 690 695 700
 Ala Ser Asn His Ala Ile Leu Gln Leu Phe Gln Gly Asp Gln Ile Trp
 705 710 715 720
 Leu Arg Leu His Arg Gly Ala Ile Tyr Gly Ser Ser Trp Lys Tyr Ser
 725 730 735
 Thr Phe Ser Gly Tyr Leu Leu Tyr Gln Asp
 740 745

<210> 186

<211> 705

<212> PRT

<213> Homo sapien

<400> 186

Ala Leu Leu Asn Val Arg Gln Pro Pro Ser Thr Thr Thr Phe Val Leu
 1 5 10 15
 Asn Gln Ile Asn His Leu Pro Pro Leu Gly Ser Thr Ile Val Met Thr
 20 25 30
 Lys Thr Pro Pro Val Thr Thr Asn Arg Gln Thr Ile Thr Leu Thr Lys
 35 40 45
 Phe Ile Gln Thr Thr Ala Ser Thr Arg Pro Ser Val Ser Ala Pro Thr
 50 55 60
 Val Arg Asn Ala Met Thr Ser Ala Pro Ser Lys Asp Gln Val Gln Leu
 65 70 75 80
 Lys Asp Leu Leu Lys Asn Asn Ser Leu Asn Glu Leu Met Lys Leu Lys
 85 90 95
 Pro Pro Ala Asn Ile Ala Gln Pro Val Ala Thr Ala Ala Thr Asp Val
 100 105 110
 Ser Asn Gly Thr Val Lys Lys Glu Ser Ser Asn Lys Glu Gly Ala Arg
 115 120 125
 Met Trp Ile Asn Asp Met Lys Met Arg Ser Phe Ser Pro Thr Met Lys

Phe Glu Ser Ile Pro Val Pro Lys Asn Ala Lys Glu Lys Glu Val Pro
 20 25 30
 Leu Glu Glu Glu Met Leu Ile Gln Ser Glu Lys Lys Thr Gln Leu Ser
 35 40 45
 Lys Thr Glu Ser Val Lys Glu Ser Glu Ser Leu Met Glu Phe Ala Gln
 50 55 60
 Pro Glu Ile Gln Pro Gln Glu Phe Leu Asn Arg Arg Tyr Met Thr Glu
 65 70 75 80
 Val Asp Tyr Ser Asn Lys Gln Gly Glu Glu Gln Pro Trp Glu Ala Asp
 85 90 95
 Tyr Ala Arg Lys Pro Asn Leu Pro Lys Arg Trp Asp Met Leu Thr Glu
 100 105 110
 Pro Asp Gly Gln Glu Lys Lys Gln Glu Ser Phe Lys Ser Trp Glu Ala
 115 120 125
 Ser Gly Lys His Gln Glu Val Ser Lys Pro Ala Val Ser Leu Glu Gln
 130 135 140
 Arg Lys Gln Asp Thr Ser Lys Leu Arg Ser Thr Leu Pro Glu Glu Gln
 145 150 155 160
 Lys Lys Gln Glu Ile Ser Lys Ser Lys Pro Ser Pro Ser Gln Trp Lys
 165 170 175
 Gln Asp Thr Pro Lys Ser Lys Ala Gly Tyr Val Gln Glu Glu Gln Lys
 180 185 190
 Lys Gln Glu Thr Pro Lys Leu Trp Pro Val Gln Leu Gln Lys Glu Gln
 195 200 205
 Asp Pro Lys Lys Gln Thr Pro Lys Ser Trp Thr Pro Ser Met Gln Ser
 210 215 220
 Glu Gln Asn Thr Thr Lys Ser Trp Thr Thr Pro Met Cys Glu Glu Gln
 225 230 235 240
 Asp Ser Lys Gln Pro Glu Thr Pro Lys Ser Trp Glu Asn Asn Val Glu
 245 250 255
 Ser Gln Lys His Ser Leu Thr Ser Gln Ser Gln Ile Ser Pro Lys Ser
 260 265 270
 Trp Gly Val Ala Thr Ala Ser Leu Ile Pro Asn Asp Gln Leu Leu Pro
 275 280 285
 Arg Lys Leu Asn Thr Glu Pro Lys Asp Val Pro Lys Pro Val His Gln
 290 295 300
 Pro Val Gly Ser Ser Ser Thr Leu Pro Lys Asp Pro Val Leu Arg Lys
 305 310 315 320
 Glu Lys Leu Gln Asp Leu Met Thr Gln Ile Gln Gly Thr Cys Asn Phe
 325 330 335
 Met Gln Glu Ser Val Leu Asp Phe Asp Lys Pro Ser Ser Ala Ile Pro
 340 345 350
 Thr Ser Gln Pro Pro Ser Ala Thr Pro Gly Ser Pro Val Ala Ser Lys
 355 360 365
 Glu Gln Asn Leu Ser Ser Gln Ser Asp Phe Leu Gln Glu Pro Leu Gln
 370 375 380
 Val Phe Asn Val Asn Ala Pro Leu Pro Pro Arg Lys Glu Gln Glu Ile
 385 390 395 400
 Lys Glu Ser Pro Tyr Ser Pro Gly Tyr Asn Gln Ser Phe Thr Thr Ala
 405 410 415
 Ser Thr Gln Thr Pro Pro Gln Cys Gln Leu Pro Ser Ile His Val Glu
 420 425 430
 Gln Thr Val His Ser Gln Glu Thr Ala Ala Asn Tyr His Pro Asp Gly
 435 440 445
 Thr Ile Gln Val Ser Asn Gly Ser Leu Ala Phe Tyr Pro Ala Gln Thr
 450 455 460
 Asn Val Phe Pro Arg Pro Thr Gln Pro Phe Val Asn Ser Arg Gly Ser
 465 470 475 480

Cys Ala Val Val Glu Phe Lys Met Glu Glu Ser Met Lys Lys Ala Ala
 115 120 125
 Glu Val Leu Asn Lys His Ser Leu Ser Gly Arg Pro Leu Lys Val Lys
 130 135 140
 Glu Asp Pro Asp Gly Glu His Ala Arg Arg Ala Met Gln Lys Ala Gly
 145 150 155 160
 Arg Leu Gly Ser Thr Val Phe Val Ala Asn Leu Asp Tyr Lys Val Gly
 165 170 175
 Trp Lys Lys Leu Lys Glu Val Phe Ser Met Ala Gly Val Val Val Arg
 180 185 190
 Ala Asp Ile Leu Glu Asp Lys Asp Gly Lys Ser Arg Gly Ile Gly Ile
 195 200 205
 Val Thr Phe Glu Gln Ser Ile Glu Ala Val Gln Ala Ile Ser Met Phe
 210 215 220
 Asn Gly Gln Leu Leu Phe Asp Arg Pro Met His Val Lys Met Asp Glu
 225 230 235 240
 Arg Ala Leu Pro Lys Gly Asp Phe Phe Pro Pro Glu Arg His Ser
 245 250 255

<210> 184
 <211> 188
 <212> PRT
 <213> Homo sapien

<400> 184
 Leu Ser Gly Ser Cys Ile Arg Arg Glu Gln Thr Pro Glu Lys Glu Lys
 1 5 10 15
 Gln Val Val Leu Phe Glu Glu Ala Ser Trp Thr Cys Thr Pro Ala Cys
 20 25 30
 Gly Asp Glu Pro Arg Thr Val Ile Leu Leu Ser Ser Met Leu Ala Asp
 35 40 45
 His Arg Leu Lys Leu Glu Asp Tyr Lys Asp Arg Leu Lys Ser Gly Glu
 50 55 60
 His Leu Asn Pro Asp Gln Leu Glu Ala Val Glu Lys Tyr Glu Glu Val
 65 70 75 80
 Leu His Asn Leu Glu Phe Ala Lys Glu Leu Gln Lys Thr Phe Ser Gly
 85 90 95
 Leu Ser Leu Asp Leu Leu Lys Ala Gln Lys Lys Ala Gln Arg Arg Glu
 100 105 110
 His Met Leu Lys Leu Glu Ala Glu Lys Lys Lys Leu Arg Thr Ile Leu
 115 120 125
 Gln Val Gln Tyr Val Leu Gln Asn Leu Thr Gln Glu His Val Gln Lys
 130 135 140
 Asp Phe Lys Gly Gly Leu Asn Gly Ala Val Tyr Leu Pro Ser Lys Glu
 145 150 155 160
 Leu Asp Tyr Leu Ile Lys Phe Ser Lys Leu Thr Cys Pro Glu Arg Asn
 165 170 175
 Glu Ser Leu Arg Gln Thr Leu Glu Gly Ser Thr Val
 180 185

<210> 185
 <211> 746
 <212> PRT
 <213> Homo sapien

<400> 185
 Asp Lys His Leu Lys Asp Leu Leu Ser Lys Leu Leu Asn Ser Gly Tyr
 1 5 10 15

gatcgtaag tacagtcctg attgcatcat aattgtgggt tccaaccag tggacattct 480
tacgtatggt acc 493

<210> 182
<211> 209
<212> PRT
<213> Homo sapien

<400> 182
Ala Phe Ser Ser Asn Pro Lys Val Gln Val Glu Ala Ile Glu Gly Gly
1 5 10 15
Ala Leu Gln Lys Leu Leu Val Ile Leu Ala Thr Glu Gln Pro Leu Thr
20 25 30
Ala Lys Lys Lys Val Leu Phe Ala Leu Cys Ser Leu Leu Arg His Phe
35 40 45
Pro Tyr Ala Gln Arg Gln Phe Leu Lys Leu Gly Gly Leu Gln Val Leu
50 55 60
Arg Thr Leu Val Gln Glu Lys Gly Thr Glu Val Leu Ala Val Arg Val
65 70 75 80
Val Thr Leu Leu Tyr Asp Leu Val Thr Glu Lys Met Phe Ala Glu Glu
85 90 95
Glu Ala Glu Leu Thr Gln Glu Met Ser Pro Glu Lys Leu Gln Gln Tyr
100 105 110
Arg Gln Val His Leu Leu Pro Gly Leu Trp Glu Gln Gly Trp Cys Glu
115 120 125
Ile Thr Ala His Leu Leu Ala Leu Pro Glu His Asp Ala Arg Glu Lys
130 135 140
Val Leu Gln Thr Leu Gly Val Leu Leu Thr Thr Cys Arg Asp Arg Tyr
145 150 155 160
Arg Gln Asp Pro Gln Leu Gly Arg Thr Leu Ala Ser Leu Gln Ala Glu
165 170 175
Tyr Gln Val Leu Ala Ser Leu Glu Leu Gln Asp Gly Glu Asp Glu Gly
180 185 190
Tyr Phe Gln Glu Leu Leu Gly Ser Val Asn Ser Leu Leu Lys Glu Leu
195 200 205
Arg

<210> 183
<211> 255
<212> PRT
<213> Homo sapien

<400> 183
Met Ala Ala Gly Val Glu Ala Ala Ala Glu Val Ala Ala Thr Glu Pro
1 5 10 15
Lys Met Glu Glu Glu Ser Gly Ala Pro Cys Val Pro Ser Gly Asn Gly
20 25 30
Ala Pro Gly Pro Lys Gly Glu Glu Arg Pro Thr Gln Asn Glu Lys Arg
35 40 45
Lys Glu Lys Asn Ile Lys Arg Gly Gly Asn Arg Phe Glu Pro Tyr Ser
50 55 60
Asn Pro Thr Lys Arg Tyr Arg Ala Phe Ile Thr Asn Ile Pro Phe Asp
65 70 75 80
Val Lys Trp Gln Ser Leu Lys Asp Leu Val Lys Glu Lys Val Gly Glu
85 90 95
Val Thr Tyr Val Glu Leu Leu Met Asp Ala Glu Gly Lys Ser Arg Gly
100 105 110

<210> 178
 <211> 440
 <212> DNA
 <213> Homo sapien

<400> 178
 gaattcggca cgaggagaag cagaaaaaca aggaatttag ccagacttta gaaaatgaga 60
 aaaatacctt actgagtcag atatcaacaa aggatgggtga actaaaaatg cttcaggagg 120
 aagtaaccaa aatgaacctg ttaaatacagc aaatccaaga agaactctct agagttacca 180
 aactaaagga gacagcagaa gaagagaaaag atgatttgga agagaggctt atgaatcaat 240
 tagcagaact taatggaagc attgggaatt actgtcagga tgttacagat gcccaaataa 300
 aaaatgagct attggaatct gaaatgaaga accttaaaaa gtgtgtgagt gaattggaag 360
 aagaaaagca gcagtttagtc aaggaaaaaa ctaagggtgga atcagaaata cgaaaggaaat 420
 atttgagaa aatacaaggt 440

<210> 179
 <211> 443
 <212> DNA
 <213> Homo sapien

<400> 179
 gaattcggca ccagcggggg gctacggcgg cggctacggc ggcgtcctga ccgcgtccga 60
 cgggctgctg gcgggcaacg agaagctaac catgcagaac ctcaacgacc gcctggcctc 120
 ctacctggac aaggtgcgcg coctggaggc ggccaacggc gagctagagg tgaagatccg 180
 cgactggtag cagaagcagg ggctggggc ctccgcgac tacagccact actacacgac 240
 catccaggac ctgcgggaca agattcttgg tgccaccatt gagaactcca ggattgtcct 300
 gcagatcgac aacgcccgtc tggctgcaga tgacttccga accaagtttg agacggaaca 360
 ggctctgcgc atgagcgtgg aggccgacat caacggcctg cgcagggtgc tggatgagct 420
 gaccctggcc aggaccgacc tgg 443

<210> 180
 <211> 403
 <212> DNA
 <213> Homo sapien

<400> 180
 gaattcggca cgaggttatg agagtcgact tcaatgttcc tatgaagaac aaccagataa 60
 caaacaacca gaggattaag gctgctgtcc caagcatcaa attctgcttg gacaatggag 120
 ccaagtcggt agtccttatg agccacctag gcgggcctga tgggtgtgcc atgcctgaca 180
 agtactcctt agagccagtt gctgtagaac tcagatctct gctgggcaag gatgttctgt 240
 tcttgaagga ctgtgtaggc ccagaagtgg agaaagcctg tgccaacca gctgctgggt 300
 ctgtcatcct gctggagaac ctccgcttcc atgtggagga agaaggggaag ggaaaagatg 360
 cttctgggaa caaggttaaa gccgagccag ccaaaataga agc 403

<210> 181
 <211> 493
 <212> DNA
 <213> Homo sapien

<400> 181
 gaattcggca ccagcagagg tctccagagc cttctctctc ctgtgcaaaa tggcaactct 60
 taaggaaaaa ctcatcgac cagttgcgga agaagaggca acagttccaa acaataagat 120
 cactgtagtg ggtgttgac agtttggtat ggctgtgtct atcagcattc tgggaaagtc 180
 tctggctgat gaacttgctc ttgtggatgt ttggaagat aagcttaaa gagaaatgat 240
 ggatctgcag catgggagct tatttcttca gacacctaaa attgtggcag ataaagatta 300
 ttctgtgacc gccaatctta agattgtagt ggtaactgca ggagtcctgc agcaagaagg 360
 ggagagtcgg ctcaatctgg tgcagagaaa tgttaatgtc ttcaaattca ttattcctca 420

gaattcggca	cgagaaatgg	cggcaggggt	cgaagcggcg	gcggaggttg	cggcgacgga	60
gatcaaaatg	gaggaagaga	gcggcgcgcc	cggcgtgccg	agcggcaacg	gggctccggg	120
ccctaagggt	gaaggagaac	gacctgctca	gaatgagaag	aggaaggaga	aaaacataaa	180
aagaggaggc	aatcgctttg	agccatatgc	caatccaact	aaaagataca	gagccttcat	240
tacaaacata	ccttttgatg	tgaaatggca	gtcacttaaa	gacctggtta	aagaaaaagt	300
tggtgaggtg	acatacgtgg	agctcttaat	ggagcgtgaa	ggaaagtcaa	ggggatgtgc	360
tggtgttgaa	ttcaagatgg	aagagagcat	gaaaaaagct	gcggaagtcc	taaaacaagca	420
tagtctgagc	ggaagaccac	tgaaagtcaa	agaagatcct	gatggtgaac	atgccaggag	480
agcaatgcaa	aaggtgatgg	ctacgactgg	tgggatgggt	atgggaccag	gtggcccagg	540
aatgatta						548

<210> 175

<211> 604

<212> DNA

<213> Homo sapien

<400> 175

gaattcggca	ccagaggacc	tccaggacat	gttcacgtgc	cataccatcg	aggagattga	60
gggcctgac	tcagcccatg	accagttcaa	gtccaccctg	ccggacgccg	atagggagcg	120
cgaggccatc	ctggccatcc	acaaggaggc	ccagaggatc	gctgagagca	accacatcaa	180
gctgtcgggc	agcaaccctt	acaccaccgt	caccccgcaa	atcatcaact	ccaagtggga	240
gaaggtgcag	cagctggtgc	caaaacggga	ccatgccctc	ctggaggagc	agagcaagca	300
gcagtccaac	gagcacctgc	gccgccagtt	cgccagccag	gccaatgttg	tggggccctg	360
gatccagacc	aagatggagg	agatcgggcg	catctccatt	gagatgaacg	ggaccctgga	420
ggaccagctg	agccacctga	agcagtatga	acgcagcatc	gtggactaca	agcccaacct	480
ggacctgctg	gagcagcagc	accagcttat	ccaggaggcc	ctcatcttcg	acaacaagca	540
caccaactat	accatggagc	acatccgcgt	gggctgggag	cagctgctca	ccaccattgc	600
ccgg						604

<210> 176

<211> 486

<212> DNA

<213> Homo sapien

<400> 176

gaattcggca	ccagccaagc	tcactattga	atccacgccg	ttcaatgtcg	cagaggggaa	60
ggaggttctt	ctactcgccc	acaacctgcc	ccagaatcgt	attggttaca	gctggtacaa	120
aggcgaaaga	gtggatggca	acagtctaat	tgtaggatat	gtaataggaa	ctcaacaagc	180
taccccgagg	ccgcataaca	gtggctcgaga	gacaatatat	cccaatgcat	ccctgctgat	240
ccagaacgtc	accagaatg	acacaggatt	ctatacccta	caagtcataa	agtcagatct	300
tgtgaatgaa	gaagcaaccg	gacagttcca	tgtatacccg	gagctgcccc	agccctccat	360
ctccagcaac	aactccaacc	ccgtggagga	caaggatgct	gtggccttca	cctgtgaacc	420
tgaggttcag	aacacaacct	acctgtggtg	ggtaaatggt	cagagcctcc	cggtcagtcc	480
caaggc						486

<210> 177

<211> 387

<212> DNA

<213> Homo sapien

<400> 177

gaattcggca	ccagggacag	cagaccagac	agtcacagca	gccttgacaa	aacgttctctg	60
gaactcaagc	tcttctccac	agaggaggac	agagcagaca	gcagagacca	tggagtctcc	120
ctcggccctt	ccccacagat	ggtgcatccc	ctggcagagg	ctcctgctca	cagcctcact	180
tetaaccttc	tggaaaccgc	ccaccactgc	caagctcact	attgaatcca	cgccgttcaa	240
tgtcgcagag	gggaaggagg	tgtttctact	tgtccacaat	ctgccccagc	atcttttttg	300
ctacagctgg	tacaaagggt	aaagagtggg	tggcaaccgt	caaattatag	gatatgtaat	360
aggaactcaa	caagctaccc	cagggcc				387

<210> 171
 <211> 547
 <212> DNA
 <213> Homo sapien

<400> 171
 gaattcggca ccagcgggat ttgggtcgca gttcttgttt gtggattgct gtgatcgta 60
 cttgacaatg cagatcttcg tgaagactct gactggtaag accatcaccc tcgaggttga 120
 gcccagtgac accatcgaga atgtcaaggc aaagatccaa gataaggaag gcatccctcc 180
 tgaccagcag aggctgatct ttgctggaaa acagctggaa gatggggcgca ccctgtctga 240
 ctacaacatc cagaaagagt ccaccctgca cctgggtgctc cgtctcagag gtgggatgca 300
 aatcttcgtg aagacactca ctggcaagac catcacctt gaggtcgagc ccagtgcac 360
 catcgagaac gtcaaaagcaa agatccagga caaggaaggc attcctcctg accagcagag 420
 gttgatcttt gccggaagc agctggaaga tgggcgcacc ctgtctgact acaacatcca 480
 gaaagagtct accctgcacc tgggtgctccg tctcagaggt gggatgcaga tcttcgtgaa 540
 gaccctg 547

<210> 172
 <211> 608
 <212> DNA
 <213> Homo sapien

<400> 172
 gaattcggca ccagagactt ctccctctga ggctcgca cccctcctca tcagcctgtc 60
 caccctcatc tacaatggtg ccctgccatg tcagtgaac cctcaagggt cactgagttc 120
 tgagtgaac cctcatggtg gtcagtgcct gtgcaagcct ggagtgggtg ggcgcgctg 180
 tgacctctgt gccctggct actatggctt tggcccaca ggctgtcaag gcgcttgct 240
 gggctgccgt gatcacacag ggggtgagca ctgtgaaagg tgcattgctg gttccacgg 300
 ggaccacagg ctgccatag ggggccagt cggccctgt ccctgtcctg aaggccctgg 360
 gagccaacgg cactttgcta cttcttgcca ccaggatgaa tattcccagc agattgtgtg 420
 ccactgcgg gcaggctata cggggctgcg atgtgaagct tgtgcccctg ggcactttgg 480
 ggaccatca aggcagggtg gccggtgcca actgtgtgag tgcagtggga acattgacct 540
 aatggatcct gatgcctgtg acccccacac ggggcaatgc ctgcgctgtt tacaccacac 600
 agagggtc 608

<210> 173
 <211> 543
 <212> DNA
 <213> Homo sapien

<400> 173
 gaattcggca ccagagatca tccgccagca gggctctggc tctacgact acgtgcgccc 60
 ccgcctcacg gctgaggacc tgttcgaggc tcggatcatc tctctcgaga cctacaacct 120
 gctccgggag ggcaccagga gcctccgtga ggctctcgag gcggagtccg cctgggtgcta 180
 cctctatggc acgggctccg tggctggtgt ctacctgcc gggtccaggc agacactgag 240
 catctaccag gctctcaaga aagggtgctg gagtgccgag gtggcccgcg tgcgtgtgga 300
 ggacacaggca gccacaggct tctgctgga cccggtgaag ggggaacggc tgactgtgga 360
 tgaagctgtg cggaagggcc tcgtggggcc cgaactgcac gaccgcctgc tctcggtga 420
 gcgggcggtc accggtacc gtgacccta caccgagcag accatctcgc tcttcaggc 480
 catgaagaag gaactgatcc ctactgagga ggccctgcgg ctgtggatgc ccagctggcc 540
 acc 543

<210> 174
 <211> 548
 <212> DNA
 <213> Homo sapien

<400> 174

gcgcgccccg ctgcagctgg agctgagcaa agtgcgtgaa gagtttaagg agctgaaagc 540
gcgcaatac 549

<210> 168

<211> 547

<212> DNA

<213> Homo sapien

<400> 168

gaattcggca	cgagatggcg	gcaggggtcg	aagcggcgcc	ggaggtggcg	gcgacggaga	60
tcaaaatgga	ggaagagagc	ggcgcgcccc	gcgtgccgag	cggcaacggg	gctccggggc	120
ctaagggtga	aggagaacga	cctgctcaga	atgagaagag	gaaggagaaa	aacataaaaa	180
gaggaggcaa	tcgctttgag	ccatatgcca	atccaaactaa	aagatacaga	gccttcatta	240
caaacatacc	ttttgatgtg	aaatggcagt	cacttaaaga	cctgggttaa	gaaaaagttg	300
gtgaggtaac	atacgtggag	ctcttaatgg	acgtgaagg	aaagtcaagg	ggatgtgctg	360
ttgttgat	caagatggaa	gagagcatga	aaaaagctgc	ggaagtccta	aacaagcata	420
gtctgagcgg	aagaccactg	aaagtcaaa	aagatcctga	tggtgaacat	gccaggagag	480
caatgcaaaa	ggctggaaga	cttggaagca	cagtatttgt	agcaaactctg	gattataaag	540
ttggctg						547

<210> 169

<211> 547

<212> DNA

<213> Homo sapien

<400> 169

gaattcggca	ccaggagtcc	gactgtgctc	gctgctcage	gccgcacccg	gaagatgagg	60
ctcgccgtgg	gagccctgct	ggtctgcgcc	gtcctggggc	tgtgtctggc	tgtccctgat	120
aaaactgtga	gatggtgtgc	agtgtcggag	catgaggcca	ctaagtgcc	gagtttccgc	180
gaccatatga	aaagcgtcat	tccatccgat	ggtccagtg	ttgcttgtgt	gaagaaagcc	240
tctaccttg	attgcatcag	ggccattgag	gcaaacgaag	cggatgctgt	gaacttgat	300
gcaggtttgg	tgtatgatgc	ttacctggct	cccaataacc	tgaagcctgt	ggtggcagag	360
ttctatgggt	caaaagagga	tccacagact	ttctattatg	ctgttgctgt	ggtgaagaag	420
gatagtggct	tccagatgaa	ccagcttcga	ggcaagaagt	cctgccacac	gggtctaggg	480
aggtcgctg	ggtggaacat	ccccataggc	ttactttact	gtgacttacc	tgagccacgt	540
aaacctc						547

<210> 170

<211> 838

<212> DNA

<213> Homo sapien

<400> 170

gaattcggca	ccagaggagc	tcggcctgcg	ctgcgccacg	atgtccgggg	agtcagccag	60
gagcttgggg	aagggaagcg	cgcccccg	gccggtccc	gagggctcga	tccgcatcta	120
cagcatgagg	ttctgcccgt	ttgctgagag	gacgcgtcta	gtcctgaagg	ccaagggaat	180
caggcatgaa	gtcatcaata	tcaacctgaa	aaataagcct	gagtgggtct	ttaagaaaaa	240
tccctttggt	ctggtgccag	ttctggaaaa	cagtcagggt	cagctgatct	acgagtctgc	300
catcacctgt	gagtacctgg	atgaagcata	cccagggaag	aagctgttgc	cggatgacct	360
ctatgagaaa	gcttgccaga	agatgatctt	agagttgttt	tctaagggtg	catccttggt	420
aggaagcttt	attagaagcc	aaaataaaga	agactatgat	ggcctaaaag	aagaatttgc	480
taaagaattt	accaagctag	aggaggttct	gactaataag	aagacgacct	tctttggtgg	540
caattctatc	tctatgattg	attacctcat	ctggccctgg	tttgaacggc	tggaagcaat	600
gaagttaaat	gagtgtgtag	accacactcc	aaaactgaaa	ctgtggatgg	cagccatgaa	660
ggaagatccc	acagtctcag	cctgtcttac	tagtgagaaa	gactggcaag	gtttcctaga	720
gctctactta	cagaacagcc	ctgaggcctg	tgactatggg	ctctgaaggg	ggcaggagtc	780
agcaataaag	ctatgtctga	tattttcctt	cactaaaaaa	aaaaaaaaaa	aactcgag	838

gaggttcagg	tggaagggtta	taattacact	ggcatgggaa	attccaccaa	taaaaaagat	180
gcacaaagca	atgctgccag	agactttgtt	aactatattg	ttcgaataaa	tgaaataaag	240
agtgaagaag	ttccagcttt	tggggtagca	tctcggcccc	cacttactga	tactcctgac	300
actacagcaa	atgctgaagg	catcttggtg	acatcgaata	tgactttgat	aataaatacc	360
ggttcctgaa	aaaaaaaaaa	aaaaaaaaac	tcgag			395

<210> 165

<211> 503

<212> DNA

<213> Homo sapien

<400> 165

gaattcggca	ccaggaacgc	tcggtgagag	gcggaggagc	ggtaactacc	ccggttgccg	60
acagctcggc	gctccttccc	gctccctcac	acaccggcct	cagcccgcac	cggcagtaga	120
agatggtgaa	agaaacaact	tactacgatg	ttttgggggt	caaacccaat	gctactcagg	180
aagaattgaa	aaaggcttat	aggaaaactgg	ccttgaagta	ccatcctgat	aagaacccaa	240
atgaaggaga	gaagtttaaa	cagattttctc	aagcttacga	agttctctct	gatgcaaaga	300
aaagggaatt	atatgacaaa	ggaggagaac	aggcaattaa	agaggggtgga	gcaggtggcg	360
gttttggtc	ccccatggac	atctttgata	tgttttttgg	aggaggagga	aggatgcaga	420
gagaaaggag	aaagtaaaat	gttgtacatc	agctctcagt	aaccctagaa	gacttatata	480
atggtgcaac	aagaaaactg	gct				503

<210> 166

<211> 893

<212> DNA

<213> Homo sapien

<400> 166

gaattcggca	cgagagggaac	ttctcttgac	gagaagagag	accaaggagg	ccaagcaggg	60
gctggggccag	aggtgccaac	atggggaaac	tgaggctcgg	ctcgggaagg	tgagagttag	120
actacatctc	aaaaaaaaaa	aaaaaaaaaa	aaaagaaaaga	aaagaaaaga	aaaaagaaag	180
aacggaagta	gttgtaggta	gtggtatggt	ggtatgagtc	tgttttctgt	tacttataac	240
aacaacaaca	acaaaaaacg	ctgaaactgg	gtaattttata	aagaaaagga	aaaaaagcag	300
aaaaaaatca	ggaagaagag	aaaggaaaag	aagacaaaata	aatgaaattt	atgtattaca	360
gttctgaagg	ctgagacatc	ccaggtaaac	ggtccacact	tggcagaggc	tttcttgctg	420
gtggagactc	tttgtggagt	cctgggacag	tgacagaagga	tcacgcctcc	ctaccgctcc	480
aagcccagcc	ctcagccatg	gcatgcccc	tggatcaggc	cattggcctc	ctcgtggcca	540
tcttcacaaa	gtactccggc	agggagggtg	acaagcacac	cctgagcaag	aaggagctga	600
aggagctgat	ccagaaggag	ctcaccattg	gctcgaagct	gcaggatgct	gaaattgcaa	660
ggctgatgga	agacttgagc	cggaacaagg	accaggaggt	gaacttccag	gagtatgtca	720
ccttcctggg	ggccttggtc	ttgatctaca	atgaagccct	caagggctga	aaataaatag	780
ggaagatgga	gacaccctct	gggggtcctc	tctgagtcaa	atccagtggg	gggtaattgt	840
acaataaatt	ttttttggtc	aaatttaaaa	aaaaaaaaaa	aaaaaaactc	gag	893

<210> 167

<211> 549

<212> DNA

<213> Homo sapien

<400> 167

gaattcggca	cgagcccaga	tcccagggtc	cgacagcgcc	cgcccagat	ccccacgcct	60
gccaggagca	agccgagagc	cagccggccg	gcgcactccg	actccgagca	gtctctgtcc	120
ttcgaccoga	gccccgcgcc	ctttccggga	cccctgcccc	gcgggcagcg	ctgccaacct	180
gcgggccatg	gagaccccgt	cccagcgggc	cgccaccgcg	agcggggcgc	aggccagctc	240
cactccgctg	tcgccacccc	gcataccccc	gctgcaggag	aaggaggacc	tgacaggagct	300
caatgatcgc	ttggcggtct	acatcgaccg	tgtgcgctcg	ctggaaacgg	agaacgcagg	360
gctgcgcctt	ctgcaccccg	agtctgaaga	ggtggtcagc	cgcgaggtgt	ccggcatcaa	420
ggccgcctac	gaggccgagc	tcggggatgc	ccgcaagacc	cttgactcag	tagccaagga	480

catgaaggaa	gatccacag	tctcagccct	gcttactagt	gagaaagact	ggcaaggttt	720
cctagagctc	tacttacaga	acagccctga	ggcctgtgac	tatgggctct	gaagggggca	780
ggagtcagca	ataaagctat	gtctgatatt	ttccttcact	aaaaaaaaa	aaaaaaaaa	840
aactcgag						848

<210> 161

<211> 432

<212> DNA

<213> Homo sapien

<400> 161

gaattcggca	cgagggcaga	ccaagatcct	ggaggaggac	ctggaacaga	tcaagctgtc	60
cttgagagag	cgagccggg	agctgaccac	tcagaggcag	ctgatgcagg	aacgggcaga	120
ggaaggggaag	ggcccaagta	aagcacagcg	cgggagccta	gagcacatga	agctgatcct	180
gcgtgataag	gagaaggagg	tggaatgtca	gcaggagcat	atccatgaac	tccaggagct	240
caaagaccag	ctggagcagc	agctccaggg	cctgcacagg	aaggtagggtg	agaccagcct	300
cctcctgtcc	cagcgagagc	aggaaatagt	ggtcctgcag	cagcaactgc	aggaagccag	360
ggaacaaggg	gagctgaagg	agcagtcact	tcagagtcaa	ctggatgagg	cccagagagc	420
cctagcccag	ag					432

<210> 162

<211> 433

<212> DNA

<213> Homo sapien

<400> 162

gattcggcac	gagccggagc	tgggttgctc	ctgctccogt	ctccaagtcc	tggtagctcc	60
ttcaagctgg	gagagggctc	tagtccctgg	ttctgaacac	tctgggggttc	tcgggtgcag	120
gccgccatga	gcaaacggaa	ggcgccgag	gagactctca	acgggggaat	caccgacatg	180
ctcacagaac	tcgcaaaactt	tgagaagaac	gtgagccaag	ctatccacaa	gtacaatgct	240
tacagaaaag	cagcatctgt	tatagcaaaa	taccacacac	aaataaagag	tggagctgaa	300
gctaagaaat	tgcttgaggt	aggaaacaaa	attgctgaaa	agattgatga	gtttttagca	360
actggaaaat	tacgtaaact	ggaaaagatt	cggcaggatg	atacagagttc	atccatcaat	420
ttcctgactc	gag					433

<210> 163

<211> 432

<212> DNA

<213> Homo sapien

<400> 163

gaattcggca	ccagatgagg	ccaacgaggt	gacggacagc	gcgtacatgg	gctccgagag	60
cacctacagt	gagtgtgaga	ccttcacgga	cgaggacacc	agcaccctgg	tgcaccctga	120
gctgcaacct	gaaggggagc	cagacagtgc	cggcggtctg	gccgtgccct	ctgagtgcct	180
ggacgccatg	gaggagcccc	accatggtgc	cctgctgctg	ctcccaggca	ggcctcacc	240
ccatggccag	tctgtcatca	cggatgatcg	ggcgaggagg	cactttgagg	actacggtga	300
aggcagtgag	gcggagctgt	ccccagagac	cctatgcaac	gggcagctgg	gctgcagtga	360
ccccgctttc	ctcacgcccc	gtccgacaaa	cgggctctcc	agcaagaagg	tggcaaggta	420
cctgcaccag	tc					432

<210> 164

<211> 395

<212> DNA

<213> Homo sapien

<400> 164

gacacttgaa	tcattgggtga	cgtaaaaaat	tttctgtatg	cctgggtgtgg	caaaaggaag	60
atgaccccat	cctatgaaat	tagagcagtg	gggaacaaaa	acaggcagaa	attcatgtgt	120

tctcagaaca	ttgctgtaca	gactgacttt	aagacagctg	attcagaggt	aaacacagat	540
caagatattg	aaaagaattt	ggataaaatg	atgacagaga	gaaccctgtt	gaaagagcgt	600
taccaggagg	tccctggacaa	acagaggcaa	gtggagaatc	agctccaagt	gcaattaaag	660
cagcttcagc	aaaggagaga	agaggaaatg	aagaatcacc	aggagatatt	aaaggctatt	720
caggatgtga	caataaagcg	ggaagaaaca	aagaagaaga	tagagaaaga	gaagaaggag	780
tttttgcaga	aggagcagga	tctgaaagct	gaaattgaga	agctttgtga	gaagggcaga	840
agagaggtgt	gggaaatgga	actggataga	ctcaagaatc	aggatggcga	aataaatagg	900
aacattatgg	aagagactga	acgggcctgg	aaggcagaga	tcttatcact	agagagccgg	960
aaagagttac	tggtactgaa	actagaagaa	gcagaaaaag	aggcagaatt	gcaccttact	1020
tacctcaagt	caactccccc	aacactggag	acagttcgtt	ccaaacagga	gtgggagacg	1080
agactgaatg	gagttcggat	aatgaaaaag	aatgttcgtg	accaatttaa	tagtcatatc	1140
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tcctcacccc	ttcctggctc	ccatggcaga	aatagccctg	gcttgggttc	ccttgtcagc	1440
cctggtgccc	aattcggcac	gaggtaccac	tggtctgtgt	gctagaggag	ggtgttgcca	1500
tagaaccagt	ggccacagtt	gtggtggtgg	tggtcagcac	tgtgggggtg	tgggtgggtc	1560
ccgggacgga	ggagggggtc	accgtgaagc	cactggttgt	gggtgtgggt	gttgtgtgta	1620
tcacacactg	aggcgtgcgt	gccgtccctg	ggctgaagga	gggggtgact	gtgaagcccg	1680
tggttgtggt	agtcggcact	ttggtagtgt	gagctgttcc	tgggggtgaa	gaggggggtg	1740
ccacagagcc	ggtggccctg	gttgtgtgtg	ccgtggtgtg	aagcactgtg	gaggtgtggg	1800
cagtctcttg	agtggaggag	ggtgtggctg	tggacatggt	ggccgtgggt	gtggtggtct	1860
gtgataggcg	ggtccaggtg	gtgcccagg	aggaggagg	gatggctgta	aagctggtag	1920
ctgtgggtgt	ggtggctgtg	cttctcagtg	ctggaagggc	ggttgagtc	cctggactgg	1980
agaaggagtg	ggcttggag	ctggtagctg	tgggtgtcgt	ggccgtgggt	ctcacatgtg	2040
gggtgccagc	agttgcctgg	gtggaggagg	cgggtggcgt	ggatccggtg	ggcaccgtca	2100
cgggagtact	tcta					2114

<210> 159

<211> 278

<212> DNA

<213> Homo sapien

<400> 159

gaattcggca	caggttaactt	tgcttggggt	atttaaaaaa	aaaaaaaaaa	aaaaaaaaag	60
tcaaatatct	gagtactaat	ttcctgaaaa	gtatgttccg	atagatgaac	agatcattaa	120
tgcagaatga	gaatcactcc	taaaataggt	aatggtaaaa	attaaattga	caattacctc	180
tctctatgca	gaaggaaata	tcacctatat	gacatcatca	tcatctattg	atacttgctg	240
gcagtgctaa	taatggtttt	aatgccaat	tgtaaaga			278

<210> 160

<211> 848

<212> DNA

<213> Homo sapien

<400> 160

gaattcggca	cgagccccag	aggagctcgg	cctgcgctgc	gccacgatgt	ccggggagtc	60
agccaggagc	ttggggaagg	gaagcgcgcc	ccggggccg	gtcccggagg	gctcgatccg	120
catctacagc	atgaggttct	gcccgtttgc	tgagaggacg	cgtctagtcc	tgaaggccaa	180
gggaatcagg	catgaagtca	tcaatatcaa	cctgaaaaat	aagcctgagt	ggttctttta	240
gaaaaatccc	tttggtctgg	tgccagttct	ggaaaacagt	cagggtcagc	tgatctacga	300
gtctgccatc	acctgtgagt	acctggatga	agcataccca	gggaagaagc	tggtgccgga	360
tgacccttat	gagaaagctt	gccagaagat	gatcttagag	ttgttttcta	aggtgccatc	420
cttggtagga	agctttatta	gaagccaaaa	taaagaagac	tatgctggcc	taaaagaaga	480
atttcgtaaa	gaatttacca	agctagagga	ggttctgact	aataagaaga	cgaccttctt	540
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<212> DNA

<213> Homo sapien

<400> 157

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<210> 158

<211> 2114

<212> DNA

<213> Homo sapien

<400> 158

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<210> 156
 <211> 2668
 <212> DNA
 <213> Homo sapien

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<210> 154

<211> 1411

<212> DNA

<213> Homo sapien

<400> 154

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<210> 155

<211> 678

<212> DNA

<213> Homo sapien

<400> 155

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<210> 153

<211> 2109

<212> DNA

<213> Homo sapien

<400> 153

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<210> 152

<211> 2179

<212> DNA

<213> Homo sapien

<400> 152

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cacgcccgtc	agtctcagca	ccaacagtac	gaaatgccat	gacctctgca	ccttcaaaag	240
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ccttggaag	tcgcttaatt	gctctgagct	tgtttctca	tctgtcagga	gtgccattaa	1020
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<210> 150

<211> 781

<212> DNA

<213> Homo sapien

<400> 150

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cccgaagggt	gaagaacgac	ctactcagaa	tgagaagagg	aaggagaaaa	acataaaaag	180
aggaggcaat	cgctttgagc	catattccaa	cccaactaaa	agatacagag	ccttcattac	240
aaatatacct	tttgatgtga	aatggcagtc	acttaaagac	ctggttaaag	aaaaagttgg	300
tgaggtaaaca	tacgtggagc	tcttaattgga	cgtgaaggga	aagtcaaggg	gatgtgctgt	360
tgttgaattc	aagatggagg	agagcatgaa	aaaagctgct	gaagttctaa	acaagcatag	420
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tctggaagat	aaagatggga	aaagtcgtgg	aataggcatt	gtgacttttg	aacagtccat	660
tgaagctgtg	caagcaatat	ctatgtttaa	tggccagttg	ctgtttgata	gaccgatgca	720
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<210> 151

<211> 3275

<212> DNA

<213> Homo sapien

<400> 151

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tctgctatcc	agtatgttgg	ctgaccacag	gctcaaaactg	gaggattata	aggatcgctt	180
gaaaagtggg	gagcatctta	atccagacca	gttggaagct	gtagagaaat	atgaagaagt	240
gctacataat	ttggaatttg	ccaaggagct	tcaaaaaacc	ttttctgggt	tgagcctaga	300
tctactaaaa	gcgcaaaaga	aggcccagag	aagggagcac	atgctaaaac	ttgagggtga	360
gaagaaaaag	cttcgaacta	tacttcaagt	tcagtatgta	ttgcagaact	tgacacagga	420
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acttgactac	ctcattaagt	tttcaaaaact	gacctgccct	gaaagaaatg	aaagtctgag	540
acaaacactt	gaaggatcta	ctgtctaaat	tgctgaactc	aggctatttt	gaaagtatcc	600
cagttcccaa	aaatgccaaag	gaaaagggaag	taccactgga	ggaagaaatg	ctaatacaat	660
cagagaaaaa	aacacaatta	tcgaagactg	aatctgtcaa	agagtcagag	tctctaattg	720
aatttgccca	gccagagata	caaccacaag	agtttcttaa	cagacgctat	atgacagaag	780
tagattattc	aaacaaacaa	ggcgaagagc	aaccttgga	agcagattat	gctagaaaac	840
caaatctccc	aaaacgttgg	gatattgctta	ctgaaccaga	tggtcaagag	aagaaacagg	900

cttcaagcag attggtatta ttaagacaaa caagaaaacg ggacagccca tgattaattt	360
gtacacagac agggaaactg gcaagctgaa gggagaggca acggtctctt ttgatgacct	420
accttcagct aaagcagcct attgactggt	450

<210> 146

<211> 451

<212> DNA

<213> Homo sapien

<400> 146

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cttcagtcgc gagacagacg gggcgagaa ggcggcgatg ctgcactgtg tgcagcgcg	180
gctgatccgc accaggagct gggcgacgag aagatccaga tctgtgagcca gatggtggag	240
ctggtggaga accgcacgcg gcaggtggac agccacgtgg agctgttcga ggcgcagcag	300
gagctgggag acacagcggg caacagcggc aaggctggcg cggacaggcc caaaggcgag	360
gcggcagcgc aggttgacaa gcccaacagc aagcgctcac ggcggcagcg caacaacgag	420
aaccgtgaga acgcgtccag caaccacgac c	451

<210> 147

<211> 400

<212> DNA

<213> Homo sapien

<400> 147

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ctgcgggctg cttcgggcca ggtcgaccc gagggccagc gcaagcagcg gcaacaggag	180
cgccaggagg acatgaggct ctgcctgcag tcagcaactt ggaatattca gacttcagac	240
cagcatcaca gattataacc ctccgtaaat catctgcac ccagctccca tcaaagcca	300
gctgaagga cccatggaca cgtgactcca gtgttctcaa caacatctta gatcaagttg	360
gtttgcacaa catttgcatc tacttgggac aaagcaagaa	400

<210> 148

<211> 503

<212> DNA

<213> Homo sapien

<400> 148

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cgagtgaagc tgcgcttttt cttaaagaagt ctggcctctc ggacattatc cttgggaaga	180
tatgggactt ggccgatcca gaaggtaaag ggttcttgga caaacagggt ttctatgttg	240
cactgagact ggtggcctgt gcacagagt gccatgaagt taccttgagc aatctgaatt	300
tgagcatgcc accgcctaaa ttacagaca ccagcagccc tctgatggtc acaccgccct	360
ctgcagaggc ccaactgggt gtgaggggtg aagaaaaggc caaatttgat gggatttttg	420
aaagcctctt gccatcaat ggtttgctct ctggagacaa agtcaagcca gtcctcatga	480
actcaaagct gcctcttgat gtc	503

<210> 149

<211> 1061

<212> DNA

<213> Homo sapien

<400> 149

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aggtcctggt tgcaactgtg tccctgctgc gccacttccc ctatgccag cggcagttcc	180

ctggaaaagg acaccacga gaagcaggac acactagttg ccctccgcca gc 1132

<210> 257

<211> 519

<212> DNA

<213> Homo sapiens

<400> 257

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cccggccggg	cccatcctct	ccatccgggt	ctgcagggac	atgatcacc	gccgctcctt	180
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tgatgaaaat	ggctccaagg	gctatggatt	tgtacacttt	gaaacacagg	aagcagctga	480
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<210> 258

<211> 596

<212> DNA

<213> Homo sapiens

<400> 258

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tatccaaatc	tgcaagtgcc	aaaagcatag	attcaaaggt	agcagacgct	gctactgaag	480
tgcagacaaa	aactactgaa	gcactgaaat	ccgaggaaaa	agccatggat	atttctgcta	540
tgcccctggt	tactccatta	tatgggcagc	cgtcatggtg	gggggatgat	gaggtg	596

<210> 259

<211> 595

<212> DNA

<213> Homo sapiens

<400> 259

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tcaggacgag	tttgatgcat	gtttggagga	gaaagatcag	tatatcagtg	ttctccagac	180
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cgtcggggaa	ccagtgggag	gtgggacttc	cgctaaaacc	ctggaaatgc	tccagcaaaag	360
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<210> 260

<211> 994

<212> DNA

<213> Homo sapiens

<400> 260

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acccagccct ttgaaattat ccatagtttt acagacagct ccaggccatg agccacaatg 180
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tgctttttat tagatctata taaataagtt aactagcaat ttagttttgt atttaagcta 960
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<210> 261

<211> 594

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (538)

<223> n=A,T,C or G

<400> 261

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tctcagaggg caggacgacc tgaaagagca gctggccatg gttgagcgca gagccaacct 180
gatgcaggct gagatcgagg agctcagggc atccctggaa cagacagaga ggagcaggag 240
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<210> 262

<211> 594

<212> DNA

<213> Homo sapiens

<400> 262

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tcggcagcaa ccctgagacg ctttacagct ctgacccta aaagggtcaaa aggcctgtct 180
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tcctccccca ggagettgct acatgtgccg gaaatctggc cactaggcca aggaatgcct 480
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<210> 263

<211> 506
 <212> DNA
 <213> Homo sapiens

<400> 263
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 tgcgatcggg ctactataaa gttctgggaa agggaaagct cccaaagcag cctgtcatcg 360
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 aaaaaaaaaa aaaaaaaaaa ctcgag 506

<210> 264
 <211> 600
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (32)
 <223> n=A,T,C or G

<400> 264
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 aaaggcctct cggagctgcy atcggagctc tacttcctca tcgcccggtt cctggaagat 180
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<210> 265
 <211> 534
 <212> DNA
 <213> Homo sapiens

<400> 265
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 ttgcgaaagg tgctggacca tcgagacaag gtatatgagc agctggccaa ataccttcaa 180
 ctgagaaatg tcattgagcg actccaggaa gctaagcact cggagttata tatgcagggtg 240
 gatttgggct gtaacttctt cgttgacaca gtggtcccag atacttcacg catctatgtg 300
 gccctgggat atggtttttt cctggagttg aacttggcag aagctctcaa gttcattgat 360
 cgtaagagct ctctcctcac agagctcagc aacagcctca ccaaggactc catgaatatc 420
 aaagcccata tccacatgtt gctagagggg cttagagaac tacaaggcct gcagaatttc 480
 ccagagaagc ctcaccattg acttcttccc cccatcctca gacattaaag agcc 534

<210> 266
 <211> 552
 <212> DNA
 <213> Homo sapiens

<400> 266

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gaattcggca ccagggcacc tccgcctcgc cgccgctagg tcggccggct ccgcccggct 60
gccgcctagg atgaatatca tggacttcaa cgtgaagaag ctggcggcgc acgcaggcac 120
cttcctcagt cgccgctgac agttcacaga agaaaagctt ggccaggctg agaagacaga 180
attggatgct cacttagaga acctccttag caaagctgaa tgtacaaaaa tatggacaga 240
aaaaataatg aaacaaactg aagtgttatt gcagccaaat ccaaagcca ggatagaaga 300
atttgtttat gagaaactgg atagaaaagc tccaagtcgt ataaacaacc cagaactttt 360
gggacaatat atgattgatg cagggactga gtttgccca ggaacagctt atggtaatgc 420
ccttattaaa tgtggagaaa ccaaaaaag aattggaaca gcagacagag aactgattca 480
aacgtcagcc ttaaattttc ttactccttt aagaaacttt atagaaggag attacaaaac 540
aattgctaaa ga
552

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<210> 267

<211> 551

<212> DNA

<213> Homo sapiens

<400> 267

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gaagcctacc agccagggtgc cgcccccccc acccccggcc cagccccctc ctgcagcggt 60
ggaagcggct cggcagatcg agcgtgaggg ccagcagcag cagcacctgt accgggtgaa 120
catcaacaac agcatgcccc caggacgcac gggcatgggg accccgggga gccagatggc 180
ccccgtgagc ctgaatgtgc cccgacccaa ccagggtgagc gggcccgtca tgcccagcat 240
gcctcccggg cagtggcagc aggcgccccct tccccagcag cagcccatgc caggcttgcc 300
caggcctgtg atatccatgc aggccagggc ggccgtggct gggccccgga tgcccagcgt 360
gcagccaccc aggagcatct caccagcgc tctgcaagac ctgctgcgga ccctgaagtc 420
gccagctcc cctcagcagc aacagcaggt gctgaacatt ctcaaatcaa acccgagct 480
aatggcagct ttcacaaaac agcgcacagc caagtacgtg gccaatcagc ccggcatgca 540
gccccagcct g
551

```

<210> 268

<211> 573

<212> DNA

<213> Homo sapiens

<400> 268

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gaattcggca ccagggttcc ttgtgggcta gaagaatcct gcaaaaatgt ctctctatcc 60
atctctcgaa gacttgaagg tagacaaagt aattcaggct caaactgctt tttctgcaaa 120
cctgcgaat ccagcaattt tgtcagaagc ttctgtcctt atccctcacg atggaaatct 180
ctatcccaga ctgtatccag agctctctca atacatgggg ctgagtttaa atgaagaaga 240
aatacgtgca aatgtggccg tggtttcttg tgcaccactt caggggcagt tggtagcaag 300
accttcagat ataaactata tgggtggctcc tgtaactggg aatgatgttg gaattcgtag 360
agcagaaaatt aagcaaggga ttctgtgaag cattttgtgt aaggatcaag atggaaaaat 420
tggactcagg cttaaatcaa tagataatgg tatatttgtt cagctagtcc aggttaattc 480
tccagcctca ttggttggtc tgagatttgg ggaccaagta cttcagatca atgggtgaaaa 540
ctgtgcagga tggagctctg ataaagcgca caa
573

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<210> 269

<211> 500

<212> DNA

<213> Homo sapiens

<400> 269

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gaatcggcac caggaaacct ttattagcag agatagctgg cttggatcag attacgggga 60
atgtggggga gccatgaaga aactaactaa aggggagcct ttggggacca gggggagaca 120
agtactatt ttgagggaga aagctctgga ttgattctga caggacactt gagtgtgaac 180
tgtccaagct aagcctctgg gtgtgtagag agagccctta cagatagata gcacctttgc 240
tttcagagtg gaaggactag ccactaagga ccagaccaag atgcatgtag gtcactgaca 300
agcacctgat gaagaggagg ggtctcctcc aagtttgtgt ttggaactcc tcctgtgttc 360

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aatttcctaa aagccataat ccagcaagct gaactcatga gaaggtctgc ttcattgtga 420
gcatggaaga cagaacacag acggaaactg cagtgatggt gtgaagacac cacggatagg 480
ttaggggcag tgaggaggaa 500

<210> 270

<211> 224

<212> DNA

<213> Homo sapiens

<400> 270

gaattcggca cgagaagact acaatctcca gggaaacctg gggcgtctcg cgcaaactgc 60
cataactgaa agtagctaag gcaccccagc cggagggaagt gagctctcct ggggcgtggt 120
tggtcgtgat ccttgcatct gttacttagg gtcaaggctt gggctcttgc ccgcagaccc 180
ttgggacgac cgggccccag cgcagctatg aacctggagc gagt 224

<210> 271

<211> 447

<212> DNA

<213> Homo sapiens

<400> 271

gaattcggca cgaggctggg cggggccccg gcgcatcgcg ggctcgggct gcggggctcc 60
ggctgcgggc gctggggccgc gaggcgcgga gcttgggagc ggagcccagg ccgtgccgcg 120
cggcgccatg aagggcaagg aggagaagga gggcgggcga cggctgggcg ctggcggcg 180
aagccccgag aagagccccg gcgcgcagga gctcaaggag cagggcaatc gtctgttcgt 240
gggcccgaag taccgcggagg cggcggcctg ctacggccgc gcgatcaccg ggaacccgct 300
ggtggccgtg tattacacca accgggcctt gtgctacctg aagatgcagc agcacgagca 360
ggccctggcc gactgccggc gcgccctgga gctggacggg cagtctgtga aggcgcactt 420
cttctggggg cagtgccagc tggagat 447

<210> 272

<211> 606

<212> DNA

<213> Homo sapiens

<400> 272

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gaggttatgt atttgcttaa acctgaccaa gtagaaggga tccagaaatc tgggactaaa 120
aaactgaaga ccgaaactga caaagaaaat gctgaagtga agtttaaaga ttttcttctg 180
tccttgaaga ctatgatgtt ttctgaagat gaggtccttt gtgtttaga cttgctaaag 240
gagaagtctg gtgtaataca agatgcttta aagaagtcaa gtaagggaga attgactacg 300
cttatacatc agcttcaaga aaaggacaag ttactcgctg ctgtgaagga agatgctgct 360
gctacaaagg atcgggtgtaa gcagttaacc caggaaatga tgacagagaa agaaagaagc 420
aatgtgggta taacaaggat gaaagatcga attggaacat tagaaaagga acataatgta 480
tttcaaaaca aaatacatgt cagttatcaa gagactcaac agatgcagat gaagtttcag 540
caagttcgtg agcagatgga ggcagagata gctcacttga agcaggaaaa tgggtatact 600
ggagaa 606

<210> 273

<211> 598

<212> DNA

<213> Homo sapiens

<400> 273

gaattcggca ccaggcccgg tcccgcggtc gcagctccag ccgcctctc cgcgagccg 60
ccgcctcagc tgctcgctct gtgggtcggt cctctccggc acttgggctc cagtgcgcgc 120
ctccaagccc ttcaggccgc ccagtgctc tcctccttct ccggccagac ccagccccgc 180
gaagatggtg gaccgcgagc aactggtgca gaaagcccgg ctggccgagc aggcggagcg 240

ctacgacgac atggccgcg ccatgaagaa cgtgacagag ctgaatgagc cactgtcgaa 300
tgaggaacga aaccttctgt ctgtggccta caagaacgtt gtgggggcac gccgctcttc 360
ctggagggtc atcagtagca ttgagcagaa gacatctgca gacggcaatg agaagaagat 420
tgagatggtc cgtgcgtacc gggagaagat agagaaggag ttggaggctg tgtgccagga 480
tgtgctgagc ctgctggata actacctgat caagaattgc agcgagacc agtacgagag 540
caaagtgttc tacctgaaga tgaaagggga ctactaccgc tacctggctg aagtggcc 598

<210> 274

<211> 536

<212> DNA

<213> Homo sapiens

<400> 274

gcaccaagag actaaacaag aaagtggatc agggagaag aaagcttcat caaagaaaca 60
aaagacagaa aatgtcttcg tagatgaacc cctatttcat gcaactactt atattccttt 120
gatggataat gctgactcaa gtctgtggt agataagaga gaggttattg atttgcttaa 180
acctgaccaa gtagaaggga tccagaaatc tgggactaaa aaactgaaga ccgaaactga 240
caaagaaaat gctgaagtga agtttaaaga ttttcttctg tccttgaaga ctatgatgtt 300
ttctgaagat gaggtcttt gtgtttaga cttgctaaag gagaagtctg gtgtaataca 360
agatgcttta aagaagtcaa gtaagggaga attgactacg cttatacatc agcttcaaga 420
aaaggacaag ttactcgctg ctgtgaagga agatgctgct gctacaaagg atcgggtgta 480
gcagttaacc caggaaatga tgacagagaa agaaagaagc aatgtggtta taacaa 536

<210> 275

<211> 494

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (379)

<223> n=A,T,C or G

<400> 275

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gcagatcttc gtgaagactc tgactggtaa gaccatcacc ctcgagggtg agcccagtga 120
caccatcgag aatgtcaagg caaagatcca agataaggaa ggcatccctc ctgaccagca 180
gaggctgatc tttgctggaa aacagctgga agatgggagc accctgtctg actacaacat 240
ccagaaagag tccaccctgc acctggtgct cgtctcaga ggtgggatgc aaatcttctg 300
gaagacactc actggcaaga ccaccacctc tgagggtggag cccagtgaaca ccatcgagaa 360
cgtcaaagca aagatccang acaaggaagg cattcctcct gaccagcaga ggttgatctt 420
tgccggaaag cagctggaag atgggcgcac cctgtctgac tacaacatcc agaaagagtc 480
taccctgcac ctgg 494

<210> 276

<211> 484

<212> DNA

<213> Homo sapiens

<400> 276

ggcttttaac cagaagtcaa acctgttcag acagaaggca gtcacagcag aaaaatcttc 60
agacaaaagg cagtcacagg tgtgcaggga gtgtgggcga ggcttttagca ggaagtcaca 120
gtcatcata caccagagga cacacacagg agaaaagcct tatgtctgcg gagagtgtgg 180
gcgaggcttt atagttgagt cagtcctccg caaccacctg agtacacact ccggggagaa 240
accttatgtg tgcagccatt gtggcgagg ctttagctgc aagccatacc tcatcagaca 300
tcagaggaca cacacaagg agaaatcgtt tatgtgcaca gtgtgtgggc gaggttttcg 360
tgaaaagtca gagctcatca agcaccagag aattcacacg ggggataagc cttatgtgtg 420
cagagattga ggccgaggct ttgtaaagga gatcatgtct caacacacac cagaggatta 480

catt

484

<210> 277

<211> 513

<212> DNA

<213> Homo sapiens

<400> 277

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gcttgaggct gccaatcaga gcttggcaga gctgagagat cagcggcagg gggagcgcct 60
ggaacatgca gcagctttgc gggccctaca agatcaggta tccatccaga gtgcagatgc 120
acaggaacaa gtggaagggc ttttggctga gaacaatgcc ttgaggacta gcctggctgc 180
cctggagcag atccaaacag caaagacca agaactgaat atgctccggg aacagaccac 240
tggtgctggca gctgagttgc agcagcagca ggctgagtag gaggacctta tgggacagaa 300
agatgacctc aactcccagc tccaggagtc attacgggcc aatagtcgac tgctggaaca 360
acttcaagaa atagggcagg agaaggagca gttgaccag gaattacagg aggtcggaa 420
gagtgcggag aagcggaagg ccatgcttgg atgagctagc aatggaaacg ctgcaagaga 480
agtccacac aaggaagagc ttgggagcag ttc 513
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<210> 278

<211> 471

<212> DNA

<213> Homo sapiens

<400> 278

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gaattcggca ccagccaagg ccctgtccct ggctcgggcc cttgaagagg ccttggaagc 60
caaagaggaa ctcgagcggg ccaacaaaat gctcaaagcc gaaatggaag acctgggtcag 120
ctccaaggat gacgtgggca agaactcca tgagctggag aagtccaagc gggccctgga 180
gacccagatg gaggagatga agacgcagct ggaagagctg gaggacgagc tgcaagccac 240
ggaggacgcc aaactgcggc tggaagtcaa catgcaggcg ctcaagggcc agttcgaaag 300
ggatctccaa gcccgggacg agcagaatga ggagaagagg aggcaactgc agagacagct 360
tcacgagtat gagacggaac tggaagacga gcgaaagcaa cgtgccctgg cagctgcagc 420
aaagaagaag ctggaagggg acctgaaaaga cctggagctt caggccgact t 471
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<210> 279

<211> 497

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (457)

<223> n=A,T,C or G

<221> misc_feature

<222> (471)

<223> n=A,T,C or G

<400> 279

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ctacctgagt ccagctgtcc cttttcttgg gactattcaa ggaggtctcc aggacggact 120
tcagatcact gtcaatggga ccgttctcag ctccagtggg accaggtttg ctgtgaactt 180
tcagactggc ttcagtggaa atgacattgc cttccacttc aaccctcggg ttgaagatgg 240
agggtacgtg gtgtgcaaca cgaggcagaa cggaagctgg gggcccagg agaggaagac 300
acacatgcct ttccagaagg ggatgccctt tgacctctgc ttcttggtgc agagctcaga 360
tttcaagggt atggtgaacg ggatcctctt cgtgcagtac ttccaccgag tgcccttcca 420
ccgtgtggac accatctccg tcaatggctc tgtgcanctg tctacatca ncttccagac 480
ccagacagtc atccaca 497
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<210> 280

<211> 544
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (451)
<223> n=A,T,C or G

<400> 280
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agacgggtga tttctgcatt tccatctgag gtaccgggtt catctcacta gggagtgcc 120
gacagtgggc gcaggccagt gtgtgtgcgc accgtgcgcg agccgaagca gggcgaggca 180
ttgcctcacc tgggaagcac aaggggtcag ggagttccct ttccgagtca aagaaagggg 240
tgacggacgc acctggaaaa tcgggtcact cccaccgaa tattgtgctt ttcagaccgg 300
cttaagaaac ggcgaccac gagactatat cccacacctg gctcagaggg tcctacgccc 360
acggaatctc gctgattgct agcacagcag tcttagatca aactgcaagg ggggcaacga 420
ggctggggga ggggcgcgcc ccattgccca ngcttgctta ggtaaacaaa gcagccggga 480
agcttgaact ggggtggagcc caccacagct caaggaggcc tgctgcctc ttagctcca 540
cctc 544

<210> 281
<211> 527
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (456)
<223> n=A,T,C or G

<400> 281
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ctgagcggtg catcgagtcc ctgattgctg tcttccagaa gtatgctgga aaggatgggt 120
ataactacac tctctccaag acagagttcc taagcttcat gaatacagaa ctagctgcct 180
tcacaaagaa ccagaaggac cctgggtgtc ttgaccgcat gatgaagaaa ctggacacca 240
acagtgatgg tcagctagat ttctcagaat ttcttaatct gattgggtggc ctagctatgg 300
cttgccatga ctcttccctc aaggctgtcc cttccagaa gcggacctga ggacccttg 360
gccctggcct tcaaaccac cccctttcct tccagccttt ctgtcatcat ctccacagcc 420
caccatccc ctgagcacac taaccacctc atgcanggcc cccctgccaa tagtaataaa 480
gcaatgtcct tttttaaaac atgaaaaaaa aaaaaaaaaa actcgag 527

<210> 282
<211> 514
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (494)
<223> n=A,T,C or G

<400> 282
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ccggctggt gctgcggggg ccccgaggag ttgaaaacta agcatgggga agagctgcaa 120
gggtgtcgtg tgtggccagg cgtctgtggg caaaacttca atcctggagc agcttctgta 180
tggaaccat gtagtgggtt cgagatgat cgagacgcag gaggacatct acgtgggctc 240
cattgagaca gaccgggggg tgcgagagca ggtgcgtttc tatgacaccc gggggctccg 300

agatggggcc gaactgcccc gacactgctt ctcttgact gatggctacg tcctgggtcta 360
tagcacagat agcagagagt cttttcagcg tgtggagctg ctcaagaagg agattgacaa 420
atccaaggac aagaaggagg tcaccatcgt ggtccttggc aacaagtgtg acttacagga 480
gcagcggcgt gtanacccaa atgtggctca acac 514

<210> 283

<211> 484

<212> DNA

<213> Homo sapiens

<400> 283

gggcgggcgg tggacagtca tggcgggccc gcgcggggct ctcatagtgc tggagggcgt 60
ggaccgcgcc ggggaagagca cgcagagccg caagctgggtg gaagcgctgt gcgcgcggcg 120
ccaccgcgcc gaactgctcc ggttcccggg aagatcaact gaaatcggca aacttctgag 180
ttctacttg caaaagaaaa gtgacgtgga ggatcaactg gtgcacctgc ttttttctgc 240
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cgtggacaga tacgcatttt ctggtgtggc cttcacccgt gccaggaga atttttccct 360
agactggtgt aaacagccag acgtgggcct tcccaaaccg gacctggtcc tgttcctcca 420
gttacagctg gcggatgctg ccaagcgggg agcgtttggc catgagcgt atgagaacgg 480
ggct 484

<210> 284

<211> 514

<212> DNA

<213> Homo sapiens

<400> 284

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acgcaccac gccctcacc ccccgagagc cgaaaatgga cccaagtggg gtcaaagtgc 120
tggaaacagc agaggacatc caggagaggc ggcagcaggt cctagaccga taccaccgct 180
tcaaggaaact ctcaaccctt aggcgtcaga agctggaaga ttctatcga ttccagttct 240
ttcaaagaga tgctgaagag ctggagaaat ggatacagga aaaacttcag attgcatctg 300
atgagaatta taaagacca accaacttgc agggaaagct tcagaagcat caagcatttg 360
aagctgaagt gcaggccaac tcaggagcca ttgttaagct ggatgaaact ggaaacctga 420
tgatctcaga agggcatttt gcattctgaaa ccatacggac ccgtttgatg gagctgcacc 480
gccagtggga attacttttg gagaagatgc gaga 514

<210> 285

<211> 383

<212> DNA

<213> Homo sapiens

<400> 285

gaattcggca cgaggccggg ctccaccgcg catcctgctc cactctggcg accgcccccg 60
gggccccgc gcgcggcgcg gcgcgcgcca tgggcgagga ggactactat ctggagctgt 120
gcgagcggcc ggtgcagttc gagaaggcga accctgtcaa ctgcgtcttc ttcatgagg 180
ccaacaagca ggtttttgct gttcgatctg gtggagctac tggcgtggta gttaaaggcc 240
cagatgatag gaatcccatc tcatttagaa tggatgacaa aggagaagtg aagtgcatta 300
agttttcctt agaaaataag atattggctg ttcagaggac ctcaaagact gtggattttt 360
gtaattttat ccctgataat tcc 383

<210> 286

<211> 943

<212> DNA

<213> Homo sapiens

<400> 286

gaattcggca ccagggccgt ggcgaggagg gagcgtgca cgggtggagcg tcgggcccgc 60

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gttcaccggc ccgtctgccc cgaccgcccaggcccgctt cccctgacct cgcgcgcacg 180
cgtggggctg gggcgcgag gctggcggtc cggcctggcc gcgactctgc ctttctttcc 240
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taggcggcgg taggggtgg ggacgcttg agtctccagg tgccaggatc cctgtccccg 480
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ccaaaacagc tggcaggact gccgtgcaca caccagcacg tcc 943
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<210> 287

<211> 1143

<212> DNA

<213> Homo sapiens

<400> 287

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gaggaagcaa agaaaatgat atcaggacta caggcccttac tgctcaatgg atccttacct 120
gaagatgaac aggagaggcc cttggccctc tgtgaaccag gtgtcaatcc cgaggaacaa 180
ctgattataa tccaaagtcg tctggatcag agtatggagg agaatacagga cttaaagaag 240
gaactgctga aatgtaaaaca agaagccaga aacttacagg ggataaagga tgccttgcat 300
cagagattga ctcagcagga cacatctgtt cttcagctca aacaagagct actgagggca 360
aatatggaca aagatgagct gcacaaccag aatgtggatc tgcagaggaa gctagatgag 420
aggaaccggc tcttgggaga atataaaaaa gagctggggc agaaggatcg ccttcttcag 480
cagcaccagg ccaagttaga agaagcactc cgaaactct ctgatgtcag ttaccaaccag 540
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gaggcagatg aggcgaccaa ctacaacagt cacaactctc aaagcaatgg ttttctcctt 660
ccaacggcag gaaaaggagc tacttcagtc agcaacagag ggaccagcga cctgcagctt 720
gttcgagatg ctctccgcag cctgcgcaac agcttcagtg gccacgatcc tcagcaccac 780
actattgaca gcttgagca gggcatttct agcctcatgg agcgctgca tgttatggag 840
acgcagaaga aacaagaaag aaaggttcgg gtcaagtcac ccagaactca agtaggtagt 900
gaataccggg agtcttgccc ccctaactca aagttgcctc actcacagag ctctccaact 960
gtcagcagca cctgtactaa agtgccttat ttactgacc ggtcaacttac gcccttcatt 1020
gtcaatatac caaagggtt ggaggaggtg acgttaaagg attttaaagc agctattgat 1080
cggaaggaa atcaccggtg tcaactcaaa gcaactggatc ctgagtttgg cactgtcaaa 1140
gag 1143
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<210> 288

<211> 881

<212> DNA

<213> Homo sapiens

<400> 288

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gtgagagcgg gccgaggaga ttggcgacgg tgtcgcccgt gttttcgttg gcgggtgcct 60
gggctggtgg gaacagccgc cogaaggaa caccatgatt tcggccgcgc agttgttggg 120
tgagttaatg ggccgggacc gaaacctagc cccggacgag aagcgacgca acgtgcggtg 180
ggaccacgag agcgtttgta aatattatct ctgtggtttt tgcctgcgg aattgttcac 240
aaatacacgt tctgatcttg gtccgtgtga aaaaattcat gatgaaaatc tacgaaaaca 300
gtatgagaag agctctcgtt tcatgaaagt tggctatgag agagattttt tgcgatactt 360
acagagctta cttgcagaag tagaacgtag gatcagacga ggccatgctc gtttggcatt 420
atctcaaac cagcagctct ctggggccgc tggcccaaca ggcaaaaatg aagaaaaaat 480
tcaggttcta acagacaaaa ttgatgtact tctgcaacag attgaagaat tagggctctg 540
```

```
aggaaaaagta gaagaagccc aggggatgat gaaattagtt gagcaattaa aagaagagag 600
agaactgcta aggtccacaa cgtcgacaat tgaaagcttt gctgcacaag aaaaacaaat 660
ggaagtgttg gaagtatgtg gagccttttt aatagtagga gatgccagat cccgggtaga 720
tgaccatttg atgggaaaaac aacacatggg ctatgccaaa attaaagcta ctgtagaaga 780
attaaaagaa aagttaagga aaagaaccga agaacctgat cgtgatgagc gtctaaaaaa 840
ggagaagcaa gaaagagaaa aaaaaaaaaa aaaaactcga g 881
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<210> 289

<211> 987

<212> DNA

<213> Homo sapiens

<400> 289

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gaattcggca cgagggactg tggtttccag gaatggtggc gtctcacgct tcttgtgctt 60
tttccttgg ggcctccgag cggctggggg tgggggactg ggcaggaggc tccctgtaaa 120
catttgact tgggctgggg caggggctgg tgttgggcaa agctgggggt ccaggctgga 180
gaagcagggg cccctccaga cgcagccttg ggagactcag catgtgcccc cctccccctca 240
tcacagaaca agacaatggt taaaaaccag aacagatgcc cagaaggggg taccatggcc 300
attaccagca tctcagacaa gggcaggcctt caaacaggga ggctgtggc aaccctccc 360
ctacgtctgg agctgagggg acagggggag ctgagaacaa agagaggaaa gaggagaaa 420
gcggcggggg aacaggcggg gagcgtgatc ttcttgcccc catcttcctc aggggttggg 480
gggtacaaag tcggcgggtg cccatcccgc caggccccgc tgcccctcag aagaggccgc 540
agtccttcag gttgttcttg atgatgacat cggtagcggc gtcaaacacg aactgcacgt 600
tcttgggtgc ggtggcgcac gtgaagtgcg tgtagatctc cttgggtgtct ttgcgcttat 660
tcaggtcctc aaacttactc tggatgtagc tggctgcctc atcataattg ttggcccctg 720
tatactcagg gaagcagatg gtcaggggac tgtgtgtgat cttctcctca aacaggctct 780
tcttgttgag gaagaggatg atggacgtgt ctgtgaacca cttgttgttg cagatgctat 840
cgaatagctt catgctctca tgcattcggt tcatctcctc gtccctcagc agcaccaagt 900
cataggcgct caaggctacg cagaagatga tggctgtgac gccctcaaag cagtggatcc 960
acttctccg ctcagaccgc tgaccac 987
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<210> 290

<211> 300

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(300)

<223> n = A,T,C or G

<400> 290

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gattcaagat gtacccatt gactttgaga aggatgatga cagcaacttt catatggatt 60
tcatcgtggc tgcattcaac ctccgggcag aaaactatga cattccttct gcagaccggc 120
acaagagcaa gctgattgca gggaagatca tcccagccat tgccacgacc acagcagccg 180
tggttggcct tgtgtgtctg gagctgtaca aggttgtgca ggggcaccga cancttgact 240
cctacangaa tgggtgcctc aacttgagcc ctgcctttct ttgggtttctc tgaaccctt 300
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<210> 291

<211> 352

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(352)

<223> n = A,T,C or G

<400> 291

aaccaagctg	ccaccggggg	tggatcggat	gcggcttgag	aggcatctgt	ctgccgagga	60
cttctcaagg	gtatttgcc	tgtcccctga	agagtttggc	aagctggctc	tgtggaagcg	120
gaatgagctc	aagaagaagg	cctctctctt	ctgatggccc	ccacctgctc	cgggacggcc	180
cccttacc	tgctgcttca	gggtttttcc	ccggcgggtt	gggaggggca	ggaggtgggg	240
tggaaatngg	gtgggcncc	ttcctcaggt	agagnggggg	gccaaaacct	ctgcngtccc	300
cggagnagac	tatggacttt	cttccccctc	acaagngtgg	gggcctcctg	ct	352

<210> 292

<211> 511

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(511)

<223> n = A,T,C or G

<400> 292

cgggtggct	gcgactcng	cctgagaaac	tcggcaagcg	cgcagtgtcg	actccccggt	60
ctatgccagg	cgcattctcag	ctaattccaa	agtaaagag	aaacttagaa	aaagattgcc	120
aattccaaat	caacatattt	agagaaaatt	ggaaaaggag	aagcttacta	cagctttatt	180
tgaggacttt	ttaaagaacg	ctgggttcta	tctgtgagct	gcaaattctg	gagcaaaaac	240
cagagacatt	gccagagcaa	acaagaacag	aaatacaaat	ggagaactgg	tcaaaagaca	300
taaccacag	ttatcttgaa	caagaaacta	cggggataaa	taaaagtag	canccagatg	360
agcaactgac	tatgaattct	gagaaaagta	tgcatcggaa	atccactgaa	ttagntaatg	420
aaataacatg	ngagaacaca	gaatggccag	gggcagagat	caacgaattt	tcnatcatc	480
agttcttata	cagatgatga	gtctgtttac	t			511

<210> 293

<211> 526

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(526)

<223> n = A,T,C or G

<400> 293

gataaaaaga	actttaatgg	aaggcactgt	tgtccaaaat	cacataaagg	gtaagagccc	60
acacggtacc	accctgctct	cctacttctc	aaaccacat	ccaccacca	gacaggagg	120
tgcanacccc	acaggaaatt	acctccggga	gactgactg	atatttttcc	ttaaaacaaa	180
aaaatggctg	tctcagacta	ataacagaac	atcttaagag	ctataccagc	tattacagcc	240
tgtaatatana	agcagctttc	taanaattcc	caagtttata	anaggcccaa	naaatgcatt	300
tattctgttg	tctattaagc	ctccatgaca	aggagaaagt	tatgagtaaa	tccttggttc	360
atcaggagtt	aagagctgtg	ngcctcatga	ggagttaana	gctgtgtgca	taagcaggtt	420
caagaaacaa	actcctgttt	gtttgcctct	ttgatgggtc	aaaaacattc	agctgctttc	480
acctctanga	caaaatgctt	aaagaattta	ctctcatcac	cttggg		526

<210> 294

<211> 601

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(601)

<223> n = A,T,C or G

<400> 294

actttaaaag	ccaaatatat	ttttaaaaga	tcatgcttat	aataagtaaa	ttacncatta	60
aggaacatc	aaaataaagt	agatgaataa	aaaggcacac	tcgaaaaatt	tgagcgagcaga	120
aaggacagt	ctttttgttt	tgtttcta	gtcggaagaa	aaagaaagag	atatattaaa	180
atcattgttt	tcaagtgaag	gtttctgtca	gttgaagtag	ttagcaatgg	cttcttttct	240
cccgtgtcca	aagcaggctc	ttcctgcgct	gacttctgag	gaggngttca	gtcctctgcc	300
atgtataggc	gatacatcaa	ggcgacggcc	actgcagaga	tggcagggat	caccagttg	360
gtccaccaac	tggaactaga	atcaatagta	gtgataagag	tttccggagg	cttgtttaac	420
tttggtctgt	catctggatg	gagctcccca	atgatgaatg	ttttggacat	ttccctggca	480
tctgtagant	gcccagacatc	ctcaaagttc	tcagtagcng	tcacctocac	ttgttccctt	540
aaaacttctt	ccccaccagg	atgctcttcc	agaaatttgg	gncaaatcgn	acaccttggtg	600
g						601

<210> 295

<211> 262

<212> DNA

<213> Homo sapien

<400> 295

cccttagccc	caagggccct	gggggcagcc	accctcccgc	ctgtcggccc	gtagatttat	60
caaggggtgt	atgggccag	ctttgggggg	ccagtcgccga	tgacttttga	ggggtgttgg	120
agaggggact	ccccactcg	cacttaactc	aacggctctc	gggccctggg	gctgttttta	180
ccatgtttgt	ttttgaagct	caggtgtctc	acgtctgggc	tgaccaggcc	gaagagagaa	240
attaaagatt	tgaggttttt	cc				262

<210> 296

<211> 598

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(598)

<223> n = A,T,C or G

<400> 296

gttagaaca	ctcagcaaaa	taaaattcct	gtttattgtt	ggacaacatt	gtttcacaca	60
tacatcaaac	aggccaaaaa	aaataaacag	caacttcata	gacaaaaaag	gaaaaaaaaa	120
gaaacctttt	atctttggcc	tttttaacca	tctcatacaa	accaactact	tatagtacag	180
ctaagtacat	acacaaaaaa	gttactggaa	tgctcggaat	aagattgttt	ttctgttgct	240
atthttgttt	tttttacaag	gntttttttc	tcctttgaga	ttataatgaa	catggncaca	300
ccacaagtaa	agtcagaagt	aggacagana	acgctccgaa	ggctggtttg	gtcatccgan	360
atcattaaaa	atggctgacc	ctaacaatat	gtacaaaaat	ataaaatgta	aataaaaaat	420
acaaacaaat	ttccttttta	aagtactttt	aagaaaaaaa	gcagggcctt	ggaagtgttg	480
gttctttttt	cctcccctgt	tgcaaattct	catggtttgg	gttgggtggn	gganancccg	540
tgtcatctgc	gggtggcact	gccccgngg	gcgggcgggc	ctctctctcg	aangngac	598

<210> 297

<211> 509

<212> DNA

<213> Homo sapien

<400> 297

agaacacagg	tgctgtgaaa	actacccta	aaagccaaaa	tgggaaagga	aaagactcat	60
atcaacattg	tcgtcattgg	acacgtagat	tcgggcaagt	ccaccactac	tggccatctg	120

atctataaat	gcggtggcat	cgacaaaaga	accattgaaa	aatttgagaa	ggaggctgct	180
gagatgggaa	agggctcctt	caagtatgcc	tgggtcttgg	ataaactgaa	agctgagcgt	240
gaacgtggta	tcaccattga	tatctccttg	tggaaatttg	agaccagcaa	gtactatgtg	300
actatcattg	atgccccagg	acacagagac	tttatcaaaa	acatgattac	agggacatct	360
caggctgact	gtgctgtcct	gattgttgct	gctgggtgtg	gtgaatttga	agctgggtatc	420
tccaagaatg	ggcaggaccc	gagagcatgc	ccttctggct	tacacactgg	gtgtgaaaca	480
actaattgtc	ggtgttaaca	aaatggatt				509

<210> 298
 <211> 267
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(267)
 <223> n = A,T,C or G

<400> 298	
gggacggggg	aaaggagacg cttcttcctc ttgctgctct tctcgttccc gagatcagcg 60
gcggcggtga	ccgcgagtggtg gtcggcaccg tctccggctc cggngcnaa caatgctgac 120
tgatagcgga	ggcggnggca cctccttnna ggaggacctg gactctgtgg ctccgcgatc 180
cgccccagct	ggggcctcgg agccgcctcc gccgggagggtg gtcgggtctgg ggatccnca 240
cgngagggctn	tttggggagg gcgggcc 267

<210> 299
 <211> 121
 <212> DNA
 <213> Homo sapien

<400> 299	
ggcacgaggg	ccctcggagc tcgtttccag atcgaggtaa gagggacttt cttaaaggcc 60
tagtctatgg	gatggggcgg cggagggaat tttttgagaa ataaaatgaa gctgcagtgt 120
a	121

<210> 300
 <211> 533
 <212> DNA
 <213> Homo sapien

<400> 300	
aagggtgcaca	gtatttgatg caggctgctg gtcttggtcg tatgaagcca aacacacttg 60
tccttggtgatt	taagaaagat tggttgcaag cagatatgag ggatgtggat atgtatataa 120
acttattttca	tgatgctttt gacatacaat atggagtagt gggtattcgc ctaaaagaag 180
gtctggatat	atctcatctt caaggacaag aagaattatt gtcatcacia gagaaatctc 240
ctggcaccaa	ggatgtggta gtaagtgtgg aatatagtaa aaagtccgat ttagatactt 300
ccaaaccact	cagtgaaaaa ccaattacac acaaagttaga ggaagaggat ggcaagactg 360
caactcaacc	actgttgaaa aaagaatcca aaggccctat tgtgccttta aatgtagctg 420
accaaagct	tcttgaagct agtacacagt ttcagaaaaa acaaggaaag aatactattg 480
atgtctgggtg	gctttttgat gatggagggt tgaccttatt gataccttac ctt 533

<210> 301
 <211> 560
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature

<222> (1)...(560)

<223> n = A,T,C or G

<400> 301

ataaatgatac	cctttttattg	taagtaatgc	gcaacactgg	cctggctttg	caactgcaagc	60
cctcggtcaa	gatatagtca	aataactatg	gctgcagggt	ccacagttcc	acaataacca	120
tggctgcacg	atccacaatt	cagacacaga	catagagctg	gggtgggtgg	aaggggcagg	180
agggtggcag	agtgcggact	gtcccagcc	ctggcctctc	catgcanagt	tggcccaggc	240
agacacaccc	catggaatga	tgagaaagt	acggcacggc	cccttcccac	agcaagcctg	300
gggctgccag	gaactgccct	tcanaacctt	tgggccagg	tcnccctgaa	nccccacaac	360
tttttatctg	gaataagtat	taaaaaaca	taaattaagc	aaacaacntg	gnccttgaag	420
gatgttgacc	nacatgggtc	acagtttttg	gcncaaaaaa	ataagggctg	gtttgctttt	480
tttggaaggc	agggtttgtg	gnttggcttt	caaatnattt	tcaaaccatt	ccccagggag	540
gganaacccc	cgggggggaa					560

<210> 302

<211> 599

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(599)

<223> n = A,T,C or G

<400> 302

gcaaagttac	aaatattattg	gtctggaaat	aaatacaaat	atctcattaa	naaactcctc	60
tggaagact	tgtgcacaat	agtttcccat	ccgtactcag	cctctcttgc	cccgatcccc	120
gacttttcta	ctcaaggcca	gggaaggcct	ccaaggngat	gggcggcagg	taacgagtca	180
ttgcctctca	cgccacctgg	aaggctggac	tacttccctc	tcccaactgc	ggggtccan	240
aaatcctcgg	gtcccagngg	ctgacttaca	atattcaatt	cactctgacc	aaacttccta	300
tganaaaatc	cacggngagc	caaaatgaaa	agtacaaggc	agtagtacag	gaacctggca	360
gccgcactgg	ccgcccanaa	acgtcagtgg	ngctgcccc	ttcggcgaaa	ggtaggggag	420
caggaaaaga	ggaagcagga	gagggaagga	aagtcccatg	gaatatgtat	tccanaatcc	480
ttacattttc	tcagccaccg	ctccccacgt	gagttccac	ccccaccccg	acaagaagca	540
aagagttctg	aggatccaag	aacgtgaccg	ggtcanacan	gttcagctac	tgagttcac	599

<210> 303

<211> 591

<212> DNA

<213> Homo sapien

<400> 303

cggagtgtga	acgtccact	gactgataga	gcgaccggcc	gaccatggcg	cccggagtgg	60
cccgcgggcc	gacgccgtac	tgagagttgc	gcctcggtgg	cgccgcgctg	ctcctgctgc	120
tcatcccggg	ggccgcgcgc	caggagcctc	ccggagctgc	ttgttctcag	aacacaaaca	180
aaacctgtga	agagtgcctg	aagaacgtct	cctgtctttg	gtgcaacact	aacaaggctt	240
gtctggacta	cccagttaca	agcgtcttgc	caccggcttc	cctttgtaaa	ttgagctctg	300
cacgctgggg	agtttgttgg	gtgaactttg	aggcgctgat	catcaccatg	tcggtagtgc	360
ggggaaccct	cctcctgggc	attgccatct	gctgctgctg	ctgctgcagg	aggaagagga	420
gccggaagcc	ggacaggagt	gaggagaagg	ccatgcgtga	gcgggaggag	aggcggatac	480
ggcaggagga	acggagagca	gagatgaaga	caagacatga	tgaaatcaga	aaaaaatatg	540
gcctgtttta	agaagaaaac	ccgtatgcta	gatttgaaaa	caactaaagc	g	591

<210> 304

<211> 441

<212> DNA

<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(441)
<223> n = A,T,C or G

<400> 304
gctggacgga gacctgctgg aggaggagga gctggaggaa gcagaggagg aggaccggtc 60
gtcgtgctg ctgctgtgc cggccgcggc caccgcctct cagaccagc agatcccagg 120
cgggtccctg gggctgtgc tgctgccagc cggcagggtc gatgccggg aggcggcggc 180
ggcggcggg gtgctgtac gaggggacga tgcccaggc atgatggcg cgatgctgtc 240
ccacgcctac ggccccggcg gttgtggggc ggccggcgcc gccctgaacg gggagcaggc 300
ggccctgctc cggagaaaga gcgtcaacac caccgagtgc gtcccgggtc ccagctccga 360
gcacgtcgcc gagatcgctg gccgccaggg ttgtaaaatt aaagcactga nagccaagac 420
aaacacgtat atcaagactc c 441

<210> 305
<211> 491
<212> DNA
<213> Homo sapien

<400> 305
tcgccatgcc cccttcttag cactgcaccg ccagggtccat gctgctgcca cccagacct 60
gggctttgcc tgccacctct gtgggcagag ctcccgaggc tgggtggccc tggttctgca 120
tctgcgggcc cattcagctg caaagcggcc catcgcttgt cccaaatgcg agagacgctt 180
ctggcgacga aagcagcttc gagctcatct gcggcggtgc caccctcccg ccccgaggc 240
ccggcccttc atatgcggca actgtggccg gagctttgcc cagtgggacc agctagtgtc 300
ccacaagcgg gtgcacgtag ctgaggccct ggaggaggcc gcagccaagg ctctggggcc 360
ccggcccagg ggccgccccg cgtgaccgc cccccggccc ggtggagatg ccgtcgaccg 420
ccccttcag tgtgcctgtt gtggcaagcg ctcccgccac aagcccaact tgatcgctca 480
ccgcgcgtg c 491

<210> 306
<211> 547
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(547)
<223> n = A,T,C or G

<400> 306
tctctttctt ttaagacagg aatgtaagcc acaacattta caaatacaat gttttaactc 60
tctacatgta ggaagccaac ctgctccttt ttgatcttct tctttggcac aacctcagtg 120
gatttctctg attcagaacg agttctaatt gatcttctct gttgcttctt ttctactgag 180
cctgtagaac cagatgttgc ttcaggagat gatacactct gcgttggctt ttcatctctc 240
tggtttggtg tagaaattat aagcctgtct tgccccctga cacttatttc tgttttgtta 300
ccaattccct ttgttgaata aacaaattga tcgataaatt tcccatcccc tgtagcattc 360
tgaagagcaa acacttggtc aattttcaca actggagaca tgttacactt ctgcaaatcc 420
aggctccctt tgtgcatccg taatggaagc tggttaaggat ttcccttgctg ccgcagtttt 480
ccaggctatt ttaacaggcg gnggctcttc ctctttccgc acttggtgtg cgctctggc 540
tatgtct 547

<210> 307
<211> 571
<212> DNA
<213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(571)
 <223> n = A,T,C or G

<400> 307
 cgctgcatgt gataatgtca tcattttattt ttaaattggtt ctaaattgca natttaagtt 60
 gatttcaaat caaccctatt ttttaattac ttttaattagg aanaaatgaa gcaaggacat 120
 acataatcta ctatatattga aggactcaaa caaatacatg ttggctgtg aattctgtac 180
 tctcaccaaa acagagataa aaatccacct aaaatacact ttccttcatt tagtgcttgt 240
 ggganaaggt caagtattgc actttaaaat tactttcatc taacatttgc cccaactttc 300
 cccctgaatt cactatatgt tttcagcaaa catgatttta taaattttaa gtataaaagc 360
 aactaggttt tctaattcaa ctttggaagg tttactttac tctacanagc tatttttgta 420
 aaacggcata tttacttaca aaattganag ataggggcat ccagctgagg tacatttcct 480
 cccttggcgt tgagtttctg gacttgggtc gggggcacag gcttgtgtga ctgccccgtg 540
 gcccgataca tggcctggac cccaggatgc g 571

<210> 308
 <211> 591
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(591)
 <223> n = A,T,C or G

<400> 308
 ctccctatgt gtctgcctac ttcattcttc ggcatttcct gcttatccaa gttcaccatt 60
 tcaggtcacc actggatata agttgcctgt atataattat caggcatttc ctgcttatcc 120
 aagttcacca tttcagggtca ccactggata tcagttgcct gtatataatt atcaggcatt 180
 tcttgcttat ccaagttcac catttcagggt caccactgga tatcagttgc ctgtatataa 240
 ttatcaggca tttcctgctt atccaagttc accatttcag gtcaccactg gatatacagtt 300
 gcctgtatat aattatcagg catttcctgc ttatccaagt tcaccatttc aggtcaccac 360
 tggatatcag ttgcctgtat ataattatca ggcatttcct gcttatccaa gttcaccatt 420
 tcaggtcacc actggatata agttgcctgt atataattat caggcatttc ctgcttatcc 480
 aaattcagca gttcagggtca ccactggata tcagttccat gtatacaatt accagatgcc 540
 accgcagtgc cctgttgggg gagcaaagga gaaatntgtg gaccgaagca t 591

<210> 309
 <211> 591
 <212> DNA
 <213> Homo sapien

<400> 309
 aggggggtgca cgtactccca actgtggtcg cgctctcacc ccttctgctg ctctcgtggc 60
 cccctcgcga tggcgggcat cctgtttgag gatattttcg atgtgaagga tattgaccgc 120
 gagggcaaga agtttgaccg aggttaagtaa gtgtctcgac tgcattgtga gagtgaatct 180
 ttcaagatgg atctaattt agatgtaaac attcaaattt accctgtaga cttgggtgac 240
 aagtttcggt tggatcatagc tagtaccttg tatgaagatg gtaccctgga tgatggtgaa 300
 tacaacccca ctgatgatag gccttccagg gctgaccagt ttgagtatgt aatgtatgga 360
 aaagtgtaca ggattgagg agatgaaact tctactgaag cagcaacacg cctgctgaga 420
 ttgagagctg ctgagtgcca gtgtccaga atcacgggat ggggccttct gtttcagctc 480
 tgcgtacgtg tcctatgggg gcctgctcat gaggtgcag ggggatgcca acaacctgca 540
 tggattcgag gtggactcca gagtttatct cctgatgaag aagctagcct t 591

<210> 310

<211> 488
<212> DNA
<213> Homo sapien

<400> 310
tggtctcaag cctgaagagg ctccgcccac aagctggccc atgaagttag caatgcctgt 60
ggcttcagtc aattgtcttg agactgtgaa gaggtgaaa gacaccttcc cgggtggaag 120
aaggagtcca ctgaaaactt atcttaaaact gaccttccc tttagtgag tcttcattcc 180
tctcccatgt gggaaaccag cctccgatgc cccggggact aggggaaaca gttggaggtc 240
cgtgccgtcc ccagcctgcc acgggtgcga ggacagccaa gtcctgagtg actcaagatg 300
cttcacttac atggaagaaa ctctaaaaac tctaccgagt ggtttttgta tatactaaag 360
ttctatttag agcttttctg ttttgggcaa gttcgtgct ccttctattt gggcactttg 420
gtttttgtac tgtcttttgt gacggcattg attgaacatt ttttactagt agtcctatga 480
cttttgta 488

<210> 311
<211> 511
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(511)
<223> n = A,T,C or G

<400> 311
cccgtttntg nagcaaaaana gggggaagat ttataggtag aggcgacaaa cctaccgagc 60
ctggtgatag ctggttggtcc aagatagaat cttagttcaa ctttaaattt gcccacagaa 120
ccctctaaat ccccttgtaa atttaactgt tagtccaaag aggaacagct ctttgacac 180
taggaaaaaa ccttgtagag agagtaaaaa atttaacacc catagtaggc ctaaaagcag 240
ccaccaatta agaaagcgtt caagctcaac acccactacc taaaaaatcc caaacatata 300
actgaactcc tcacacccaa ttggaccaat ctatcacctc atagaagaac taatgttagt 360
ataagtaaca tgaaaacatt ctctccgca taagcctgcy tcagattaaa aactgaact 420
gacaattaac agcccaatat ctacaatcaa ccaacaagtc attattaccc tcaactgtcaa 480
cccaacacag gcatgctcat aaggaaaggt t 511

<210> 312
<211> 591
<212> DNA
<213> Homo sapien

<400> 312
gaacttgctg tgaaggaagc agaaactgat gaaataaaaa ttttgctgga agaaagcaga 60
gcccagcaga aggagacctt gaaatctctt cttgaacaag agacagaaaa tttgagaaca 120
gaaattagta aactcaacca aaagattcag gataataatg aaaattatca ggtgggctta 180
gcagagctaa gaactttaat gacaattgaa aaagatcagt gtatttccga gtttaattagt 240
agacatgaag agaactctaa tatacttaaa gctgaattaa acaaagtaac atctttgcat 300
aaccaagcat ttgaaataga aaaaaacctt aaagaacaaa taattgaact gcagagtaaa 360
ttggattcag aattgagtgc tcttgaaaga caaaaagatg aaaaaattac ccaacaagaa 420
gagaaatacg aagctattat ccagaacctt gagaaagaca gacaaaaatt ggtcagcagc 480
caggagcaag acagagaaca gttaattcag aagcttaatt gtgaaaaaga tgaagctatt 540
cagactgccc taaaagaatt taaattggag agagaagttg ttgagaaaga g 591

<210> 313
<211> 373
<212> DNA
<213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(373)
 <223> n = A,T,C or G

<400> 313
 ttgattttta ttctgnatth tattactgaa atangttgtc ctantnatcc caccacacaa 60
 taaaaatnln acccangccc cccntttctt tncctnatnc cctnttccac cacaccatcc 120
 cggaacaagt gctccaggat tccctgcca ctggccatth tggagtgtgn ccattgggta 180
 gcaatgtgga aaccaccaag gcctttgtgg anaaaatgga ggggggtgag ggagnccan 240
 gaggggctna tttgagggcc tttgccactt gctcataggc gagctcnatc tcctcntnat 300
 ctgnacangt ggaagcaaat tcttcccggg cgtnggnant gctnaagnac cgatgcactc 360
 cccggaaggc ctn 373

<210> 314
 <211> 591
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(591)
 <223> n = A,T,C or G

<400> 314
 cccgtgccgc cgccgcctcc tgggaagaga ggaagcggga gaggagccca cgtcgcctgt 60
 caccacaatat ctccagccgc gcagtcocga agagtgtgaa atgttcgcct gcgccaagct 120
 cgctgcacc cctctctga tccgagctgg atccagagtt gcatacagac caatttctgc 180
 atcagtgtta tctcgaccag aggctagtag gactggagag ggctctacgg tattttaatgg 240
 ggcccagaat ggtgtgtctc agctaataca aaggaggtt cagaccagtg caatcagcag 300
 agacattgat actgctgcca aatttattgg tgcaggtgct gcaacagtag gagggtgctg 360
 ttctggtgct ggtattggaa cagtctttgg cagccttatc attggttatg ccagaaaccc 420
 ttcgctgaag cagcagctgt tctcatatgc tatcctggga tttgccttgt ctgaagctat 480
 gggctctctt tgtttgatgg ttgctttctt gattttgttt gccatgtaac aaattactgc 540
 ttgacatgtt ggcattcata ttaattacng atgtaattct gtgtatctta c 591

<210> 315
 <211> 591
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(591)
 <223> n = A,T,C or G

<400> 315
 aagcccttca ccaacaaaga tgcctatact tgtgcaaatt gcagtgcctt tgtccacaaa 60
 ggctgcccag aaagtctagc ctctgtgca aaggtcaaaa tgaagcagcc caaagggagc 120
 cttcaggcac atgacacatc atcactgccc acggctatta tgagaaacaa gccctcacag 180
 cccaaggagc gtctctggtc cgcagtcctc ctgggtgatg aaaccgctac caccaccaata 240
 tttgccaata gacgatccca gcagagtgtc tgcctctcca aaagtgtctc catacagaac 300
 attactggag ttggcaatga tgagaacatg tcaaacacct ggaaattcct gtctcattca 360
 acagactcac taaataaaat cagcaaggtc aatgagtgaa cagaatcact tactgatgag 420
 ggtacagaca tgaatgaagg acaactactg ggagactttg agattgagtc caaacagctg 480
 gaagcagagt cttggagtcg gataatagac agcaagtttc taaaacagcc aaaagaaaga 540
 tgtgggtcaa acngcgagaa gtaatatatg agttggatgc agacagagtt t 591

<210> 316
 <211> 591
 <212> DNA
 <213> Homo sapien

<400> 316
 gtttttataa gaataaaaatt ccattcaagc cagatgggtgt ttacattgaa gaagttctaa 60
 gtaaatggaa aggagattat gaaaaactgg agcacaacca cacttacatt caatggcttt 120
 tccccctgag agaacaaggc ttgaacttct atgccaaaga actaactaca tatgaaattg 180
 aggaattcaa aaaaacaaaa gaagcaatta gaagattcct cctggcttat aaaatgatgc 240
 tagaattttt tggaaataaaa ctgactgata aaactggaaa tgttgctcgg gctgttaact 300
 ggcaggaaaag atttcagcat ctgaatgagt ccagcacaa ctatttaaga atcactcgta 360
 ttcttaaaag ccttgggtgag ctgggatatg aaagttttaa atctcctctt gtaaaattta 420
 ttcttcatga agctcttgtg gagaatacta ttccaatat taagcagagt gctctagagt 480
 attttgttta tacaattaga gacagaagag aaaggagaaa gctcctgcgg ttcgcccaga 540
 aacactacac gccttcagag aactttatct ggggaccgcg ctcgaaaaga a 591

<210> 317
 <211> 323
 <212> DNA
 <213> Homo sapien

<400> 317
 ccaagctacg gaagcaagtg gaagagattt ttaatttgaa atttgctcaa gctcttggac 60
 tcaccgaggc agtaaaagta ccatatcctg tgtttgaatc aaaccggag ttcttctatg 120
 tggaaggctt gccagagggg attcccttcc gaagccctac ctgggttggg attccacgac 180
 ttgaaaggat cgtccacggg agtaataaaa tcaagttcgt tgttaaaaaa cctgaactag 240
 ttaatttcta cttgctctct gggatggcta gtaaaataaa cactaaagct ttgcagtcct 300
 ccaaaagacc acgaagtcct ggg 323

<210> 318
 <211> 591
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(591)
 <223> n = A,T,C or G

<400> 318
 gatggcgtag ttggcttggg gactggcgcg gcgttcgtgt ccgagttctc tgcagggtcac 60
 tagtttcccg gtagttcagc tgcacatgaa tagaacagca atgagagcca gtcagaagga 120
 ctttggaaat tcaatgaatc aagtgaact cttagaaaaag gatccaggaa acgaagtga 180
 gctaaaactc tacgcgctat ataagcaggc cactgaagga ccttgtaaca tgcccaaacc 240
 aggtgtatth gacttgatca acaaggccaa atgggacgca tggaatgccc ttggcagcct 300
 gcccaaggaa gctgccaggc agaactatgt ggatttgggt tccagtttga gtccttcatt 360
 ggaatcctct agtcaggtgg agcctggaac agacaggaaa tcaactgggt ttgaaactct 420
 ggtggtgacc tccgaagatg gcatcacaaa gatcatgttc aaccggccca aaaagaaaaa 480
 tgccataaac actgagatgt atcatgaaat tatgcgtgca cttaaagctg ccagcaanga 540
 tgactcaatc atcacttggt ttaacaggaa atggtgacta ttacagtagn g 591

<210> 319
 <211> 591
 <212> DNA
 <213> Homo sapien

<400> 319

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gaattcggca cgagggttgct gctaagcgaa cgcccttttg agcttacgga ggccttctga      60
aagacttcac tgctactgac ttgtctgaat ttgtctgcaa ggctgccttg tctgctggca      120
aagtctcacc tgaacacagt gacagtgtga ttatgggcaa tgcctgcag agttcttcag      180
atgctatata tttggcaagg catgttggtt tgcgtgtggg aatcccaaag gagacccag      240
ctctcacgat taataggctc tgtggttctg gttttcagtc cattgtgaat ggatgtcagg      300
aaatttgtgt taaagaagct gaagttgttt tatgtggagg aaccgaaagc atgagccaag      360
ctccctactg tgtcagaaat gtgcgttttg gaaccaagct tggatcagat atcaagctgg      420
aagattcttt atgggtatca ttaacagatc agcatgtcca gctcccatg gcaatgactg      480
cagagaatct tgctgtaaaa cacaaaataa gcagagaaga atgtgacaaa tatgccctgc      540
agtcacagca gagatggaaa gctgctaata atgctggcta cttaaatgat g              591

```

<210> 320

<211> 591

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(591)

<223> n = A,T,C or G

<400> 320

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ggctccggcg tctgcagggg tcgccgagct aaccogtggc taggcgagtg gggcggggcg      60
gccggcacca tgtcgaggca ggcgaaccgt ggcaccgaga gcaagaaaat gagctctgag      120
ctcttcaccc tgacctatgg tgccctggtc acccagctat gtaaggacta tgaaaatgat      180
gaagatgtga ataaacagct ggacaaaatg ggccttaaca ttggagtcg gctgattgaa      240
gatttcttgg ctcggtcaaa tgttgggagg tgccatgact ttccggaaac tgcggatgtc      300
attgccaagg tggcgttcaa gatgtacttg ggcattcact caagcattac taattggagc      360
ccagctggtg atgaattctc cctcattttg gaaaataacc ccttgggtgga ctttgtggaa      420
cttcctgata accactcatc ccttatttat tccaatctct tgtgtggggg gttgcgggga      480
gctttggaga tgggtccagat ggctngngga ggcccaagtt tgtccaggac accctnaaag      540
gagacgggng tgacagaaat ccggatgaga ttcatcaggc ggattganga c              591

```

<210> 321

<211> 260

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(260)

<223> n = A,T,C or G

<400> 321

```

ctgcttggtt ccacacgtgg gccgccgtag gtattccgac cggtaatcc tcctattggt      60
gtgcagcagc cacattgaag gatagagtgg cagcagaggc caaggatcgt gagttgatgg      120
agtttctgct tgaaaatgaa gggaagtctg ggggaggtct ccacagcgta gctgaggggg      180
tgcggctaag tccagagcct ggcagggagg gagtaaggga cttagcaggg gcggaggagt      240
tctgcggngg anaggagggg

```

<210> 322

<211> 559

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(559)

<223> n = A,T,C or G

<400> 322

ttccacatga	catggagtgt	gaagctggat	gagcacatca	ttccactggg	aagcatggca	60
nttaacagca	tctcaaaact	gactnanctc	accagtcctt	ccatgtattc	acttcctaata	120
gcacccactc	tggcanacct	gnaggacnat	acacatgaag	ncantgatga	tcagccagan	180
aancctcact	ttgactctcg	canngtgata	tttgagctgg	attcatgcaa	tggmagtggg	240
aaagtttgcc	ttgtctacaa	aagtgggaaa	ccagnattag	cagaanacac	tgagatctgg	300
ttcctgnaca	nancgttata	ctggcatttt	ctcacanaca	cctttactgc	ctattaccgc	360
ctgctcatca	cccacctggg	cctgccccag	tggcaatatg	ccttcccagc	tatggcatta	420
gcccacaggc	caagcaatgg	ttcagcatgt	ataaacctat	cacctacaac	acaaacctgc	480
tcacagaaga	naccgactcc	tttgtgaata	agctagatcc	canctnagtg	tttaagagca	540
agaacaagat	cgttatccc					559

<210> 323

<211> 492

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(492)

<223> n = A,T,C or G

<400> 323

cctgtctccc	agccgtacca	gcgagggctc	ggccggcagc	gccgggctgg	ggggcgggcg	60
cgccggcgcc	ggagccgggg	tgggtgcagg	cgccggcggg	ggcagcgggc	cgagcagcgg	120
cgccggggcc	ggggggctgc	aaccagcag	cgccggctgg	ggcgccggc	cctccagccc	180
cagcccgtcg	gtggtgagcg	agaaggagaa	ggaagagttg	gagcggtgc	agaaagagga	240
ggaggagagg	aagaagaggc	tgcagctgta	tgtgttcgtg	atgcgctgca	tcgcctaccc	300
ctttaatgcc	aagcagccca	ccgacatggc	tcgcccggcag	cagaagatca	gcaaacagca	360
gctgcagaca	gtcaaggacc	ggtttcaggc	tttcctcaat	ggggaaaccc	anacatggc	420
tgacgaagcc	ttcatgaacc	gctgtngcag	agttactatg	aggtgttcct	gaagaccacc	480
cgtgtggccg	ca					492

<210> 324

<211> 474

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(474)

<223> n = A,T,C or G

<400> 324

aatttcagca	acatacttct	caattttctc	aggatttaaa	atcttgaggg	attgatctcg	60
cctcatgaca	gcaagttcaa	tgtttttgcc	acctgactga	accacttcca	ggagtgcctt	120
gatcaccagc	ttaatggtca	natcatctgt	ttcaatggct	tcgtcagtat	agttcttctc	180
cagnaactca	cgcactgact	tggcaccgcc	gcctatggca	ttggccttcc	aggcatggta	240
tgtgcccag	gggtcagtct	gatagagcct	aggagtggca	tcaaagtcga	aaccacgat	300
gagggcagag	atgccaaacg	gcctgcgccc	attgctctgc	gtataacgct	gcttcanact	360
ggcagatgag	cggtgatgt	actccacagt	gaccgggtcc	tccacagtca	gccggtggct	420
ctggcactcc	acccgggccc	tgttgatgac	tatccttgca	tcggcggtga	ggcc	474

<210> 325

<211> 532

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(532)

<223> n = A,T,C or G

<400> 325

gaggagacag	gacagagcgt	ctggagaggc	aggaggacac	cgagttcccc	gtgttggcct	60
ccaggtcctg	tgcttgcgga	gccgtccggc	ggctgggatc	gagccccgac	aatgggcaac	120
gcgcaggagc	ggccgtcaga	gactatcgac	cgcgagcgga	aacgcctggg	cgagacgctg	180
caggcggact	cgggactgct	gttggacgcg	ctgctggcgc	ggggcggtgt	caccgggcca	240
gagtacgagg	cattggatgc	actgcctgat	gccgagcgca	gggtgcgccg	cctactgctg	300
ctggtgcagg	gcaagggcga	ggccgcctgc	caggagctgc	tacgctgtgc	ccagcgtacc	360
gcgggcgcgc	cggaccccg	ttgggactgg	cagcacgtgg	gtccgggcta	ccgggaccgc	420
agctatgacc	ctccatgcc	aggccactgg	acgccggagg	caccgggctc	ggggaccaca	480
tgccccgggt	tgcccagact	tcagaccctg	acgaggncgg	gggccctgag	gg	532

<210> 326

<211> 322

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(322)

<223> n = A,T,C or G

<400> 326

caaaattaac	atttttatta	aatcaagtta	aaaaaaatgt	tcagtgtana	aaagtcaaca	60
agggttttta	caaaaccaaa	atataccttt	ttatacaata	tatgtatata	ttagcagcaa	120
actacttctg	anattctctt	tcttttatgt	tcttctagtt	attttaaaga	aagcataaac	180
aatgtatatt	agtatggaat	gtcagcaaat	ccactcttag	tcctttattc	tgtgatttgg	240
gccttctaca	aaatactttg	tgattctcac	taatgaatat	taagaacata	cccaatttta	300
actaaaaagt	agtgaacag	tg				322

<210> 327

<211> 387

<212> DNA

<213> Homo sapien

<400> 327

aaaaccgtgt	actattagcc	atgggtcaacc	ccaccgtgtt	cttcgacatt	gccgtcgacg	60
gcgagccctt	gggccgcgtc	tcctttgagc	tgtttgcaga	caaggtccca	aagacagcag	120
aaaattttcg	tgctctgagc	actggagaga	aaggatttgg	ttataagggt	tcctgctttc	180
acagaattat	tccagggttt	atgtgtcagg	gtgggtgactt	cacacgccat	aatggcactg	240
gtggcaagtc	catctatggg	gagaaatttg	aagatgagaa	cttcataccta	aagcatacgg	300
gtcctggcat	cttgtccatg	gcaaagtctg	gacccaacac	aaatggttcc	cagtttttca	360
tctgcactgc	caagactgag	tggttgg				387

<210> 328

<211> 502

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(502)

<223> n = A,T,C or G

<400> 328

agcagcccg	cgccgccc	gcgcggcg	gcggcaagg	tccgggccag	catgggggct	60
tcgtggtgac	tgtcaagcaa	gagcgcgcg	aggggtccacg	cgccggcgag	aaggggtccc	120
acgaggagga	gccggtgaag	aaacgcggct	ggcccaagg	caagaagcg	aagaagattc	180
tgccgaatg	gcccaggca	ccggtcacgg	gctacgtg	cttcctgaac	gagcgggcg	240
agcagatccg	cacgcgccac	ccgcatctgc	cctttcccga	gatcaccaag	atgctggg	300
ccgagtggag	caagctgcag	ccaacggaaa	agcagcggt	cctggatgag	gccnagagag	360
agaagcagca	gtacatgaag	gagctgcgg	cgtaccagca	gtctgaagcc	tataagatgt	420
gcacggagaa	gatccaggag	aagaagatca	agaaagaaga	ctcgagctct	gggctcatga	480
acactcttct	gaatggacac	aa				502

<210> 329

<211> 463

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(463)

<223> n = A,T,C or G

<400> 329

caagtgac	attttaattt	acaattttta	ccaataaaaa	ggattagttt	acaaaaagg	60
aagtccttta	tacaaaataa	ggacaatttg	taaaganaat	ccactgtcat	gttttgcctt	120
gtcaagtcaa	aactcaaata	gcttgttttg	gtaaaattat	tccagaaaca	taatccagac	180
aaaatcaata	acgtcatcag	cttcctaacc	atgtttaana	ggaataactt	catgaacatt	240
ttgccctgaa	ctgaanagtt	ctaaataactt	gtaaaccttt	aggaaaaaat	gactgctcgc	300
aggcagcttg	actggttaaga	gggtacacca	nagactccgg	gtcactcact	gtcagaatat	360
tcttatacat	acaatgagtc	tccacgcctg	tacaatgagt	gtcgtgcaac	ataattggag	420
taatggcctc	taaaatttta	caagtaaact	ttattgnggc	ccc		463

<210> 330

<211> 500

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(500)

<223> n = A,T,C or G

<400> 330

taattataga	tctacaaaat	atgaaatgta	ttccaagaat	gcagaaaaac	catctagaag	60
caaaaggact	ataaaacaaa	aacagagaag	aaaattcatg	gctaaaccag	ctgaagaaca	120
gcttgatgtg	ggacagtcta	aagatgaaaa	catacatata	tcacatatta	ccaagacga	180
atttcaaaga	aattcagaca	gaaatatgga	agagcatgaa	gagatgggaa	atgatttgt	240
ttccaaaaaa	acagatgcc	cctgtgggaa	gcaagaaaag	tagcactaga	aaagataagg	300
aagaatctaa	aaagaagcgc	ttttccagt	agtccaagaa	caaacttgtn	cctgaagaag	360
tgacttcaac	tgtcacgaaa	agtcgaanaa	tttccangcg	tccatctgat	tggtgggtgg	420
taaaancaga	ggagagtcct	gtttatagca	attcttcagt	aagaaatgaa	ttaccaantg	480
catcacaatn	ntgcccggaa					500

<210> 331

<211> 494

<212> DNA

<213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(494)
 <223> n = A,T,C or G

<400> 331
 tctctctctc tctcaaaatt acagtgttca ttgtcattga cctcagcagc aaatttgact 60
 tgaattcact taggatcgca ggaatcaggg gaaagtgatt ttaaagggtg tttctccagc 120
 acattttaag aaaagggacc aaaagttatt ttagcttcct caatagattg catgttgctt 180
 attaggataa taaattaata ttaaattgcaa tataatgtctt gnctttatta tggcatctat 240
 ttaggagttg ttcaaatcac tgcagttagg ctctgcaaat aaaataatgn aacctattat 300
 catggatcta atgnactgna actttatcag tgaaaggnaa aatctcaaat aacaagtaca 360
 aacattggac aattaacctat aaagatttgt aaaaggaaaa tttttccata gatttcattc 420
 ttggcatttt gtaaagacga ccctgcagnc ccctgtttgn aactttttta ataaaataga 480
 catctgttta cttg 494

<210> 332
 <211> 538
 <212> DNA
 <213> Homo sapien

<400> 332
 aaagaacaaa tggaacgcga tgggtgttct gaacaagagt ctcaaccgtg tgcatttatt 60
 gggataggaa atagtgcaca agaaatgcag cagctaaact tggaaggaaa gaactattgc 120
 acagccaaaa cattgtatat atctgactca gacaagcgaa agcacttcat gttgtctgta 180
 aagatgttct atggcaacag tgatgacatt ggtgtgttcc tcagcaagcg gataaaaagtc 240
 atctccaaac cttccaaaaa gaagcagtc ttgaaaaatg ctgacttatg cattgcctca 300
 ggaacaaagg tggctctgtt taatcgacta cgatcccaga cagttagtac cagatacttg 360
 catgtagaag gaggtaattt tcatgccagt tcacagcagt ggggagcctt ttttattcat 420
 ctcttgatg atgatgaatc agaaggagaa gaattcacag tccgagatgg ctacatccat 480
 tatggacaaa cagtcaaact tgtgtgctca gttactggca tggcactccc aagattga 538

<210> 333
 <211> 499
 <212> DNA
 <213> Homo sapien

<400> 333
 ctcagcctgc gggactgctc ggctcggctt ctaggcgggtt ttgatgaaca cctggcttta 60
 ttcttgcaat gaagaaagg tctcaacaaa aaatattctc caaagcaaag ataccatcat 120
 catctcactc tctatccca tcatctatgt ccaatatgag atctagggtca ctttcacctt 180
 tgattggatc agagactcta ccttttcatt ctggaggaca gtggtgtgag caagttgaga 240
 ttgcagatga aaacaatatg cttttggact atcaagacca taaaggagct gattcacatg 300
 caggagttag atatattaca gaggccctca ttaaaaaact tactaaacag gataatttgg 360
 ctttgataaa atctctgaac ctttcacttt ctaaaagacgg tggcaagaaa ttttaagtata 420
 ttgagaattt ggaaaaatgt gttaaacttg aagtactgaa tctcagctat aatctaatag 480
 ggaagattga aaagtcgga 499

<210> 334
 <211> 561
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(561)
 <223> n = A,T,C or G

<400> 334

ttccccgtag	ttcagctgca	catgaataga	acagcaatga	gagccagtca	gaaggacttt	60
gaaaattcaa	tgaatcaagt	gaaactcttg	aaaaaggatc	caggaaacga	agtgaagcta	120
aaactctacg	cgctatataa	gcaggccact	gaaggacctt	gtaacatgcc	caaaccagggt	180
gtatttgact	tgatcaacaa	ggccaaatgg	gacgcatgga	atgcccttgg	cagcctgccc	240
aaggaagctg	ccaggcgagaa	ctatgtggat	ttggtgtcca	gtttgagtc	ttcattggaa	300
tcctctagtc	aggtggagcc	tggaacagac	aggaaatcaa	ctgggtttga	aactctggtg	360
gtgacctccg	aagatggcat	cacaaagatc	atgttcaacc	cggcccaaaa	agaaaaatgc	420
cataaacact	gagatgtatc	atgaaattat	gcgtgcactt	aaagctgcca	gcaaggatga	480
ctcaatcatc	actgttttaa	cangaaatgg	tgactattac	agtagtggga	atgatctgac	540
taacttcnct	gatattcccc	c				561

<210> 335

<211> 551

<212> DNA

<213> Homo sapien,

<400> 335

aagctggtca	tggtgggga	gaccaccaac	tcccgcggcc	agcggctgcc	ccagaaggga	60
gacgtggaga	tgctgtgcg	cgggcogccc	tgccagggct	tcagcggcat	gaaccgcttc	120
aattcgcgca	cctactccaa	gttcaaaaac	tctctggtgg	tttcttctct	cagctactgc	180
gactactacc	ggccccggtt	cttctctctg	gagaatgtca	ggaactttgt	ctccttcaag	240
cgctccatgg	tcctgaagct	caccctccgc	tgctgtgtcc	gcattgggcta	tcagtgcacc	300
ttcggcgctg	tcagggcgg	tcagtacggc	gtggcccaga	ctaggaggcg	ggccatcatc	360
ctggcccgcg	cccctggaga	gaagctccct	ctgttcccgg	agccactgca	cgtgtttgct	420
ccccgggcct	gccagctgag	cgtggtgggt	ggatgacaag	aagtttgatga	gcaacataac	480
caggttgagc	tcgggtcctt	tccggaccat	acggtgcgag	aaacgatgtc	cgacctgccg	540
gaagtgcgga	a					551

<210> 336

<211> 540

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(540)

<223> n = A,T,C or G

<400> 336

aggcttatgt	ctactgaagg	caataaacga	ggaatgatcc	agcttattgt	tgcaaggaga	60
ataagcaagt	gcaatgagct	gaagtcacct	gggagccccc	ctggacctga	gctgccatt	120
gaaacagcgt	tgatgatag	agaacgaaga	atttcccatt	ccctctacag	tgggattgag	180
gggcttgatg	aatcgccag	cagaaatgct	gccttcagta	ggataatggg	taaataaccag	240
ctgtccccta	cagtgaatat	gcccgaagat	gacactgtca	ttatagaaga	tgacagggtg	300
ccagtgcctc	ctccacatct	ctctgaccag	tcctcttcca	gctcccatga	tgatgtgggg	360
tttgtgacgg	cagatgctgg	tacttgggcc	aaggctgcaa	tcagtgatcc	agccgactgc	420
tctttgagtc	cagatgttga	tccagttcct	gcttttcaac	gaaaaaggat	ttggacgtca	480
gaagtatgtc	agaaaaacgc	accaaagcaa	ttttcanatg	ccagtcaatt	ggatttcggt	540

<210> 337

<211> 422

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(422)

<223> n = A,T,C or G

<400> 337

gcagcaggaa	cagttacagc	agcagcagca	acagcagctg	ttgcaacagc	agcaggaaca	60
attgcagcag	caacaactgc	agcctcctcc	cctggagccc	gaggaggagg	aagagggtgga	120
gctggagctc	atgccggtgg	acctggggtc	agagcaggag	ctggagcagc	agcggcagga	180
gttggagcgg	cagcaggagc	tggaaacggca	gcaggagcag	cggcagctgc	agctcaaact	240
gcaggagagag	ctgcagcagc	tggagcaaca	gctggagcag	cagcagcagc	agctggagca	300
gcaggaggtg	cagctggagc	tgaccccggt	ggagctaggc	gcccagcagc	aggagggtgca	360
gctggagctg	acccccgtgc	agccggagct	gcagctggaa	ctggtgccan	cccagggggc	420
gg						422

<210> 338

<211> 601

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(601)

<223> n = A,T,C or G

<400> 338

catcttacga	acgctctatg	atgtcttatg	agcgggtctat	gatgtcccct	atggctgaac	60
gctctatgat	gtcagcctac	gagcgtctta	tgatgtcagc	ctacgagcgc	tctatgatgt	120
cccctatggc	tgagcgtctt	atgatgtcag	cttatgaacg	ctccatgatg	tcagcttatg	180
aacgctccat	gatgtcccca	atggctgata	gatctatgat	gtccatgggt	gctgaccggt	240
ctatgatgtc	gtcatactct	gtgctgacc	ggctctatgat	gtcatcgta	tctgcagctg	300
accgatctat	gatgtcatct	tatactgctg	atcggttaac	gatgtctatg	gctgctgatt	360
cttacaccga	ttcttacact	gacacatata	cagaggcata	tatgggtgcca	cctttgcctc	420
ctgaagagcc	cccaacaatg	ccaccgttgc	cacctgagga	gccaccaatg	acaccaccat	480
tgctnctga	ggaaccaccc	agaggggtcca	gcattgcccc	cttgagcagt	cagcattaac	540
cagcttgaaa	atacttggcc	ctacanangg	tgccatcatt	accatctgaa	gagctgtatc	600
g						601

<210> 339

<211> 440

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(440)

<223> n = A,T,C or G

<400> 339

agagggagga	ggcccaactg	gtgatgctgc	tgtgtgctgct	gctgccgccg	ccgccgcctc	60
tattgctgat	actctagtgg	ggctggaagg	gtgggttccta	ttcgacccat	cgccaaccag	120
agacagaggg	aaaaaaaaaa	ccggcagcca	ctgctgatgt	tgggttcgga	ggctgcatcc	180
gactcgggtca	caaggaaaat	ggattcagtt	tgcattctctc	cctccttttaa	acagcttctc	240
cgggtctcag	catggtatca	aagcttgaaa	gagagaagac	tcaagaagcg	aagaggattc	300
gtgagctgga	gcagcgcaag	cacacggtgc	tggtgacaga	actcaaagcc	aagctccatg	360
aggagaagat	gaaggagctg	caggctgtga	gggagaacct	tatcaagcag	cacgacagga	420
aatgtcaang	acggtgaagg					440

<210> 340

<211> 450

<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(450)
<223> n = A,T,C or G

<400> 340
gatttccagg ggcggatatt gagtgtcgac ccagaggaag aaagggagga gggcccgcct 60
aggattcctc aggccgacca gtggaagtct tcaaacaaga gcctgggtga ggctctgggg 120
ctggaagccg aggggtgcagt tcctgagaca cagactttga ccggatggag taaggggttc 180
attggcatgc acagggaaat gcaagtcaac cccatttcaa agcggatggg gcccatgact 240
gtggtcagga tggacgcttc agtccagcca ggcccttttc ggaccctgct ccagtttctt 300
tatacgggac aactggatga aaaggaaaag gatttggtgg gcctggctca gatcgcagag 360
gtcctcgaga tgttcgattt gaggatgatg gtggaaaaca tcatgaacaa ggaagccttc 420
atgaaccagg agattacgaa nncctttcac 450

<210> 341
<211> 451
<212> DNA
<213> Homo sapien

<400> 341
aacagctatt aaaacagaaa atggatgaac ttcataagaa gttgcatcag gtggtggaga 60
catcccata ggaatctgcc gcttcccagg aaagggtccga ggtaaatcca gcacgtatgg 120
ggccaagtgt aggtctccag caggaactga gagcgccatg tcttccagta acctatcagc 180
agacaccagt gaacatggaa aagaacccaa gagaggcacc tctgttgtt cctcctttgg 240
caaatgctat ttctgcagct ttggtgtccc cagccaccag ccagagcatt gctcctctg 300
ttcctttgaa agcccagaca gtaacagact ccatgtttgc agtggccagc aaagatgctg 360
gatgtgtgaa taagagtact catgaattca agccacagag tggagcagag atcaaagaag 420
ggtgtgaaac acataaggtt gccaacacaa g 451

<210> 342
<211> 498
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(498)
<223> n = A,T,C or G

<400> 342
ctcaagcagg ctattgaaga ggaaggaggc gatccagata atattgaatt aactgtttca 60
actgatactc caaacaagaa accaactaaa ggcaaaggta aaaaacatga agcagatgag 120
ttgagtggag atgcttctgt gggaagatga tgctttttatc aaggactgtg aattggagaa 180
tcaagaggca catgagcaag atggaaatga tgaactaaaag gactctgaag aatttggtga 240
aaatgaagaa gaaaatgtgc attccaagga gttactctct gcagaagaaa acaagagagc 300
tcatgaatta atagaggcag aaggaataga agatatagaa aaagaggaca tcgaaagtca 360
ggaaattgaa gctcaagaag gtgaagatga taccttttcta acagcccaag atgggtgagga 420
agaagaaaat gagaaagata tagcagggtt ctgggtgatgg cncacaagaa gtatntaaac 480
ctcttccttc aaaaaggg 498

<210> 343
<211> 491
<212> DNA
<213> Homo sapien

<400> 343
 ccgaccccta ctcggcggcg caactccaca accagtacgg ccccatgaat atgaacatgg 60
 gtatgaacat ggcagcagcc gcggcccacc accaccacca ccaccaccac cccccgggtg 120
 cctttttccg ctatatcgcg cagcagtgca tcaagcagga gctaattctgc aagtggatcg 180
 accccgagca actgagcaat cccaagaaga gctgcaacaa aactttcagc accatgcacg 240
 agctggtgac acacgtctcg gtggagcacg tcggcggccc ggagcagagc aaccacgtct 300
 gcttctggga ggagtgtccg cgcgagggca agcccttcaa ggccaaatac aaactggtca 360
 accacatccg cgtgcacaca ggcgagaac ccttccctgc ccttccgggt gtggcaaagt 420
 cttcgcgcgc tccgagaacc tcaagatcca caaaaggacc acacagggga gaagccgtcc 480
 agtggagttg a 491

<210> 344

<211> 412

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(412)

<223> n = A,T,C or G

<400> 344
 gtgcgtgtc ttcccgttg cgtcagggac ctgcccgaact cagtggccgc catggcatca 60
 gatgaaggca aactttttgt tggagggctg agttttgaca ccaatgagca gtgcgtggag 120
 caggtcttct caaagtacgg acagatctct gaagtgttgg ttgtgaaaga caggagagacc 180
 cagagatctc ggggatttgg gtttgcacc tttgagaaca ttgacgacgc taaggatgcc 240
 atgatggcca tgaatgggaa gtctgtagat ggacggcaga tccgagtaga ccaggcaggc 300
 aagtcgtcan acaaccgatc ccgtgggtac cgtgggtggct ctgccggggg ccgggggttc 360
 ttccgtgggg gcccgangac ggggcccgtg ggttctctaa aagaagaggg ga 412

<210> 345

<211> 498

<212> DNA

<213> Homo sapien

<400> 345
 aactagtctc gggccatcct ttctgcgcac ccggtgtcgc tgggctgcac cccgggcccgg 60
 gacgtccgcc gggcacggga gggggccaag atgccgatca ataaatcaga gaagccagaa 120
 agctgcgata atgtgaagggt tgttgttagg tgccggcccc tcaatgagag agagaaatca 180
 atgtgttaca aacaggctgt cagtgtggat gagatgaggg gaactatcac tgtacataag 240
 actgattctt ccaatgaacc tccaaagaca tttacttttg atactgtttt tggaccagag 300
 agtaaacaaac ttgatgttta taacttaact gcaagaccta ttattgattc tgtacttgaa 360
 ggctacaatg ggactatttt tgcataatgga caaaccggaa caggcaaaac ttttaccatg 420
 gaaaggtgtc gagctattcc tgaacttaga ggaataattc cccaatttct ttgctcacia 480
 tatttgggcc atatttgc 498

<210> 346

<211> 427

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(427)

<223> n = A,T,C or G

<400> 346

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agatggcggg cgccgtgaga actttgcagg aacagctgga aaaggccaaa gagagtctta      60
agaacgtgga tgagaacatt cgcaagctca cggggcgga tccgaatgac gtgaggccca      120
tccaagccag attgctggcc ctttctgggc ctggtggagg tagaggacgt ggtagtttat      180
tactgaggcg tggattctca gatagtggag gaggaccccc agccaaacag agagaccttg      240
aaggggcagt cagtaggctg ggcggggagc gtcggaccag aagagaatca cgccaggaaa      300
gcgaccggga ggatgatgat gttaaaaagc cagcattgca gtcttcannt gtagctacct      360
cccaaagagc gccccacgta gagaccttat ccagggatca aaattttgga tgaaaaaggg      420
gaaagcc                                         427

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<210> 347
 <211> 280
 <212> DNA
 <213> Homo sapien

```

<400> 347
cacagaaagt tctccgctcc cagacatggg tccctcggtt tctgcctcg gaagcgcagc      60
agcaggcatc gtgggaagggt gaagagcttc cctaaggatg acccgctcaa gccgggtccac      120
ctcacagcct tcctgggata caaggctggc atgactcaca tcgtgcggga agtcgacagg      180
ccgggatcca aggtgaacaa gaaggagggt gtggaggctg tgaccattgt agagacacca      240
cccatggtgg ttgtgggcat tgtgggctac gtggaacccc      280

```

<210> 348
 <211> 411
 <212> DNA
 <213> Homo sapien

```

<400> 348
caactatgat gtgcctgaaa aatgggcacg attctatact gcagaagtag ttcttgcatt      60
ggatgcaatc cattccatgg gttttattca cagagatgtg aagcctgata acatgctgct      120
ggataaatct ggacatttga agttagcaga ttttgggtact tgtatgaaga tgaataagga      180
aggcatggta cgatgtgata cagcggttgg aacacctgat tataatttccc ctgaagtatt      240
aaaatcccaa ggtggtgatg gttattatgg aagagaatgt gactggtggt cggttgggg      300
atttttatac gaaatgcttg taggtgatac acctttttat gcagattcct tggttggaa      360
ttacagtaaa attatgaacc attaaaaatt cacttacctt tctgatgat a              411

```

<210> 349
 <211> 408
 <212> DNA
 <213> Homo sapien

```

<400> 349
gatgggcacg tctcgggaca actggcacaa gcgcccga aa accgggggca agagaaagcc      60
ctaccacaag aagcggaagt atgagttggg gcgcccagct gccaacacca agattggccc      120
ccgcccacac cacacagtcc gtgtgcgggg aggttaacaag aaataccgtg ccctgaggtt      180
ggacgtgggg aatttctcct ggggctcaga gtgtgtgact cgtaaaacaa ggatcatcga      240
tgttgtctac aatgcatcta ataacgagct ggttcgtacc aagacctggt tgaagaattg      300
catcgtgctc atcgacagca caccgtaccg acagtggtag gagtccact atgcgctgcc      360
cctggggccg aagaaggag ccaaactgac ttctgaggaa gaagaaaa              408

```

<210> 350
 <211> 409
 <212> DNA
 <213> Homo sapien

```

<400> 350
ggttccccca gctctgggta cccggctctg catcgcgtcg ccatgatggg ccatcgtcca      60
gtgctcgtgc tcagccagaa cacaagcgt gaatccggaa gaaaagttca atctggaaac      120
atcaatgctg ccaagactat tgcagatata atccgaacat gtttgggacc caagtcctat      180

```

atgaagatgc ttttggaccc aatgggaggc attgtgatga ccaatgatgg caatgccatt	240
cttcgagaga ttcaagtcca gcatccagcg gccaaagtcca tgatcgaaat tagccggacc	300
caggatgaag aggttggaga tgggaccaca tcagtaatta ttcttgacagg ggaaatgctg	360
tctgtagctg agcacttcct ggagcagcag atgcacccaa caggtgggg	409

<210> 351
 <211> 226
 <212> DNA
 <213> Homo sapien

<400> 351	
aatcccaaac atataactga actcctcaca cccaattgga ccaatctatc accctataga	60
agaactaatg ttagtataag taacatgaaa acattctcct ccgcataagc ctgcgtcaga	120
ttaaaacact gaactgacaa ttaacagccc aatatctaca atcaaccaac aagtcattat	180
taccctcact gtcaacccaa cacaggcatg ctcataagga aaggtt	226

<210> 352
 <211> 410
 <212> DNA
 <213> Homo sapien

<400> 352	
gcggaggggc tggctgggca ggaggggttg gcggggcagc agggccgcgg ccatggggag	60
cttgaaggag gagctgctca aagccatctg gcacgccttc accgcactcg accaggacca	120
cagcggcaag gtctccaaagt cccagctcaa ggtcctttcc cataacctgt gcacgggtgt	180
gaaggttctc catgacccag ttgcccttga agagcacttc agggatgatg atgaggggtcc	240
agtgtccaac cagggtcaca tgccttattt aaacagggtc attttggaag aggtccaaga	300
caactttgac aagattgaat tcaataggat gtgttggacc ctctgtgtca aaaaaaacct	360
cacaaagaat cccctgctca ttacagaaga agatgcattt aaaatatggg	410

<210> 353
 <211> 380
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(380)
 <223> n = A,T,C or G

<400> 353	
gagtttattt agaaagtatc atagtgtaaa caaacaatt gtaccacttt gattttcttg	60
gaatacaaga ctcgatgatc aaagctgaag ttgtgtgtac aagactcttg acagttgtgc	120
ttctctagga ggntgggttt ttttaaaaaa agaattatct gngaaccata cgtgattaat	180
aaagatttcc tttaaggcan aggctggtcn agatgctgct gttatcttct gcctcagaca	240
gacagtataa gnggtcttgt ttctaagatt cctaccacca gttacttttg gccaaagtatc	300
cacatcccct tgcgtatggg aggnnggtga anagtgttgg atgcaaagng gttattatgg	360
gaagnagctc natggtaaaa	380

<210> 354
 <211> 379
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(379)
 <223> n = A,T,C or G

```

<400> 354
caacacatct ttattaaaca cctgaagtta ctgggaggag gccatgatgc tggacacact      60
gtcaaagtca atctttctcca caatgttctt gggtttaatg ctctcttctt ggctacagan      120
gaanatctgc cccgactngt cggcaactcca gccgtatttg ctcatccaca cctttagctg      180
gctgtccgac aganccccga gcatntcggc cagcagccan cggncaatgt gctggtaagt      240
gatacccaca acatggcaga taaactttcg gacanagtct tcaaagccag ttataccttc      300
caagagggtcc atgttttcat ccagggttg ccanaagcct ggaaatggca ggtctccaac      360
aggccccca ggtacaaaa                                     379

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```

<210> 355
<211> 499
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(499)
<223> n = A,T,C or G

```

```

<400> 355
gtccagagct gctggtgctc ccgttcccca gaccctaccc ctatcccag tggagccgga      60
gtgcgggggc gccccaccac cgccctcacc atggtgctgt tggcagcagc ggtctgcaca      120
aaagcaggaa aggtatttgt ttctcgacag tttgtggaaa tgaccgaac tcggattgag      180
ggcttattag cagcttttcc aaagctcatg aacactggaa aacaacatac gtttgttgaa      240
acagagagtg taagatatgt ctaccagcct atggagaaac tgtatatggt actgatcact      300
acaaaaaaca gcaacatttt agaagatttg gagaccctaa ggctcttctc aagagtgatc      360
cctgaatatt gcgagcctta gaagagaatg aaatatctga gcaactgntt gatttgattt      420
ttgcttttga tgaaaaatgtc gcactgggat acccgggang aatgttaact tggcacagat      480
canaaccttt cacagaaaa                                     499

```

```

<210> 356
<211> 511
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(511)
<223> n = A,T,C or G

```

```

<400> 356
gggcttctgc tgagggggca ggcggagctt gaggaaaccg cagataagtt tttttctctt      60
tgaaagatag agattaatac aactacttaa aaaatatagt caataggtta ctaagatatt      120
gcttagcggt aagtttttaa cgtaatttta atagcttaag attttaagag aaaatatgaa      180
gacttagaag agtagcatga ggaaggaaaa gataaaaagg ttctaaaaaca tgacggagggt      240
tgagatgaag cttcttcatg gagtaaaaaa tgtattttaa agaaaattga gagaaaggac      300
tacagagccc cgaattaata ccaatagaag ggcaatgctt ttagattaaa atgaagggtga      360
cttaaacagc ttaaaagtta ntttaaaagt ttaggtgat taaaataatt tgaaggcgat      420
cttttaaaaa gagattaaac ccgaaggatg ttaaaagacc ttgaaatcca tgacgccagg      480
gagaattgcc gtcattttaa gcctagttaa c                                     511

```

```

<210> 357
<211> 511
<212> DNA
<213> Homo sapien

```

```

<220>

```


<221> misc_feature
<222> (1)...(511)
<223> n = A,T,C or G

<400> 357
gatacttcac atttccttag ggaacgggagc ccgagggggtc cgttcggccc tcttcctctc 60
gctggggccga caccocgctg taggaccgta acccttagtc ccaatgcctc cgtaagcgga 120
gttgagtggg tgcctgtggt tggagctgtg gaggtgtccc cgggtggcgag cgcgccgaga 180
actgcggtca cttaagtttt ccgtgtgcgg gttgcaagga gcgtgcgtgc gtctggtata 240
atttggtctc ctgagattct gcttacaaga aaggagtggg aaataccctt ggaaagaaaa 300
ctaaaacagt aagaaaacca aaacttattt ttacatggnt gtcagcacat ttaccgatat 360
ggacactttt cccaataatt tcctcctggt ggagacagtg gattgacagg ttctcagtcg 420
gaattccaga aaatgttaa ttgatgaaaa gggtacnatg tgagcatcat aaagntaatt 480
attaanacac tgaaggctga acacacaagg g 511

<210> 358
<211> 401
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(401)
<223> n = A,T,C or G

<400> 358
acggatgaag atgatgacct tcaagaaaat gaagacaata aacaacataa agaaagcttg 60
aaaagagtga cctttgcttt accagatgat gcggaaactg aagatacagg tgttttaaat 120
gtaaagaaaa attctgatga agttaaatcc tcctttgaaa aaagacagga aaagatgaat 180
gaaaaaattg catctttaga aaaagagttg ttagaaaaaa agcccggtggc agcttcaggg 240
ggaagtgaca gcacagaaga ggccagagaa cacctcctgg aggagaccct acctttgcca 300
tctgcccgat ggccctgtga ttacagagga acccccttca ctggagattt cttaaacnga 360
ngatagagat cngnttggga tatgtntcct taagaaaacc t 401

<210> 359
<211> 511
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(511)
<223> n = A,T,C or G

<400> 359
gcgatgcccg cgcgcccagg acgcctcctc ccgctgctgg cccggccggc ggccctgact 60
gcgctgctgc tgctgctgct gggccatggc ggcggcgggc gctggggcgc ccggggccag 120
gaggcggcgg cggcgggcggc ggacggggccc cccgcggcag acggcgagga cggacaggac 180
ccgcacagca agcacctgta cacggccgac atgttcacgc acgggatcca gagcgcccgc 240
gcacttcgtc atgttcttcg cgccctgggtg tggacacttg ccagcggctt gcagccgant 300
ttggaatgac cttggganga acaaatataa cagcatggaa agaatgccaa aagtctatgt 360
ggnttaaagt ggacttgac nggccacttc gactngtget cccccaaggg gngggaagat 420
accacctta aaacttttca accaagccaa aaactttgaa aaccaggtct cggattcaaa 480
atggaaaact gatgttcaac ctgaacaaga a 511

<210> 360
<211> 511
<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(511)

<223> n = A,T,C or G

<400> 360

tactgggaga	ctttgagatt	gagtccaaac	agctggaagc	agagtcttgg	agtcggataa	60
tagacagcaa	gtttctaaaa	cagcaaaaga	aagatgtggg	caaacggcaa	gaagtaatat	120
atgagttgat	gcagacagag	tttcatcatg	tcccgaactct	caagatcatg	agtgggtgtg	180
cnagccnggg	gatgatggcg	gatctgnttt	ttgagcanca	gatggtagaa	aaagctgggt	240
ccctgtttgg	atgagcttga	tcagtatccc	ataccatttc	tttccagagg	attcttggag	300
ccggaaagaa	nggagcttcc	ttgggtggg	aaaaagtga	aaagaacttt	ctcttcaana	360
aggatagggg	gatgtgcttt	gtaaaatcan	tttttcagg	ngganaatgc	cnnaaccgtt	420
ttaaagaaaa	acatnttggg	naagtttttg	tgggccaaca	ttaccgggtc	ttgtaaacct	480
accttcaaa	aacctttttg	cccagggtta	a			511

<210> 361

<211> 411

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(411)

<223> n = A,T,C or G

<400> 361

gctcagcggc	ccgatccac	ggaagcgcgc	tcggaggggt	gggaccggc	cggaccggag	60
atggcgccgc	cagcggggcg	ggcggcgccg	gcggcctcgg	acttgggctc	cgccgcagtg	120
ctcttggctg	tgcacgcgcg	ggtgaggccg	ctgggcgcgcg	ggccagacgc	cgaagcacia	180
cttgccggag	ctgcagctta	acgcggaccc	tgagaagcct	ggcgcttncc	gctggaactt	240
cttggcgccg	gacctggggc	ggtaatttga	gtggccctga	gtcattttct	caccatccag	300
gccaccaca	cgactaagct	cacaagaagg	ctgaactnnc	tgattctnaa	cctagaanta	360
cgtgcattct	tcagtgcng	aagaaatgac	aacataccac	tggaactct	g	411

<210> 362

<211> 511

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(511)

<223> n = A,T,C or G

<400> 362

cgggggacgc	ggctgccttg	gcccctcagc	gctcgcgtct	tttccggcag	ttggaacgct	60
tctgtttgtc	ctcaccgcta	accgcctgtt	gccccctgtc	tcagagtccc	tcacgcgtcc	120
cctcccgctc	ttggctcggt	ggctgccgcc	gccggggctt	cgccagcctt	caagtcgaga	180
ctactggccg	aaggggcgtc	tgcggctctc	cgccgtcccc	agccctgcct	ctccctgggc	240
tctgccatgg	caatgacagg	ctcaacacct	tgctcatcca	tgagtaacca	cacaaaggaa	300
agggtgacaa	tgacaaaag	tgacactgga	gaatttttat	agcaacctta	tcgctcacat	360
gaagaacgag	aaatgagaca	aaagaagtta	gaaaaagggg	atggaagaag	aaggcctaaa	420
aaaatgaagg	agaaaaccaa	cttccgaaga	tcaaccacat	tgcttcggaa	anggaaacaa	480
aantttcttt	cgtttgaaan	aaaaacaaan	a			511

<210> 363
 <211> 401
 <212> DNA
 <213> Homo sapien

<400> 363
 caggatctgg ggagaaagag ccccatccct tctctctctg ccaccatttc ggacaccccg 60
 cagggactcg ttttgggatt cgcactgact tcaaggaagg acgcgaaccc ttctctgacc 120
 ccagctcggg cggccacctg tctttgccgc ggtgaccctt ctctcatgac cctgcggtgc 180
 cttgagccct ccgggaatgg cggggaaggg acgcggagcc agtgggggac cgcggggtcg 240
 gcggaggagc catccccgca ggcggcgcgt ctggcgaaag ccctgcggga gctcggtcag 300
 acaggatggt actggggaag tatgactggt aatgaagcca aagagaaatt aaaagaggca 360
 ccagaaggaa ctttcttgat tagagatagc tcgcattcag a 401

<210> 364
 <211> 401
 <212> DNA
 <213> Homo sapien

<400> 364
 agtcaaaggt ttcttttccc tttttaccat ggtttctaca aaaataacct tcaggaaaaa 60
 gaaaatcagg aaaaaaattt tttttcaata atcttattcc ctatattaaa ttagatttga 120
 agaggattaa cgttggttta gtttgggtcc agatcagcct tataacaacat ttctaaactc 180
 atttgtactt ttaaaaaatt taaacacaga cttctaaaat tacttgatgt aagtaattta 240
 aatcacttat gaccaagtta ttaaccttat gaatcagaag tctgaccctt gtaggaaatt 300
 atattcacat ataaagtaca tcagatcttt gccatatatt gatggttatt atgcataaac 360
 acattgagtt gtgttggaag cagatttata aacctgcatg t 401

<210> 365
 <211> 361
 <212> DNA
 <213> Homo sapien

<400> 365
 atctggagtt gcacaaatag ttcttttagaa cataaaacta aatggattta tacataacag 60
 ttacattcag catttaagag aggcagtaca aaaatgtgtt ctgcttttat ctgatataaa 120
 ttgcatgtaa taccatgatt taaacaatat cagttatat aactaatgcc atgagatata 180
 tcttactcag aacgtctgat gtttcccata atagacagaa aaaatgcagt tgtatgagca 240
 actgagtttc ttttcatctt caaattcatt tgtgatggtg ggaagatcta aggacaatcc 300
 ttccattgaa gaagtaggaa aaacagttca gcactgttct gaactcatca aaaatgaaat 360
 t 361

<210> 366
 <211> 401
 <212> DNA
 <213> Homo sapien

<400> 366
 cgggagcagc agaggtctag cagccggggc cgcggggccg ggggcctgag gaggccacag 60
 gacgggctc ttcccggcta gtggagcccc gcgcggggcc cgctgcggcc gcaccgtgag 120
 gggaggagc cagaggaggac gcagcgccgg ctgccggcgg gaggaagcgc tccaccaggg 180
 cccccgacgg cactcgttta accacatccg cgcctctgct ggaaacgctt gctggcgcc 240
 gtcaccggtt ccctccattt tgaaagggaa aaaggctctc cccacccatt ccctgcccc 300
 taggagctgg agccggagga gccgcgctca tggcggttcag cccgtggcag atcctgtccc 360
 ccgtgcagtg ggcgaaatgg acgtggtctg cgttacgcgg c 401

<210> 367

<211> 401
 <212> DNA
 <213> Homo sapien

<400> 367
 catggagtcg ggcaagatgg cgcctcccaa gaacgctccg agagatgcct tggatgatggc 60
 acagatcctg aaggatatgg gaatcacaga gtatgaacca aggggtataa atcaaatgtt 120
 ggaatttgct ttccgttatg tgactacaat tctggatgat gcaaaaattt attcgagcca 180
 tgctaagaaa cctaagtgtg atgcagatga tgtgagactg gcaatccagt gtcgtgctga 240
 ccaatctttt acctctctc ccccaagaga ttttttactg gatatcgcaa ggcagaaaaa 300
 tcaaacccct ttgccactga ttaagccata tgcaggacct agactgccac ctgatagata 360
 ctgcttaaca gctccaaact ataggctgaa gtccttaatt a 401

<210> 368
 <211> 401
 <212> DNA
 <213> Homo sapien

<400> 368
 cggagcggta ggagcagcaa tttatccgtg tgcagcccca aactggaaag aagatgctaa 60
 ttaaagtga gacgctgacc ggaaaggaga ttgagattga cattgaacct acagacaagg 120
 tggagcgaat caaggagcgt gtggaggaga aagaggggaat cccccacaa cagcagaggc 180
 tcatctacag tggcaagcag atgaatgatg agaagacagc agctgattac aagattttag 240
 gtggttcagt ccttcacctg gtgttggtc tgagaggagg aggtggtctt aggcagtgat 300
 ggaccctcca ttttacctct ttaccctgtc gctcataatg aggcataata tatcctctca 360
 ctctctggga caccatagcc ctgccccctc ccctggatgc c 401

<210> 369
 <211> 174
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(174)
 <223> n = A,T,C or G

<400> 369
 gcgagnnngg cgccaagcgc ggggccggag cggccttccc ggagtccttt gcgcggcacc 60
 tggcgacaaa atggctgccc gagggagacg ggcggagcct cagggccggg aggctccggg 120
 ccccgcgggc ggtggcgggt gcgggagccg ttgggctgag tcgggatcgg ggac 174

<210> 370
 <211> 375
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(375)
 <223> n = A,T,C or G

<400> 370
 tgcttttcca actttattta gaaaaacaaa tccaggtccc agtgccccct gtaccctccc 60
 cgaccccgag cataatttaa ataacttana gacagagttg gagggagggg acagganagg 120
 ttggggtcac ggtggaagga ggaaganagc cactacagc cgccgcagcg cccgcttctt 180
 gtccgtcttt ttcttgccg ccagcttctt atcgcgctcg ccagcatgct tnttgccat 240
 gggaccctca gcccctccc ggccccctgg ggccccaggg tcggtggagg aagcttcagt 300

gccactggcc agggcccgcg cggcttcggc cctgccgctg ggcccgcgg cgccccctg 360
gatctctgtg agcag 375

<210> 371
<211> 375
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(375)
<223> n = A,T,C or G

<400> 371
taaattctaa aaaatatttt aatacttgaa aacttctaaa aaaaaaggta aggtaacatg 60
ttctttcaaa agtgaatttc acatgcaaac cattaattat atttatttta ctgngagata 120
aaagcaaaac ataacattcg gagaaagaga ccagtaactg acctatttat tttatattat 180
attaatgnga atcttcatta gaaatgtgat aacgttattg cacaaacaaa accgtgggca 240
gaaacatccc agcaatgcag gggcgcccat accgggttac aagggatgtc cagcatgtgt 300
ttccctggaa cactcanagt ctgcactttt cctgcaaatg ggaccatgtc tgattattta 360
ttatgaaaga acact 375

<210> 372
<211> 164
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(164)
<223> n = A,T,C or G

<400> 372
cgctctgtnt cctcaacctc tacctggcgg aggttatatg taaagtcaga tgtgccactg 60
aacttgacag acacaaaatt ctactgcatt tgggctttat aatggaagc ctgctctttt 120
tagtggtgaa cttgacttgc gcaatgctag ttcatggaga tgtc 164

<210> 373
<211> 401
<212> DNA
<213> Homo sapien

<400> 373
gcgctggtcg cctttgccta cctgcagctg tggcggctgc tctgtaccg cgagcggcgg 60
ctgagttacc agagcctctg cctcttcctc tgtctcctgt gggcagcgt caggaccacc 120
ctcttctccg ccgccttctc gctcagcggc tccctgccct tgctccggcc gcccgctcac 180
ctgcacttct tccccactg gctgctctac tgcttccct cctgtctcca gttctccacg 240
ctctgtctcc tcaacctcta cctggcggag gttatatgta aagtcagatg tgccactgaa 300
cttgacagac acaaaattct actgcatttg ggctttataa tggcaagcct gctcttttta 360
gtggtgaact tgacttgccg aatgctagtt catggagatg t 401

<210> 374
<211> 401
<212> DNA
<213> Homo sapien

<400> 374
ggaatgatac cattcagatt gatttgaga ctggcaagat tactgatttc atcaagttcg 60

```

acactggttaa cctgtgtatg gtgactggag gtgctaacct aggaagaatt ggtgtgatca 120
ccaacagaga gaggcaccct ggatcttttg acgtgggttca cgtgaaagat gccaatggca 180
acagctttgc cactcgactt tccaacattt ttgttattgg caagggcaac aaaccatgga 240
tttctcttcc ccgaggaaag ggtatccgcc tcaccattgc tgaagagaga gacaaaagac 300
tggcggccaa acagagcagt gggtgaaatg ggtccctggg tgacatgtca gatctttgta 360
cgtaattaaa aatattgttg caggattaat agcaaaaaaa a 401

```

```

<210> 375
<211> 401
<212> DNA
<213> Homo sapien

```

```

<400> 375
gagcggagtc cgctggctga cccgagcgt ggtctccgcc gggaaccctg gggcatggag 60
aggtctgagt acctcgcccg cggcgcacgc tgcattcgcg agccaggccg aggacgtgag 120
ggtggagggc tcctttcccg tgacctgct tccgggagac ggtgtggggc ctgagctgat 180
gcacgccgtc aaggaggtgt tcaaggctgc cgctgtccca gtggagtcc aggagcacca 240
cctgagttag gtgcagaata tggcatctga ggagaagctg gagcaggtgc tgagttccat 300
gaaggagAAC aaagtggcca tcattggaaa gattcatacc ccgatggagt ataaggggga 360
gctagcctcc tatgatatgc ggctgaggcg taagttggac t 401

```

```

<210> 376
<211> 284
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(284)
<223> n = A,T,C or G

```

```

<400> 376
ggaacaaggt cgtgaaaaaa aaggtcttgg tgagggtgcc ccatttcatt tgcctcatt 60
ctctgcgcct ttgcagagc ttccancagc tggtagttg gccagagca tccggaggtt 120
cacaacctct gtggtccgta ggagccacta tgaggagggc cctgggaaga atttgccatt 180
ttcagtgga aacaagtggc cgttactagc taagatgtgt ttgtactttg gatctgcatt 240
tgctacaccc ttccttgtn taagacacca actgcttaaa acat 284

```

```

<210> 377
<211> 401
<212> DNA
<213> Homo sapien

```

```

<400> 377
atztatgtta ttgcactctc ggtgtgattt atcgtatgta tctgataggt tttatgaatt 60
gttttgagtt gtaaactcct atacccttta ttaaaatgga cctaattaag tgatttatgc 120
tttgtgcaat ttcttaaact agatctctct aggattgaag ggatccatag gtatctttca 180
cttagtgtga agcctagtag tatactttta tattcctgaa gagagaccag cattaacata 240
aagagagaag tcttaggaaa aaatatacct aagaattatt tttaaaattc atactgtgaa 300
ggagaatctg cctgcctatt tcctctccaa atttcagaaa ataacacaga gtgctatttg 360
cctgaacttt aatgagcttg actttgttat gattcaggga g 401

```

```

<210> 378
<211> 401
<212> DNA
<213> Homo sapien

```

```

<400> 378

```

```

ccagaacaca ggtgtcgtga aaactacccc taaaagcoaa aatgggaaag gaaaagactc 60
atatcaacat tgtcgtcatt ggacacgtag attcgggcaa gtccaccact actggccatc 120
tgatctataa atgcggtggc atcgacaaaa gaaccattga aaaatttgag aaggaggctg 180
ctgagatggg aaagggctcc ttcaagtatg cctgggtcct ggataaactg aaagctgagc 240
gtgaacgtgg tatcaccatt gatatctcct tgtggaaatt tgagaccagc aagtactatg 300
tgactatcat tgatgcccca ggacacagag actttatcaa aaacatgatt acagggacat 360
ctcaggctga ctgtgctgtc ctgattgttg ctgctggtgt t 401

```

<210> 379

<211> 401

<212> DNA

<213> Homo sapien

<400> 379

```

tcagatatca ggtggcttct tcaaatgatt ttttaagtatc tcgatgatga tgaagaacaa 60
agacatcaat caggattcag gaagacagct tttgcggaaa atgcttaaag ggaagcatca 120
aggattggtg ttgatatttg aaagttaaag agtgggtatac ttttattcag tcaacacatg 180
acaaatgtaa aaggcactca tttgtttgtc ctggaagaag cctggcagca ttccattcag 240
acatctgccc ttctatcgtc ccacttttta cttattgcag tcctttcagt ctgaatatat 300
cctcctgacg catcttctgc cgtccgaaat gactccctgc tcccagatcc tgtagccctt 360
attattgaca cctttcattt agaaatttag cacatgtcac a 401

```

<210> 380

<211> 401

<212> DNA

<213> Homo sapien

<400> 380

```

cctgactctc tgaggctcat tttgcagttg ttgaaattgt cccgcagtt ttcaatcatg 60
tctgaaccaa tcagagtcct tgtgactgga gcagctggtc aaattgcata ttcactgctg 120
tacagtattg gaaatggatc tgtctttggt aaagatcagc ctataattct tgtgctgttg 180
gatatcacc ccatgatggg tgtcctggac ggtgtcctaa tggaaactgca agactgtgcc 240
cttcccctcc tgaaagatgt catcgcaaca gataaagaag acgttgctt caaagacctg 300
gatgtggcca ttcttgtggg ctccatgcc aagaagggaag gcatggagag aaaagattta 360
ctgaaagcaa atgtgaaaat cttcaaatcc cagggtgcag c 401

```

<210> 381

<211> 401

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> {1}...(401)

<223> n = A,T,C or G

<400> 381

```

ggggcttcgc tggcagtcgt aacggcaagc ttgagcaacg cggtaaaaat attgcttcgg 60
tgggtgacgc ggtacagctg tccaagggcn ttngtaacgg gaatgccgaa gcgtgggaaa 120
aaggagcgcg tggcggaaga cggggatgag ctcaggacag agccagaggc caagaagagt 180
aagacggcgg caaagaaaaa tgacaaagag gcagcaggag agggcccagc cctgtatgag 240
gacccccag atcagaaaac ctccccagt ggcaaacctg ccacactcaa gatctgctct 300
tggaatgtgg atgggcttcg agcctggatt aagaagaaag gattagattg ggtaaaggaa 360
gaagccccag atatactgtg ccttcaagag accaaatgtt c 401

```

<210> 382

<211> 491

<212> DNA

<213> Homo sapien

<400> 382

gagcagcccc	cggcgggctga	aagccggggc	agaagtgctg	gtctcggctg	ggattccggg	60
cttgggtcca	cagaggcggc	gactgcggtg	ggagggaaga	ggttttggac	gcgctggcct	120
cccgcgctg	tgcattgcag	cattatttca	gttcaaaatg	aactatatgc	ctggcaccgc	180
cagcctcatc	gaggacattg	acaaaaagca	cttggttctg	cttcgagatg	gaaggacact	240
tataggcttt	ttaagaagca	ttgatcaatt	tgcaaaacta	gtgctacatc	agactgtgga	300
gcgtattcat	gtgggcaaaa	aatacgggtg	tattcctcga	gggatttttg	tggtcagagg	360
agaaaatgtg	gtcctactag	gagaaataga	cttggaagag	gagagtgaca	caccctcca	420
gcaagtatcc	attgaagaaa	ttctagaaga	acaaagggtg	gaacagcaga	ccaagctgga	480
agcagagaag	t					491

<210> 383

<211> 491

<212> DNA

<213> Homo sapien

<400> 383

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<210> 384

<211> 491

<212> DNA

<213> Homo sapien

<400> 384

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aaactgcagg	cacaagtgcg	cattggtggg	aaaggaactg	ctcgcagaaa	gaagaagggtg	420
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<210> 385

<211> 483

<212> DNA

<213> Homo sapien

<400> 385

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cct 483

<210> 386
<211> 491
<212> DNA
<213> Homo sapien

<400> 386
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ttaagaattt agccagcagg gaaaatttcc aggtttgaga atgttctaata gtaaatattt 480
aatcataata c 491

<210> 387
<211> 491
<212> DNA
<213> Homo sapien

<400> 387
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<210> 388
<211> 491
<212> DNA
<213> Homo sapien

<400> 388
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<210> 389
<211> 511
<212> DNA
<213> Homo sapien

<220>
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<222> (1)...(511)

<223> n = A,T,C or G

<400> 389

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ttcanactaa	cctcaaagta	cggcatgtgc	agtgtttaag	tgcaanaagt	attttcattc	240
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atttcctggt	tgatctcaga	aatatatgga	tgatctttgc	cgtgagctac	ttccatgatt	420
gcaatggcct	tcttcagggc	tttctccoct	gcggctttgt	gttcaggcc	catgtagagt	480
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<210> 390

<211> 1984

<212> DNA

<213> Homo sapien

<400> 390

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<210> 391

<211> 429

<212> PRT

<213> Homo sapien

<400> 391

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      35      40      45
Leu Ser Val Leu His Ala Leu Leu Tyr Ala Ala Leu Phe Ala Phe Ala
      50      55      60
Tyr Leu Gln Leu Trp Arg Leu Leu Leu Tyr Arg Glu Arg Arg Leu Ser
      65      70      75      80
Tyr Gln Ser Leu Cys Leu Phe Leu Cys Leu Leu Trp Ala Ala Leu Arg
      85      90      95
Thr Thr Leu Phe Ser Ala Ala Phe Ser Leu Ser Gly Ser Leu Pro Leu
      100     105     110
Leu Arg Pro Pro Ala His Leu His Phe Phe Pro His Trp Leu Leu Tyr
      115     120     125
Cys Phe Pro Ser Cys Leu Gln Phe Ser Thr Leu Cys Leu Leu Asn Leu
      130     135     140
Tyr Leu Ala Glu Val Ile Cys Lys Val Arg Cys Ala Thr Glu Leu Asp
      145     150     155     160
Arg His Lys Ile Leu His Leu Gly Phe Ile Met Ala Ser Leu Leu
      165     170     175
Phe Leu Val Val Asn Leu Thr Cys Ala Met Leu Val His Gly Asp Val
      180     185     190
Pro Glu Asn Gln Leu Lys Trp Thr Val Phe Val Arg Ala Leu Ile Asn
      195     200     205
Asp Ser Leu Phe Ile Leu Cys Ala Ile Ser Leu Val Cys Tyr Ile Cys
      210     215     220
Lys Ile Thr Lys Met Ser Ser Ala Asn Val Tyr Leu Glu Ser Lys Gly
      225     230     235     240
Met Ser Leu Cys Gln Thr Val Ile Val Gly Ser Val Val Ile Leu Leu
      245     250     255
Tyr Ser Ser Arg Ala Cys Tyr Asn Leu Val Val Val Thr Ile Ser Gln
      260     265     270
Asp Thr Leu Glu Ser Pro Phe Asn Tyr Gly Trp Asp Asn Leu Ser Asp
      275     280     285
Lys Ala His Val Glu Asp Ile Ser Gly Glu Glu Tyr Ile Val Phe Gly
      290     295     300
Met Val Leu Phe Leu Trp Glu His Val Pro Ala Trp Ser Val Val Leu
      305     310     315     320
Phe Phe Arg Ala Gln Arg Leu Asn Gln Asn Leu Ala Pro Ala Gly Met
      325     330     335
Ile Asn Ser His Ser Tyr Ser Ser Arg Ala Tyr Phe Phe Asp Asn Pro
      340     345     350
Arg Arg Tyr Asp Ser Asp Asp Asp Leu Pro Arg Leu Gly Ser Ser Arg
      355     360     365
Glu Gly Ser Leu Pro Asn Ser Gln Ser Leu Gly Trp Tyr Gly Thr Met
      370     375     380
Thr Gly Cys Gly Ser Ser Ser Tyr Thr Val Thr Pro His Leu Asn Gly
      385     390     395     400
Pro Met Thr Asp Thr Ala Pro Leu Leu Phe Thr Cys Ser Asn Leu Asp
      405     410     415
Leu Asn Asn His His Ser Leu Tyr Val Thr Pro Gln Asn
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<210> 392
 <211> 1584
 <212> DNA
 <213> Homo sapiens

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<210> 393
 <211> 191
 <212> PRT
 <213> Homo sapiens

<400> 393
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 Ser Glu Met Ile Glu Thr Gln Glu Asp Ile Tyr Val Gly Ser Ile Glu
 35 40 45
 Thr Asp Arg Gly Val Arg Glu Gln Val Arg Phe Tyr Asp Thr Arg Gly
 50 55 60
 Leu Arg Asp Gly Ala Glu Leu Pro Arg His Cys Phe Ser Cys Thr Asp
 65 70 75 80
 Gly Tyr Val Leu Val Tyr Ser Thr Asp Ser Arg Glu Ser Phe Gln Arg
 85 90 95
 Val Glu Leu Leu Lys Lys Glu Ile Asp Lys Ser Lys Asp Lys Lys Glu
 100 105 110
 Val Thr Ile Val Val Leu Gly Asn Lys Cys Asp Leu Gln Glu Gln Arg
 115 120 125
 Arg Val Asp Pro Asp Val Ala Gln His Trp Ala Lys Ser Glu Lys Val
 130 135 140

Lys Leu Trp Glu Val Ser Val Ala Asp Arg Arg Ser Leu Leu Glu Pro
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 Phe Val Tyr Leu Ala Ser Lys Met Thr Gln Pro Gln Ser Lys Ser Ala
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 Phe Pro Leu Ser Arg Lys Asn Lys Gly Ser Gly Ser Leu Asp Gly
 180 185 190

<210> 394
 <211> 1937
 <212> DNA
 <213> Homo sapiens

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<210> 395
 <211> 1675
 <212> DNA
 <213> Homo sapiens

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<210> 396

<211> 559

<212> PRT

<213> Homo sapiens

<400> 396

```

Gly Ser Pro Ser Ser Gly Tyr Pro Ala Leu His Arg Val Ala Met Met
                    5              10              15
Gly His Arg Pro Val Leu Val Leu Ser Gln Asn Thr Lys Arg Glu Ser
                20              25              30
Gly Arg Lys Val Gln Ser Gly Asn Ile Asn Ala Ala Lys Thr Ile Ala
                35              40              45
Asp Ile Ile Arg Thr Cys Leu Gly Pro Lys Ser Met Met Lys Met Leu
                50              55              60
Leu Asp Pro Met Gly Gly Ile Val Met Thr Asn Asp Gly Asn Ala Ile
                65              70              75              80
Leu Arg Glu Ile Gln Val Gln His Pro Ala Ala Lys Ser Met Ile Glu
                85              90              95
Ile Ser Arg Thr Gln Asp Glu Glu Val Gly Asp Gly Thr Thr Ser Val
                100             105             110
Ile Ile Leu Ala Gly Glu Met Leu Ser Val Ala Glu His Phe Leu Glu
                115             120             125
Gln Gln Met His Pro Thr Val Val Ile Ser Ala Tyr Arg Lys Ala Leu
                130             135             140
Asp Asp Met Ile Ser Thr Leu Lys Lys Ile Ser Ile Pro Val Asp Ile
                145             150             155             160
Ser Asp Ser Asp Met Leu Asn Ile Ile Asn Ser Ser Ile Thr Thr
                165             170             175
Lys Ala Ile Ser Arg Trp Ser Ser Leu Ala Cys Asn Ile Ala Leu Asp
                180             185             190
Ala Val Lys Met Val Gln Phe Glu Glu Asn Gly Arg Lys Glu Ile Asp
                195             200             205
Ile Lys Lys Tyr Ala Arg Val Glu Lys Ile Pro Gly Gly Ile Ile Glu
                210             215             220

```

Asp Ser Cys Val Leu Arg Gly Val Met Ile Asn Lys Asp Val Thr His
 225 230 235 240
 Pro Arg Met Arg Arg Tyr Ile Lys Asn Pro Arg Ile Val Leu Leu Asp
 245 250 255
 Ser Ser Leu Glu Tyr Lys Lys Gly Glu Ser Gln Thr Asp Ile Glu Ile
 260 265 270
 Thr Arg Glu Glu Asp Phe Thr Arg Ile Leu Gln Met Glu Glu Glu Tyr
 275 280 285
 Ile Gln Gln Leu Cys Glu Asp Ile Ile Gln Leu Lys Pro Asp Val Val
 290 295 300
 Ile Thr Glu Lys Gly Ile Ser Asp Leu Ala Gln His Tyr Leu Met Arg
 305 310 315 320
 Ala Asn Ile Thr Ala Ile Arg Arg Val Arg Lys Thr Asp Asn Asn Arg
 325 330 335
 Ile Ala Arg Ala Cys Gly Ala Arg Ile Val Ser Arg Pro Glu Glu Leu
 340 345 350
 Arg Glu Asp Asp Val Gly Thr Gly Ala Gly Leu Leu Glu Ile Lys Lys
 355 360 365
 Ile Gly Asp Glu Tyr Phe Thr Phe Ile Thr Asp Cys Lys Asp Pro Lys
 370 375 380
 Ala Cys Thr Ile Leu Leu Arg Gly Ala Ser Lys Glu Ile Leu Ser Glu
 385 390 395 400
 Val Glu Arg Asn Leu Gln Asp Ala Met Gln Val Cys Arg Asn Val Leu
 405 410 415
 Leu Asp Pro Gln Leu Val Pro Gly Gly Gly Ala Ser Glu Met Ala Val
 420 425 430
 Ala His Ala Leu Thr Glu Lys Ser Lys Ala Met Thr Gly Val Glu Gln
 435 440 445
 Trp Pro Tyr Arg Ala Val Ala Gln Ala Leu Glu Val Ile Pro Arg Thr
 450 455 460
 Leu Ile Gln Asn Cys Gly Ala Ser Thr Ile Arg Leu Leu Thr Ser Leu
 465 470 475 480
 Arg Ala Lys His Thr Gln Glu Asn Cys Glu Thr Trp Gly Val Asn Gly
 485 490 495
 Glu Thr Gly Thr Leu Val Asp Met Lys Glu Leu Gly Ile Trp Glu Pro
 500 505 510
 Leu Ala Val Lys Leu Gln Thr Tyr Lys Thr Ala Val Glu Thr Ala Val
 515 520 525
 Leu Leu Leu Arg Ile Asp Asp Ile Val Ser Gly His Lys Lys Lys Gly
 530 535 540
 Asp Asp Gln Ser Arg Gln Gly Gly Ala Pro Asp Ala Gly Gln Glu
 545 550 555

<210> 397

<211> 307

<212> PRT

<213> Homo.sapiens

<400> 397

Arg Glu Ser Arg Ser Arg Ala Met Glu Glu Glu Ala Ser Ser Pro Gly
 5 10 15
 Leu Gly Cys Ser Lys Pro His Leu Glu Lys Leu Thr Leu Gly Ile Thr
 20 25 30
 Arg Ile Leu Glu Ser Ser Pro Gly Val Thr Glu Val Thr Ile Ile Glu
 35 40 45
 Lys Pro Pro Ala Glu Arg His Met Ile Ser Ser Trp Glu Gln Lys Asn
 50 55 60

Asn Cys Val Met Pro Glu Asp Val Lys Asn Phe Tyr Leu Met Thr Asn
 65 70 75 80
 Gly Phe His Met Thr Trp Ser Val Lys Leu Asp Glu His Ile Ile Pro
 85 90 95
 Leu Gly Ser Met Ala Ile Asn Ser Ile Ser Lys Leu Thr Gln Leu Thr
 100 105 110
 Gln Ser Ser Met Tyr Ser Leu Pro Asn Ala Pro Thr Leu Ala Asp Leu
 115 120 125
 Glu Asp Asp Thr His Glu Ala Ser Asp Asp Gln Pro Glu Lys Pro His
 130 135 140
 Phe Asp Ser Arg Ser Val Ile Phe Glu Leu Asp Ser Cys Asn Gly Ser
 145 150 155 160
 Gly Lys Val Cys Leu Val Tyr Lys Ser Gly Lys Pro Ala Leu Ala Glu
 165 170 175
 Asp Thr Glu Ile Trp Phe Leu Asp Arg Ala Leu Tyr Trp His Phe Leu
 180 185 190
 Thr Asp Thr Phe Thr Ala Tyr Tyr Arg Leu Leu Ile Thr His Leu Gly
 195 200 205
 Leu Pro Gln Trp Gln Tyr Ala Phe Thr Ser Tyr Gly Ile Ser Pro Gln
 210 215 220
 Ala Lys Gln Trp Phe Ser Met Tyr Lys Pro Ile Thr Tyr Asn Thr Asn
 225 230 235 240
 Leu Leu Thr Glu Glu Thr Asp Ser Phe Val Asn Lys Leu Asp Pro Ser
 245 250 255
 Lys Val Phe Lys Ser Lys Asn Lys Ile Val Ile Pro Lys Lys Lys Gly
 260 265 270
 Pro Val Gln Pro Ala Gly Gly Gln Lys Gly Pro Ser Gly Pro Ser Gly
 275 280 285
 Pro Ser Thr Ser Ser Thr Ser Lys Ser Ser Ser Gly Ser Gly Asn Pro
 290 295 300
 Thr Arg Lys
 305

<210> 398

<211> 416

<212> DNA

<213> Homo sapiens

<400> 398

agaattcggc acgaggattg cctatctcca gtgcaacaac catcaagtgt gctgaaagtc 60
 ttcagccggt tgctgcagca gtggaagaaa gggctacagg tccagtcttg ataagcaccg 120
 ccgactttga ggggcctatg ccagtgccgc cccagaagc tgaaagtcct cttgcctcaa 180
 ccagcaagga ggagaaggat gaatgtgctc tcatttccac tagcatagca gaagaatgtg 240
 aggtttctgt ttccggtgta gttgttgaaa gtgaaaatga gcgagctggc acagtcattg 300
 aagaaaaaga cgggagtggc atcatctcta cgagctcggg ggaagactgt gagggcccag 360
 tgtccagtgc tgtccctcaa gaggaaggcg acccctcagt cacaccagcg gaagag 416

<210> 399

<211> 259

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(259)

<223> n = A,T,C or G

<400> 399
caaagaattc ggcacgaggg ggcgacctgc attcggacgt caccgaggcc atgctgtacg 60
aaaagttcag ccccgcgggg cctgtgctgt ncatccgggt ctgccngat atgatcacc 120
gccgctccct gggtatgcc tacgncaact tccancaacc ggccgacgt gatcgggctt 180
tggacacat gaactttgat gtgattnagg gaaanccaat cttatcntg tnnnaatcat 240
aggnatcctt ctttgacaa 259

<210> 400
<211> 410
<212> DNA
<213> Homo sapiens

<400> 400
ggcacgaggg gagagcggac cccagagagc cctgagcagc cccaccgccc ccgccggcct 60
agttaccatc acaccccggg aggagccgca gctgcccgag ccggccccag tcaccatcac 120
cgcaaccatg agcagcgagg ccgagaccca gcagccgccc gccgcccccc cccgccgccc 180
ccgccctcag cgcgcgcgac accaagcccc gcaactacggg cagcggcgca gggagcggtg 240
gcccgggcgg cctcacatcg gcggcgccctg ccggcgggga caagaaggtc atcgcaacga 300
aggttttggg aacagtaaaa tggttcaatg taaggaaagg atatggtttc atcaacagga 360
atgacaccaa ggaagatgta tttgtacacc agactgccat aaagaagaat 410

<210> 401
<211> 433
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(433)
<223> n = A,T,C or G

<400> 401
ggnacgagga atcatggcgg ctgcgctgtt cgtgctgctg ggattcgcgc tgctgggcac 60
ccacggagcc tccggggctg ccggcacagt cttcactacc gtagaagacc ttggctccaa 120
gatactctc acctgctcct tgaatgacag cgccacagag gtcacagggc accgctggct 180
gaaggggggc gtggtgctga aggaggacgc gctgcccgcc cagaaaacgg agttcaagg 240
ggactccgac gaccagtggg gagagtactc ctgcgtcttc ctccccgagc ccatgggcac 300
ggccaacatc cagctccacg ggccctcccag agtgaaggcc gtgaagtcgt cagaacacat 360
caacgagggg gagacggcca tgctggtctg caagtcagag tccgtgccac ctgtcactga 420
ctgggcctgg tac 433

<210> 402
<211> 434
<212> DNA
<213> Homo sapiens

<400> 402
ggcacgaggc tcggactgag caggactttc cttatcccag ttgattgtgc agaatacact 60
gcctgtcgct tgtcttctat tcaccatggc ttcttctgat atccagggtga aagaactgga 120
gaagcgtgcc tcaggccagg cttttgagct gattctcagc cctcgggtcaa aaggatctgt 180
tccagaattc cccctttccc ctccaaagaa gaaggatctt tccctggagg aaattcagaa 240
gaaattagaa gctgcagaag aaagacgcaa gtcccatgaa gctgagggtc tgaagcagct 300
ggctgagaaa cgagagcacg agaaagaagt gcttcagaag gcaatagaag agaacaacaa 360
cttcagtaaa atggcagaag agaaactgac ccacaaaatg gaagctaata aagagaaccg 420
agaggcacia atgg 434

<210> 403
<211> 435

<212> DNA

<213> Homo sapiens

<400> 403

```
ggcacgagga actgctgttg ccattcaaac cattgaggag catcctgcat cttttgactg 60
gagctctttt aagccaatgg gatttgaagt atcatttctg aagtttcttg aggagtctgc 120
agtgaagcag aagaaaaata ctgacaaaga ccatccgaat actggaaaca aaaaaggatc 180
ccattcaaat tcaagaaaaa atattgataa gactgctgtg actagtggaa atcatgtatg 240
tccttgtaaa gaaagcgaaa cgtttgtaaa gtttgccaat ccatcacagc ttcagtgcag 300
tgataatgta aaaattgttt tagacaagaa tcttaaagat tgcactgagc ttgtcttaaa 360
gcaacttcag gaaatgaaac ctaccgtcag tctgaaaaaa cttgaagtac attcaaata 420
tccagatatg tctgt 435
```

<210> 404

<211> 416

<212> DNA

<213> Homo sapiens

<400> 404

```
aaagaattcg gcacgaggcg ccgctccgcc acgaccaccg ccgcctcctg ccctgcagcc 60
accgccaccg cctgtgtcgc cgccgcctcg ggaccggctg tatgattagg ccacaatctt 120
caatgagtaa acatattcct caattctgtg gtgttcttgg tcacacattt atggagtctt 180
tgaagggcag tggagattac tgccaggcac agcacgacct ctatgcagac aagtgaactg 240
tagaaactga ttactgtctc accaagaagc ccccataaga gtggttatcc tggacacaga 300
agtgttgaat tgaaatccac agagcatttt acaagagttc tgacctggat ggggtaaacc 360
tcagtgcact tcttttctgt tggcctcagt attactggat tgaagaattg ctgctt 416
```

<210> 405

<211> 435

<212> DNA

<213> Homo sapiens

<400> 405

```
ggcacgaggg ctgccggagg gtcgttttaa agggcccgcg cgttgccgcc ccctcggccc 60
gccatgtctg tatccgtgcc gctgtgtctc ggccctcctc gcctggccgt cgccgagcct 120
gccgtctact tcaaggagca gtttctggac ggagacgggt ggacttcccg ctggatcgaa 180
tccaaacaca agtcagattt tggcaaattc gttctcagtt ccggcaagtt ctacggtgac 240
gaggagaaag ataaagggtt gcagacaagc caggatgcac gcttttatgc tctgtcggcc 300
agtttcgagc ctttcagcaa caaaggccag acgctggtgg tgcagttcac ggtgaaacat 360
gagcagaaca tcgactgtgg gggcggtat gtgaagctgt ttcctaatag tttggaccag 420
acagacatgc acgga 435
```

<210> 406

<211> 424

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(424)

<223> n = A,T,C or G

<400> 406

```
gcccaaacc actccacctt actaccagac aaccttagcc aaaccattta cccaaataaa 60
gtataggcga tagaaattga aacctggcgc aatagatata gtaccgcaag ggaaagatga 120
aaaattataa ccaagcataa tatagcaagg actaaccctt ataccttctg cataatgaat 180
taactagaaa taactttgca aggagagcca aagctaagac ccccgaaacc agacgagcta 240
cctaagaaca gctaaaagag cacaccgctc tatgtagcaa aatagtggga agatttatag 300
```

```

gtagaggcga caaacctacc gagcctgggt atagctgggt gtccaagata gaatcttagt 360
tcaactttta atttgcccac agaaccctct aaatcccctt gnaaatttta ctgntagctc 420
aaag                                              424

```

```

<210> 407
<211> 423
<212> DNA
<213> Homo sapiens

```

```

<400> 407
gctcctaccg ggcacgtgg tgccgcgct gctgcctccc gctgcgcctg aaccagtg 60
ctgcagccat ggctcccgcc cagctcgctt tatttagtgt ctctgacaaa accggccttg 120
tggaatttgc aagaaacctg accgctcttg gtttgaatct ggctgcttcc ggagggactg 180
caaaagctct cagggatgct ggtctggcag tcagagatgt ctctgagttg acgggatttc 240
ctgaaatggt ggggggacgt gtgaaaactt tgcctcctgc agtccatgct ggaatcctag 300
ctcgtaatat tccagaagat aatgctgaca tggccagact tgatttcaat cttataagag 360
ttgttgctg caatctctat ccctttgtaa agacagtggc ttctccaggt gtaagtgtg 420
agg                                              423

```

```

<210> 408
<211> 424
<212> DNA
<213> Homo sapiens

```

```

<400> 408
gaaaaaaaat agcttactga attctataag atgtgtggga atctcaccta tcaaaaatag 60
gtaaaaagag cctccaaacc tgctttgatt ttattcacct attcttttag gccaggaa 120
aatttacctc tcaactatct gttccctctt gctatcttgt ggagtctcta aagacaaagg 180
tataaagagc ttttggtagg tgaattaata atcaactaga tggcatttcc aaatgggatt 240
gcacatactg tggggcaagt cccaagtga cttcaaagt agacgtttat ttgagtaatc 300
cttcagagatt aacaataatc ataatagcag ttaccacttc ctgagtactt tctatatgcc 360
atgtattgag cttgctcact tctttatgtg gattcttatt taatcttaat accaagatga 420
ggtg                                              424

```

```

<210> 409
<211> 398
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(398)
<223> n = A,T,C or G

```

```

<400> 409
gctcgactct tagcttgctg gggacggtaa cggggacccg gtgtctgctc ctgtgcctt 60
cgctccttaa tccctagcca ctatgcgtga gtgcctctcc atccacgttg gccaggctg 120
tgtccagatt ggcaatgcct gctgggagct ctactgcctg gaacacggca tccagcccga 180
tggccagatg ccaagtgaac agaccattgg gggaggagat gactccttca acaccttct 240
cagtgaagcg ggcgctggca agcacgtgcc cgggctgng tttgtagact tggaaacccac 300
agtnattgat gaagntcgna ctggcaccta cccgcaggtc ttncaccctg ancanntcat 360
nacaggcaag gaagatgctg ncaaataact atgcccga 398

```

```

<210> 410
<211> 423
<212> DNA
<213> Homo sapiens

```

<400> 410

```
gccccacccc acctgcccgc tgcggctctc cgcgggagat ctcaccgttc tggagacagg 60
gctcgcctcg tctcacgctg cccggccagc ccgcttctct gcccgagcc atgaatctca 120
gtagcgccag tagcacggag gaaaaggcag tgacgaccgt gctctggggc tgcgagctca 180
gtcaggagag gcggaacttg accttcagac ccagctgga ggggaagcag agctgcaggc 240
tggtgttca tacgatttgc ttgggggaga aagccaaaga ggagatgcat cgcgtggaga 300
tcctgcccc agcaaaccag gaggacaaga agatgcagcc ggtcaccatt gcctactcc 360
aggcctcagt cctccccatg gtctccatgg taggagtgca gctttctccc ccagttactt 420
tcc 423
```

<210> 411

<211> 424

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(424)

<223> n = A,T,C or G

<400> 411

```
gcggaggcga ctagcggcgg cgggagcggc gccgagaggc cgtgcgggac gcgggcgcca 60
ggaccggccg aacgcagagg ttgattcttc accacactga aaccattagg aaaaatcctt 120
gtggttaaca gcagaggctt cagagtgtaa cctgtactcg ggcctagaaa ttatttaaaa 180
tggcgactga tacgtctcaa ggtgaactcg tccatcctaa ggcactcca cttatagtag 240
gagctcagct gatccacgcg gacaagttag gtgagaaggt agaagatagc accatgccga 300
ttcgtogaac tgtgaattct acccgggaaa ctctcccaa aagcaagctt gctgaagggg 360
aggaagaaan gccagaacca gacataagtt cagaggaatc tgtctccact gtagaagaac 420
aaga 424
```

<210> 412

<211> 430

<212> DNA

<213> Homo sapiens

<400> 412

```
ggcacgaggg gaagccggcg ccagttcgcg gggctccggg ccgccactca gagctatgag 60
ctacggccgc cccctcccg atgtggaggg tatgacctcc ctcaagggtg acaacctgac 120
ctaccgcacc tcgcccgaca cgctgaggcg cgtcttcgag aagtacgggc gcgtcggcga 180
cgtgtacatc ccgcgggatc gctacaccaa ggagtccgc ggcttcgcct tcgttcgctt 240
tcacgacaag cgcgacgctg aggacgctat ggatgccatg gacggggccg tgctggacgg 300
ccgcgagctg cgggtgcaaa tggcgcgcta cggcgcccc ccggactcac accacagccg 360
ccggggaccg ccaccccgca ggtacggggg cggtggtctac ggacgccgga gccgcagccc 420
taggcggcgt 430
```

<210> 413

<211> 429

<212> DNA

<213> Homo sapiens

<400> 413

```
ggcacgaggt cggcccggcc atcttgtggg aagagctgaa gcaggcgctc ttggctcggc 60
gcggcccgt gcaatccgtg gaggaacgcg ccgccgagcc accatcatgc ctgggcactt 120
acaggaaagg ttcggctcg tggtcaccaa ccgattcgac cagttatttg acgacgaatc 180
ggaccccttc gaggtgctga aggcagcaga gaacaagaaa aaagaagccg gcgggggcgg 240
cgttgggggc cctggggcca agagcgagc tcaggcccg gcccagacca actccaacgc 300
ggcaggcaaa cagctgcga aggagtccta gaaagaccgc aagaaccgc tgccccccag 360
cgttggcgtg gttgacaaga aagaggagac gcagccgccc gtggcgctta agaaagaagg 420
```

aataagacg

429

<210> 414

<211> 429

<212> DNA

<213> Homo sapiens

<400> 414

```
ggcacgagga cgggcccggc tgccggcccc cgctctgccc tgcataataa aatggctaata 60
caggtgaatg gtaatgCGGT acagttaaaa gaagaggaag aaccaatgga tacttccagt 120
gtaactcaca cagaacacta caagacactg atagaggcag gcctcccaca gaaggtggca 180
gaaagacttg atgaaatatt tcagacagga ttggtagctt atgtcgatct tgatgaaaga 240
gcaattgatg ctctcaggga atttaatgaa gaaggagctc tgtctgtact acagcagttc 300
aaggaaagtg acttatcaca tgttcagaac aaaagtgcac ttttatgtgg agttatgaag 360
acctacaggc agagagagaa acaggggagc aaggtgcaag agtccacaaa gggacctgat 420
gaagcgaag                                     429
```

<210> 415

<211> 398

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(398)

<223> n = A,T,C or G

<400> 415

```
gcggtcgtaa gggctgagga tttttggtcc gcacgctcct gctcctgact caccgctggt 60
cgctctcgcc gaggaacaag tcggtcagga agcccgcgcg caacagccat ggcttttaag 120
gataccggaa aaacacccgt ggagccggag gtggcaattc accgaattcg aatcaccta 180
acaagccgca acgtaaaatc cttggaaaag gtgtgtgctg acttgataag aggcgcaaaa 240
gaaaagaatc tcaaagtact ttgagaatca ctacaagaaa aactccttgt ggtgaagggt 300
ctaagacgtg ggatcgtttc cagatgagaa ttcacaagcg actcattgac ttgcacagtc 360
cttctgagat tgtaagcan attacttcca tcantatt 398
```

<210> 416

<211> 269

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(269)

<223> n = A,T,C or G

<400> 416

```
gccgaggcag gaagctgtga gtgcgcgggt gcgggggcgc attgtggcta cggctttgcg 60
tccccggcgg gcagccccag gctgggtcccc gcctccgctc tccccaccgg cggggaaagc 120
agctggtgtg ggaggaaaag ctocatcccc cgccccctct ctcccgctgt tggctggcan 180
gatcttttgg cagtctctgt gntcncctcc ccgnccggat cctnctgacc ctganattcn 240
nggtntnacn nnccgtncac gccttgntt 269
```

<210> 417

<211> 408

<212> DNA

<213> Homo sapiens

<400> 417

```
ggccgggaga accgttcgcg gaggaaggc gaactagtgt tgggatggcc accaactggg 60
ggagcctctt gcaggataaa cagcagctag aggagctggc acggcaggcc gtggaccggg 120
ccctggctga gggagtattg ctgaggacct cacaggagcc cacttcctcg gaggtggtga 180
gctatgcccc attcacgctc ttccccctac tgggtccccag tgccctgctg gagcaagcct 240
atgctgtgca gatggacttc aacctgctag tggatgctgt cagccagaac gctgccttcc 300
tggagcaaac tctttccagc accatcaaac aggatgactt taccgctcgt ctctttgaca 360
tccacaagca agtcctaata gagggcattg cccagactgt gttcctgg 408
```

<210> 418

<211> 402

<212> DNA

<213> Homo sapiens

<400> 418

```
gagccgggca gccgcttccc gcccccgagc aggagccggg gcgagcggag cagagccgag 60
gtcggggcgc gagcggagcc ggctgagcgg gcgccgagct cccgccatgg cccggaacac 120
gctgtcctcg cgcttccgccc ggggtggacat cgacgaattt gacgagaaca aatttgtgga 180
cgagcaggag gaggcggcgg cggcggcggc ggagccaggc ccggacccga gcgaggtgga 240
cgggctcctg cggaaggggg acatgcttcg ggcattccat gcagccttgc ggaactctcc 300
cgtcaaacacc aagaatcaag ctgtgaagga gcgagcccag ggcgtggtgc tgaaagtgct 360
cacaaaacttc aagagcagtg agattgagca ggctgtgcag tc 402
```

<210> 419

<211> 406

<212> DNA

<213> Homo sapiens

<400> 419

```
gcccgggcta gccgcctggg ttgggctttg tagctgctcc gcaggcccag cccggggcgc 60
gctgcgagag tcctaggcgg tgcgcggcct cctgcctcct ccctcctcgg cggtcgcggc 120
ccgccggcct ccgcggtgcc tgccttcgct ctacggttga ggagctcaag cttgggaaaa 180
tgggtgtgcat tccttgatc gtcatccag ttctgctctg gatctacaaa aaattcctgg 240
agccatatat ataccctctg gtttccccct tcgttaagtc gtatatggcc taaaaaaga 300
attcaaagaa atccaatgat ccaaacaaaa gggcaaaagt aaaaactttt aaaggggtgc 360
aagaacattg aaatgggaat taccacaacca aaaaaggga cccaac 406
```

<210> 420

<211> 371

<212> DNA

<213> Homo sapiens

<400> 420

```
cagccatcgt ggtgtgttct tgactccgct gctcgccatg tcttctcaca agactttcag 60
gattaagcga ttctggcca agaaacaaaa gcaaaatcgt cccattcccc agtggattcg 120
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 Met Lys Thr Glu Trp Lys Ser Asn Val Tyr Leu Ala Arg Ser Arg Ile
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 Gln Gly Leu Gly Leu Tyr Ala Ala Arg Asp Ile Glu Lys His Thr Met
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<211> 174

<212> PRT

<213> Homo sapiens

<400> 426

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<210> 429

<211> 732

<212> DNA

<213> Homo sapiens

<400> 429

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<211> 2843

<212> DNA

<213> Homo sapiens

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<211> 640

<212> DNA

<213> Homo sapiens

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<210> 432

<211> 2068

<212> DNA

<213> Homo sapiens

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cataacatct gtgaaatcaa tggacagaat gtcattggat tgaaggactc tcaaattgca 840
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ttactgactt tcctagaata gtttctctac tggaaacctg atgcttttat aagccattgt 1260
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tttcaagaga ttgtgatgat tcttaaatct taactacct cacttaatat gcttgaactg 1560
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<210> 433

<211> 1723

<212> DNA

<213> Homo sapiens

<400> 433

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aatgggaccg ttctcagctc cagtgggaacc aggtttgctg tgaactttca gactggcttc 240
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cagaagggga tgccctttga cctctgcttc ctggtgcaga gctcagattt caagtgatg 420
gtgaacggga tcctcttctg gcagtacttc caccgcgtgc ccttccaccg tgtggacacc 480
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ccagctgtct gctcctggtg ggaggtggcc tcctcagccc ctctctctg acctttaacc 1560
tcactctcac ctgcaccgt gcaccaaccc ttacccctc ctggaaagca ggctgatgg 1620
cttcccactg gcctccacca cctgaccaga gtgttctctt cagaggactg gctcctttcc 1680
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<210> 434

<211> 1702

<212> PRT

<213> Homo sapiens

<400> 434

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Ala Ala Val Leu Gln Ser Cys Thr Ala Phe Ile Glu Arg Tyr Gly Ile
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Val Asp Gly Ile Tyr Arg Leu Ser Gly Val Ala Ser Asn Ile Gln Arg
      20              25              30
Leu Arg His Glu Phe Asp Ser Glu His Val Pro Asp Leu Thr Lys Glu
      35              40              45
Pro Tyr Val Gln Asp Ile His Ser Val Gly Ser Leu Cys Lys Leu Tyr
      50              55              60
Phe Arg Glu Leu Pro Asn Pro Leu Leu Thr Tyr Gln Leu Tyr Glu Lys
      65              70              75              80
Phe Ser Asp Ala Val Ser Ala Ala Thr Asp Glu Glu Arg Leu Ile Lys
      85              90              95
Ile His Asp Val Ile Gln Gln Leu Pro Pro Pro His Tyr Arg Thr Leu
      100             105             110
Glu Phe Leu Met Arg His Leu Ser Leu Leu Ala Asp Tyr Cys Ser Ile
      115             120             125
Thr Asn Met His Ala Lys Asn Leu Ala Ile Val Trp Ala Pro Asn Leu
      130             135             140
Leu Arg Ser Lys Gln Ile Glu Ser Ala Cys Phe Ser Gly Thr Ala Ala
      145             150             155             160
Phe Met Glu Val Arg Ile Gln Ser Val Val Val Glu Phe Ile Leu Asn
      165             170             175
His Val Asp Val Leu Phe Ser Gly Arg Ile Ser Met Ala Met Gln Glu

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				180						185				190		
Gly	Ala	Ala	Ser	Leu	Ser	Arg	Pro	Lys	Ser	Leu	Leu	Val	Ser	Ser	Pro	
		195					200					205				
Ser	Thr	Lys	Leu	Leu	Thr	Leu	Glu	Glu	Ala	Gln	Ala	Arg	Thr	Gln	Ala	
	210					215					220					
Gln	Val	Asn	Ser	Pro	Ile	Val	Thr	Glu	Asn	Lys	Tyr	Ile	Glu	Val	Gly	
225					230					235					240	
Glu	Gly	Pro	Ala	Ala	Leu	Gln	Gly	Lys	Phe	His	Thr	Ile	Ile	Glu	Phe	
				245					250						255	
Pro	Leu	Glu	Arg	Lys	Arg	Pro	Gln	Asn	Lys	Met	Lys	Lys	Ser	Pro	Val	
			260					265					270			
Gly	Ser	Trp	Arg	Ser	Phe	Phe	Asn	Leu	Gly	Lys	Ser	Ser	Ser	Val	Ser	
		275					280					285				
Lys	Arg	Lys	Leu	Gln	Arg	Asn	Glu	Ser	Glu	Pro	Ser	Glu	Met	Lys	Ala	
	290					295					300					
Met	Ala	Leu	Lys	Gly	Gly	Arg	Ala	Glu	Gly	Thr	Leu	Arg	Ser	Ala	Lys	
305					310					315					320	
Ser	Glu	Glu	Ser	Leu	Thr	Ser	Leu	His	Ala	Val	Asp	Gly	Asp	Ser	Lys	
				325					330					335		
Leu	Phe	Arg	Pro	Arg	Arg	Pro	Arg	Ser	Ser	Ser	Asp	Ala	Leu	Ser	Ala	
			340					345					350			
Ser	Phe	Asn	Gly	Glu	Met	Leu	Gly	Asn	Arg	Cys	Asn	Ser	Tyr	Asp	Asn	
		355					360					365				
Leu	Pro	His	Asp	Asn	Glu	Ser	Glu	Glu	Glu	Gly	Gly	Leu	Leu	His	Ile	
	370					375					380					
Pro	Ala	Leu	Met	Ser	Pro	His	Ser	Ala	Glu	Asp	Val	Asp	Leu	Ser	Pro	
385					390					395					400	
Pro	Asp	Ile	Gly	Val	Ala	Ser	Leu	Asp	Phe	Asp	Pro	Met	Ser	Phe	Gln	
				405					410					415		
Cys	Ser	Pro	Pro	Lys	Ala	Glu	Ser	Glu	Cys	Leu	Glu	Ser	Gly	Ala	Ser	
			420					425					430			
Phe	Leu	Asp	Ser	Pro	Gly	Tyr	Ser	Lys	Asp	Lys	Pro	Ser	Ala	Asn	Lys	
		435					440					445				
Lys	Asp	Ala	Glu	Thr	Gly	Ser	Ser	Gln	Cys	Gln	Thr	Pro	Gly	Ser	Thr	
	450					455					460					
Ala	Ser	Ser	Glu	Pro	Val	Ser	Pro	Leu	Gln	Glu	Lys	Leu	Ser	Pro	Phe	
465					470					475					480	
Phe	Thr	Leu	Asp	Leu	Ser	Pro	Thr	Glu	Asp	Lys	Ser	Ser	Lys	Pro	Ser	
				485					490					495		
Ser	Phe	Thr	Glu	Lys	Val	Val	Tyr	Ala	Phe	Ser	Pro	Lys	Ile	Gly	Arg	
			500					505					510			
Lys	Leu	Ser	Lys	Ser	Pro	Ser	Met	Ser	Ile	Ser	Glu	Pro	Ile	Ser	Val	
		515					520									

				645						650						655.
Met	Leu	Ala	Leu	Ala	Leu	Ala	Glu	Ser	Ala	Gln	Gln	Ala	Ser	Thr	Gln	
			660						665					670		
Ser	Leu	Lys	Arg	Pro	Gly	Thr	Ser	Gln	Ala	Gly	Tyr	Thr	Asn	Tyr	Gly	
		675						680					685			
Asp	Ile	Ala	Val	Ala	Thr	Thr	Glu	Asp	Asn	Leu	Ser	Ser	Ser	Tyr	Ser	
	690					695					700					
Ala	Val	Ala	Leu	Asp	Lys	Ala	Tyr	Phe	Gln	Thr	Asp	Arg	Pro	Ala	Glu	
705					710					715					720	
Gln	Phe	His	Leu	Gln	Asn	Asn	Ala	Pro	Gly	Asn	Cys	Asp	His	Pro	Leu	
				725					730					735		
Pro	Glu	Thr	Thr	Ala	Thr	Gly	Asp	Pro	Thr	His	Ser	Asn	Thr	Thr	Glu	
			740						745					750		
Ser	Gly	Glu	Gln	His	His	Gln	Val	Asp	Leu	Thr	Gly	Asn	Gln	Pro	His	
		755					760					765				
Gln	Ala	Tyr	Leu	Ser	Gly	Asp	Pro	Glu	Lys	Ala	Arg	Ile	Thr	Ser	Val	
	770					775					780					
Pro	Leu	Asp	Ser	Glu	Lys	Ser	Asp	Asp	His	Val	Ser	Phe	Pro	Glu	Asp	
785					790					795					800	
Gln	Ser	Gly	Lys	Asn	Ser	Met	Pro	Thr	Val	Ser	Phe	Leu	Asp	Gln	Asp	
				805					810					815		
Gln	Ser	Pro	Pro	Arg	Phe	Tyr	Ser	Gly	Asp	Gln	Pro	Pro	Ser	Tyr	Leu	
			820					825					830			
Gly	Ala	Ser	Val	Asp	Lys	Leu	His	His	Pro	Leu	Glu	Phe	Ala	Asp	Lys	
		835					840					845				
Ser	Pro	Thr	Pro	Pro	Asn	Leu	Pro	Ser	Asp	Lys	Ile	Tyr	Pro	Pro	Ser	
	850					855					860					
Gly	Ser	Pro	Glu	Glu	Asn	Thr	Ser	Thr	Ala	Thr	Met	Thr	Tyr	Met	Thr	
865					870					875					880	
Thr	Thr	Pro	Ala	Thr	Ala	Gln	Met	Ser	Thr	Lys	Glu	Ala	Ser	Trp	Asp	
				885					890					895		
Val	Ala	Glu	Gln	Pro	Thr	Thr	Ala	Asp	Phe	Ala	Ala	Ala	Thr	Leu	Gln	
			900					905					910			
Arg	Thr	His	Arg	Thr	Asn	Arg	Pro	Leu	Pro	Pro	Pro	Pro	Ser	Gln	Arg	
		915					920						925			
Ser	Ala	Glu	Gln	Pro	Pro	Val	Val	Gly	Gln	Val	Gln	Ala	Ala	Thr	Asn	
	930					935					940					
Ile	Gly	Leu	Asn	Asn	Ser	His	Lys	Val	Gln	Gly	Val	Val	Pro	Val	Pro	
945					950					955					960	
Glu	Arg	Pro	Pro	Glu	Pro	Arg	Ala	Met	Asp	Asp	Pro	Ala	Ser	Ala	Phe	
				965					970					975		
Ile	Ser	Asp	Ser	Gly	Ala	Ala	Ala	Ala	Gln	Cys	Pro	Met	Ala	Thr	Ala	
		980					985						990			
Val	Gln	Pro	Gly	Leu	Pro	Glu	Lys	Val	Arg	Asp	Gly	Ala	Arg	Val	Pro	
		995					1000					1005				
Leu	Leu	His	Leu	Arg	Ala	Glu	Ser	Val	Pro	Ala	His	Pro	Cys	Gly	Phe	
	1010					1015					1020					
Pro	Ala	Pro	Leu	Pro	Pro	Thr	Arg	Met	Met	Glu	Ser	Lys	Met	Ile	Ala	
1025					1030					1035					1040	
Ala	Ile	His	Ser	Ser	Ser	Ala	Asp	Ala	Thr	Ser	Ser	Ser	Asn	Tyr	His	
				1045					1050					1055		
Ser	Phe	Val	Thr	Ala	Ser	Ser	Thr	Ser	Val	Asp	Asp	Ala	Leu	Pro	Leu	
		1060					1065					1070				
Pro	Leu	Pro	Val	Pro	Gln	Pro	Lys	His	Ala	Ser	Gln	Lys	Thr	Val	Tyr	
		1075					1080					1085				
Ser	Ser	Phe	Ala	Arg	Pro	Asp	Val	Thr	Thr	Glu	Pro	Phe	Gly	Pro	Asp	
	1090					1095					1100					
Asn	Cys	Leu	His	Phe	Asn	Met	Thr	Pro	Asn	Cys	Gln	Tyr	Arg	Pro	Gln	

1105		1110		1115		1120
Ser Val Pro Pro His	His Asn Lys Leu Glu Gln His Gln Val Tyr Gly					
	1125		1130		1135	
Ala Arg Ser Glu Pro Pro Ala Ser Met Gly Leu Arg Tyr Asn Thr Tyr						
	1140		1145		1150	
Val Ala Pro Gly Arg Asn Ala Ser Gly His His Ser Lys Pro Cys Ser						
	1155		1160		1165	
Arg Val Glu Tyr Val Ser Ser Leu Ser Ser Ser Val Arg Asn Thr Cys						
	1170		1175		1180	
Tyr Pro Glu Asp Ile Pro Pro Tyr Pro Thr Ile Arg Arg Val Gln Ser						
1185		1190		1195		1200
Leu His Ala Pro Pro Ser Ser Met Ile Arg Ser Val Pro Ile Ser Arg						
	1205		1210		1215	
Thr Glu Val Pro Pro Asp Asp Glu Pro Ala Tyr Cys Pro Arg Pro Leu						
	1220		1225		1230	
Tyr Gln Tyr Lys Pro Tyr Gln Ser Ser Gln Ala Arg Ser Asp Tyr His						
	1235		1240		1245	
Val Thr Gln Leu Gln Pro Tyr Phe Glu Asn Gly Arg Val His Tyr Arg						
	1250		1255		1260	
Tyr Ser Pro Tyr Ser Ser Ser Ser Ser Tyr Tyr Ser Pro Asp Gly						
1265		1270		1275		1280
Ala Leu Cys Asp Val Asp Ala Tyr Gly Thr Val Gln Leu Arg Pro Leu						
	1285		1290		1295	
His Arg Leu Pro Asn Arg Asp Phe Ala Phe Tyr Asn Pro Arg Leu Gln						
	1300		1305		1310	
Gly Lys Ser Leu Tyr Ser Tyr Ala Gly Leu Ala Pro Arg Pro Arg Ala						
	1315		1320		1325	
Asn Val Thr Gly Tyr Phe Ser Pro Asn Asp His Asn Val Val Ser Met						
	1330		1335		1340	
Pro Pro Ala Ala Asp Val Lys His Thr Tyr Thr Ser Trp Asp Leu Glu						
1345		1350		1355		1360
Asp Met Glu Lys Tyr Arg Met Gln Ser Ile Arg Arg Glu Ser Arg Ala						
	1365		1370		1375	
Arg Gln Lys Val Lys Gly Pro Val Met Ser Gln Tyr Asp Asn Met Thr						
	1380		1385		1390	
Pro Ala Val Gln Asp Asp Leu Gly Gly Ile Tyr Val Ile His Leu Arg						
	1395		1400		1405	
Ser Lys Ser Asp Pro Gly Lys Thr Gly Leu Leu Ser Val Ala Glu Gly						
	1410		1415		1420	
Lys Glu Ser Arg His Ala Ala Lys Ala Ile Ser Pro Glu Gly Glu Asp						
1425		1430		1435		1440
Arg Phe Tyr Arg Arg His Pro Glu Ala Glu Met Asp Arg Ala His His						
	1445		1450		1455	
His Gly Gly His Gly Ser Thr Gln Pro Glu Lys Pro Ser Leu Pro Gln						
	1460		1465		1470	
Lys Gln Ser Ser Leu Arg Ser Arg Lys Leu Pro Asp Met Gly Cys Ser						
	1475		1480		1485	
Leu Pro Glu His Arg Ala His Gln Glu Ala Ser His Arg Gln Phe Cys						
	1490		1495		1500	
Glu Ser Lys Asn Gly Pro Pro Tyr Pro Gln Gly Ala Gly Gln Leu Asp						
1505		1510		1515		1520
Tyr Gly Ser Lys Gly Ile Pro Asp Thr Ser Glu Pro Val Ser Tyr His						
	1525		1530		1535	
Asn Ser Gly Val Lys Tyr Ala Ala Ser Gly Gln Glu Ser Leu Arg Leu						
	1540		1545		1550	
Asn His Lys Glu Val Arg Leu Ser Lys Glu Met Glu Arg Pro Trp Val						
	1555		1560		1565	
Arg Gln Pro Ser Ala Pro Glu Lys His Ser Arg Asp Cys Tyr Lys Glu						

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1570      1575      1580
Glu Glu His Leu Thr Gln Ser Ile Val Pro Pro Pro Lys Pro Glu Arg
1585      1590      1595      1600
Ser His Ser Leu Lys Leu His His Thr Gln Asn Val Glu Arg Asp Pro
      1605      1610      1615
Ser Val Leu Tyr Gln Tyr Gln Pro His Gly Lys Arg Gln Ser Ser Val
      1620      1625      1630
Thr Val Val Ser Gln Tyr Asp Asn Leu Glu Asp Tyr His Ser Leu Pro
      1635      1640      1645
Gln His Gln Arg Gly Val Phe Gly Gly Gly Gly Met Gly Thr Tyr Val
      1650      1655      1660
Pro Pro Gly Phe Pro His Pro Gln Ser Arg Thr Tyr Ala Thr Ala Leu
1665      1670      1675      1680
Gly Gln Gly Ala Phe Leu Pro Ala Glu Leu Ser Leu Gln His Pro Glu
      1685      1690      1695
Thr Gln Ile His Ala Glu
      1700

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<210> 435
<211> 160
<212> PRT
<213> Homo sapiens

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<400> 435
Pro Phe Gln Gln Val Gly Arg Cys Asn Pro Ser Pro Gln Thr Arg Pro
      5      10      15
Gly Pro Ala Ser Lys Val Lys Gln Asp Met Pro Pro Pro Gly Gly Tyr
      20      25      30
Gly Pro Ile Asp Tyr Lys Arg Asn Leu Pro Arg Arg Gly Leu Ser Gly
      35      40      45
Tyr Ser Met Leu Ala Ile Gly Ile Gly Thr Leu Ile Tyr Gly His Trp
      50      55      60
Ser Ile Met Lys Trp Asn Arg Glu Arg Arg Arg Leu Gln Ile Glu Asp
      65      70      75      80
Phe Glu Ala Arg Ile Ala Leu Leu Pro Leu Leu Gln Ala Glu Thr Asp
      85      90      95
Arg Arg Thr Leu Gln Met Leu Arg Glu Asn Leu Glu Glu Glu Ala Ile
      100      105      110
Ile Met Lys Asp Val Pro Asp Trp Lys Val Gly Glu Ser Val Phe His
      115      120      125
Thr Thr Arg Trp Val Pro Pro Leu Ile Gly Glu Leu Tyr Gly Leu Arg
      130      135      140
Thr Thr Glu Glu Ala Leu His Ala Ser His Gly Phe Met Trp Tyr Thr
145      150      155      160

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<210> 436
<211> 396
<212> PRT
<213> Homo sapiens

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<400> 436
Arg Ala Gln Glu Ala Ala Ala Ala Ala Asp Gly Pro Pro Ala Ala
      5      10      15
Asp Gly Glu Asp Gly Gln Asp Pro His Ser Lys His Leu Tyr Thr Ala
      20      25      30
Asp Met Phe Thr His Gly Ile Gln Ser Ala Ala His Phe Val Met Phe

```

```
<210> 437
<211> 92
<212> PRT
<213> Homo sapiens
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<400> 437
Ala Glu Met Asp Pro Leu Arg Ala Gln Gln Leu Ala Ala Glu Leu Glu
                    5              10              15
Val Glu Met Met Ala Asp Met Tyr Asn Arg Met Thr Ser Ala Cys His
                20              25              30
Arg Lys Cys Val Pro Pro His Tyr Lys Glu Ala Glu Leu Ser Lys Gly

```

35 40 45
 Glu Ser Val Cys Leu Asp Arg Cys Val Ser Lys Tyr Leu Asp Ile His
 50 55 60
 Glu Arg Met Gly Lys Lys Leu Thr Glu Leu Ser Met Gln Asp Glu Glu
 65 70 75 80
 Leu Met Lys Arg Val Gln Gln Ser Ser Gly Pro Ala
 85 90

<210> 438
 <211> 303
 <212> PRT
 <213> Homo sapiens

<400> 438
 Lys Asn Pro Ala Lys Met Ser Leu Tyr Pro Ser Leu Glu Asp Leu Lys
 5 10 15
 Val Asp Lys Val Ile Gln Ala Gln Thr Ala Phe Ser Ala Asn Pro Ala
 20 25 30
 Asn Pro Ala Ile Leu Ser Glu Ala Ser Ala Pro Ile Pro His Asp Gly
 35 40 45
 Asn Leu Tyr Pro Arg Leu Tyr Pro Glu Leu Ser Gln Tyr Met Gly Leu
 50 55 60
 Ser Leu Asn Glu Glu Glu Ile Arg Ala Asn Val Ala Val Val Ser Gly
 65 70 75 80
 Ala Pro Leu Gln Gly Gln Leu Val Ala Arg Pro Ser Ser Ile Asn Tyr
 85 90 95
 Met Val Ala Pro Val Thr Gly Asn Asp Val Gly Ile Arg Arg Ala Glu
 100 105 110
 Ile Lys Gln Gly Ile Arg Glu Val Ile Leu Cys Lys Asp Gln Asp Gly
 115 120 125
 Lys Ile Gly Leu Arg Leu Lys Ser Ile Asp Asn Gly Ile Phe Val Gln
 130 135 140
 Leu Val Gln Ala Asn Ser Pro Ala Ser Leu Val Gly Leu Arg Phe Gly
 145 150 155 160
 Asp Gln Val Leu Gln Ile Asn Gly Glu Asn Cys Ala Gly Trp Ser Ser
 165 170 175
 Asp Lys Ala His Lys Val Leu Lys Gln Ala Phe Gly Glu Lys Ile Thr
 180 185 190
 Met Thr Ile Arg Asp Arg Pro Phe Glu Arg Thr Ile Thr Met His Lys
 195 200 205
 Asp Ser Thr Gly His Val Gly Phe Ile Phe Lys Asn Gly Lys Ile Thr
 210 215 220
 Ser Ile Val Lys Asp Ser Ser Ala Ala Arg Asn Gly Leu Leu Thr Glu
 225 230 235 240
 His Asn Ile Cys Glu Ile Asn Gly Gln Asn Val Ile Gly Leu Lys Asp
 245 250 255
 Ser Gln Ile Ala Asp Ile Leu Ser Thr Ser Gly Thr Val Val Thr Ile
 260 265 270
 Thr Ile Met Pro Ala Phe Ile Phe Glu His Ile Ile Lys Arg Met Ala
 275 280 285
 Pro Ser Ile Met Lys Ser Leu Met Asp His Thr Ile Pro Glu Val
 290 295 300

<210> 439
 <211> 378
 <212> PRT

<213> Homo sapiens

<400> 439

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Val Val Pro Ser Thr Lys Asp Phe Leu Val Gly Val Lys Gly Ser Gly
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Gly His Arg Gly Gly Gly Glu Met Ala Phe Ser Gly Ser Gln Ala Pro
      20              25              30
Tyr Leu Ser Pro Ala Val Pro Phe Ser Gly Thr Ile Gln Gly Gly Leu
      35              40              45
Gln Asp Gly Leu Gln Ile Thr Val Asn Gly Thr Val Leu Ser Ser Ser
      50              55              60
Gly Thr Arg Phe Ala Val Asn Phe Gln Thr Gly Phe Ser Gly Asn Asp
      65              70              75              80
Ile Ala Phe His Phe Asn Pro Arg Phe Glu Asp Gly Gly Tyr Val Val
      85              90              95
Cys Asn Thr Arg Gln Asn Gly Ser Trp Gly Pro Glu Glu Arg Lys Thr
      100              105              110
His Met Pro Phe Gln Lys Gly Met Pro Phe Asp Leu Cys Phe Leu Val
      115              120              125
Gln Ser Ser Asp Phe Lys Val Met Val Asn Gly Ile Leu Phe Val Gln
      130              135              140
Tyr Phe His Arg Val Pro Phe His Arg Val Asp Thr Ile Ser Val Asn
      145              150              155              160
Gly Ser Val Gln Leu Ser Tyr Ile Ser Phe Gln Asn Pro Arg Thr Val
      165              170              175
Pro Val Gln Pro Ala Phe Ser Thr Val Pro Phe Ser Gln Pro Val Cys
      180              185              190
Phe Pro Pro Arg Pro Arg Gly Arg Arg Gln Lys Pro Pro Gly Val Trp
      195              200              205
Pro Ala Asn Pro Ala Pro Ile Thr Gln Thr Val Ile His Thr Val Gln
      210              215              220
Ser Ala Pro Gly Gln Met Phe Ser Thr Pro Ala Ile Pro Pro Met Met
      225              230              235              240
Tyr Pro His Pro Ala Tyr Pro Met Pro Phe Ile Thr Thr Ile Leu Gly
      245              250              255
Gly Leu Tyr Pro Ser Lys Ser Ile Leu Leu Ser Gly Thr Val Leu Pro
      260              265              270
Ser Ala Gln Arg Phe His Ile Asn Leu Cys Ser Gly Asn His Ile Ala
      275              280              285
Phe His Leu Asn Pro Arg Phe Asp Glu Asn Ala Val Val Arg Asn Thr
      290              295              300
Gln Ile Asp Asn Ser Trp Gly Ser Glu Glu Arg Ser Leu Pro Arg Lys
      305              310              315              320
Met Pro Phe Val Arg Gly Gln Ser Phe Ser Val Trp Ile Leu Cys Glu
      325              330              335
Ala His Cys Leu Lys Val Ala Val Asp Gly Gln His Leu Phe Glu Tyr
      340              345              350
Tyr His Arg Leu Arg Asn Leu Pro Thr Ile Asn Arg Leu Glu Val Gly
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Gly Asp Ile Gln Leu Thr His Val Gln Thr
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<210> 440

<211> 2239

<212> DNA

<213> Homo sapiens

<400> 440

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<210> 441

<211> 5981

<212> DNA

<213> Homo sapiens

<400> 441

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<210> 442

<211> 337

<212> DNA

<213> Homo sapiens

<400> 442

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<210> 443

<211> 739

<212> DNA

<213> Homo sapiens

<400> 443

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<210> 444

<211> 738

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

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<223> n = A,T,C or G

<400> 444

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<210> 445

<211> 716

<212> DNA

<213> Homo sapiens

<400> 445

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<210> 446

<211> 641

<212> DNA

<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(641)
<223> n = A,T,C or G

<400> 446
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<210> 447
<211> 652
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(652)
<223> n = A,T,C or G

<400> 447
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<210> 448
<211> 677
<212> DNA
<213> Homo sapiens

<400> 448
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677

<210> 449

<211> 603

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(603)

<223> n = A,T,C or G

<400> 449

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gggggagggg aatgtgaatg tggcctggcc canagaactc cccatttcat cgattttgca 240
ttgggcgata gaggaagcag atgtcggggc tgcctgcctt ggtctanagg agatggctgg 300
ggccacttcc cacagggtga agtggcagcg gctcagcaag gggagcctgg ccaccagggg 360
ctgggacatg cgctcactgg aacctttgtg cttggccctc ggcagcgcgg ctgtggtccc 420
gtgtgaggtg tgctgggggt ggggtgtgggt ggctgggtgt ggcagcttgt gccagagtga 480
cacaggcctc cctggggttg gatgggggca agttaaaaag ctgaaaagggt acttggcttt 540
ctgagggcgg gcttggggagc aggccttgca gganaccatg ttctctgtcc tcagcagatc 600
cac 603
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<210> 450

<211> 678

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(678)

<223> n = A,T,C or G

<400> 450

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tcatcatgtg attaaaagtg gtgattcagt ggggaactggg aatgttttta gctgggtgga 120
gaaggctgcc tacactgggc actgttttag attctcatat catttaaaca gcaaggaggt 180
tcagggaaga ataaccgtag ccttgggtaa tccactaggg cttttgtgag taggagagct 240
gatacctcac attcttagca ggtgaaaact tgccatgatg gaaacagata gtgaagagtt 300
actgacgtat cccaaattat atgctgtgac ataaattccc agcatgccca gccctgattt 360
ctgagttcat aagtaattct agtgaacctt agtaggaatt ctgggtaaga aaatgaggtt 420
gccattggtc ttgtttgcat caccaagacc agacatccag aagagcccct caccttgaaa 480
agcagacaça ttttaaatta accccctcct tcccactcac cttcatctcc ctaagagttt 540
tggccattta attccacatt ttgaaaggaa tacattgggtg aaatttggga agagaatctg 600
tgctatgcaa tgtttcatta aaatcttcag tttttcaagt ctctctaaaa ataatttgta 660
gatctatctt ggatggat 678
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<210> 451

<211> 651

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(651)

<223> n = A,T,C or G

<400> 451
tttttcatca acaaaaatca agcattttcn tttttttgaa acaagaaaag cgcctcgtan 60
aaaccaagat tctgtacaat attctaacat tatatgtaca taaaattata ttactcataa 120
ctatatgtgaa aagtcttatt tgtagaatat ggctggcaac aaagaaagac ccataccatt 180
tagcgtttga agcagggcag gtagcaagag aacattagca aagacacctt tgtgcctgga 240
tacacaatcc tgctactaag ttatgtgact aaccagcaca ctctaagttc tgtggtttgt 300
tcgttgtttc acattctagt agggaaattct gcagcaggcg atgcgaaaaa naanacatgg 360
tcaaataaaa tgtgaaatgc tgtttaaaat ctgcatattg gctatgataa tgggtttgng 420
aatccaagtt gcattggaag ttcaactcatt ctccattcat tatgcatgcc tccagtgtatt 480
taatgaattt cagcagggng aaaagacagc tttgaacaga tcagatgggc tgtgagtcn 540
attcttgatt ctttttcctc atttggtccc tgaatgttg anaaaactgg tttgttacac 600
tggggaagga gagagtgaag accctccagt tggttcctca gtcagctccg t 651

<210> 452
<211> 679
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(679)
<223> n = A,T,C or G

<400> 452
gaattcgaac cccttcgcat tgctcagccn nctaccactg ctaagagcca tctccaccag 60
aagcctggcc agacctggaa gaacaaagag catcatctct ctgacagaga gtttgtgttc 120
aaagaacctc agcaggtagt acgtagagct cctgagccac gagtgtattga cagagagggg 180
gtgtatgaaa tcagcctgtc acccacaggt gtatctaggg tctgtttgta tcctggcttt 240
gttgacgtga aagaagctga ctggatattg gaacagcttt gtcaagatgt tccctggaaa 300
cagaggaccg gcatcagaga ggatataact tatcagcaac caagacttac agcatggtat 360
ggagaacttc cttacactta ttcaagaatc actatggaac caaatcctca ctggcaccct 420
gtgctgcgca cactaaagaa ccgcattgaa gagaacactg gccacacctt caactcctta 480
ctctgcaatc tttatcgcaa tgagaaggac agcgtggact ggacagtgat tgatgaaccc 540
tcactagggg ggtgccccat tattgcttca ctaagttttg gtgccacacg cacatttgag 600
atgagaaaag agccaccacc agaagagaat ggagactaca catatgtgga aagagtgaag 660
atacccttgg atcatggta 679

<210> 453
<211> 630
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(630)
<223> n = A,T,C or G

<400> 453
gaattcgaac cccttcggaa ggccaaggng ntagaaggng gctccggccc cagctgtcgt 60
gaagaagcag gaggctaaga aagtgttgaa tcccctgttt gagaaaaggc ctaagaattt 120
tggcattgga caggacatcc agcccaaaag agacctcacc cgctttgtga aatggccccg 180
ctatatcagg ttgcagcggc agagagccat cctctataag cggtgaaag tgcctcctgc 240
gattaaccag ttcaccagag ccctggaccg ccaaacagct actcagctgc ttaagctggc 300
ccacaagtac agaccagaga caaagcaaga gaagaagcag agactgttgg cccggggcga 360
gaagaaggct gctggcaaaag gggacgtccc aacgaagaga ccacctgtcc ttcgagcagg 420
agttaacacc cgtcaccacc ttggtggaga acaagaaagc tcagctggtg gtgattgcac 480
acgacgtgga tcccatcgag ctggtgtgtc tcttgcttgc cctgtgtcgt aaaatggggg 540

tccttactg cattatcaag ggaaaggcaa gactgggacg tctagtccac aggaagacct 600
gcaccactgt cgccttccac aggtgaactc 630

<210> 454
<211> 677
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(677)
<223> n = A,T,C or G

<400> 454
gaattcgaac cccttcgccc gcatgcgga catccccttg gcccagggg cagactggcg 60
cgatctgccc aacatcgagg tgcggctctc agacggcacc atggccagga agctgcggtg 120
taccacccat gacaggaaga acggccgcag cagctctggg gccctccgtg gggctctgctc 180
ctgctgggaa gccggcaaa cctgcgaccc cgcagccagg cagttcaaca ccctcatccc 240
ctggtgcctg ccccacaccg ggaaccggca caaccactgg gctggcctct atggaaggct 300
cgagtgggac ggcttcttca gcacaaccgt caccaacccc gagcccatgg gcaagcaggg 360
ccgctgctc caccagagc agcaccgtgt ggtgagcgtg cgggagtgtg cccgctccca 420
gggcttccct gacacctacc ggctcttcg caacatcctg gacaagcacc ggcagggtggg 480
caatgccgtg ccaccgcccc tggcaaagcc attggcttgg agatcaagct ttgtattgtt 540
ggccaaagcc cgagagagt cctcagctaa aataaaggag gaggaagctg ctaaggacta 600
gttctgcctt cccgtcaccc ctgtttcttg caccaggaat ccccacaat gcacttgatg 660
gtggggtttt aacatgt 677

<210> 455
<211> 598
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(598)
<223> n = A,T,C or G

<400> 455
ttttttggtt tataggagag atttatttga agaaatatta caacatataa aaactacata 60
aagtcttaat ttccactcat acagtggtag atttgatata atgcataata aaaaactttt 120
aaaatccaga atgcacaaag tactgcacaa tttgatcact aaatcattag ttgataagcg 180
aacctcacac aacagcttca tgtcagccaa ggccacaaac accatgtacc acacatgtga 240
acggacagat tgacatgtta aaaacacaac atcagtgcac gttggggatt cctggtgcca 300
gaaacagggg tgacgggagg gcagaactag tccttagcag cttcctcctc ctttatttta 360
gctgaggcac tctctcgggc tttggccaac atacaaagct tgatctccaa gccaatggct 420
ttggccaggg gcggtggcac ggcatggccc acctgccggt gcttngtcca ggatgttgcc 480
cgaagagccg gtaggtggtc aagggaagcc cctggggaag cgggcacact cccggacgct 540
naccacacgg tgctgntttt ggggtggagca ccgcggcctt gcttgcccat gggctcgg 598

<210> 456
<211> 574
<212> DNA
<213> Homo sapiens

<400> 456
ggaattcgaa ccccttcggg gcggggagcc ccgtagaacc gaggggggtcg gcccgggggt 60
cccgggggag gtggagatgg tgaaggggca gccgttcgac gtgggcccgc gctacacgca 120
gttgacgtac atcggcgagg gcgcgtacgg catggtcagc tcggcctatg accacgtgcg 180

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caagaactcgc gtggccatca agaagatcag ccccttcgaa catcagacct actgccagcg 240
cacgctccgg gagatccaga tcctgctgcg cttccgccat gagaatgtca tcggcatccg 300
agacattctg cgggcggtcca ccctggaagc catgagagat gtctacattg tgcaggacct 360
gatggagact gacctgtaca agttgctgaa aagccagcag ctgagcaatg accatatctg 420
ctacttcttc taccagatcc tgcggggcct caagtacatc cactccgcca acgtgctcca 480
ccgagatcta aagccctcca acctgcttca tcaacaccac ctggcgacct ttaaaatttg 540
tgaatttccg gcctggcccc cggattgccc gaat 574
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<210> 457

<211> 546

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(546)

<223> n = A,T,C or G

<400> 457

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ttttttgaca catctctata tttatatatt agacgggtca gggagggtggc aggggcgccc 60
ggctctccac gccccccagc tccacttctg ctccaccacac acagaagcag cgaggggcacg 120
cgaagtgaca gctttgacag ggaggggatt cggccccggc tggtcctca gggatgctag 180
cccttgagac taaggaatgt tccttcaggg aaactagggg ggggtttgaa tganatgagg 240
ggggcaggca tggccctgag tccctactca gcgcccccca ccctccacct ctgcccttca 300
gcagggttggg gcagccagaa cccttccatt ccagaactgc cagagactgg gacgctgggg 360
aaggtaaggg gcgagcagca gcagcgggag attgaactgg ggccacctga gctcccgagg 420
ccccgtggg agggcggggtg gggaggaaaaa ggccttggcc tgcttgaagc tggaggcctc 480
agcaaaggag agaggtggcc aggcccatgc tccaccccg cctgggctgc caanggtccc 540
gggctg 546
```

<210> 458

<211> 674

<212> DNA

<213> Homo sapiens

<400> 458

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gaattcgaac cccttcggtg ttattaagaa ctaagagaat agcttgccag atacaaatgg 60
aaacaccttc caaatgagtc ggagaaaatg tcttgagta ttatgggtaa aatagcaaa 120
agcttgggaa tacagtttgc taatatcaag tccttaacaa cgaccattct tcattcaaga 180
ttagttgtgt ataaatacat gcttcttcag gagttgactt agaaaacaag caaacaaca 240
aacatcagaa actattttaca actgggagca atccttgaag aacataaaga atataaatat 300
caacaaaggc tgaaaactct tttttagatt aaagatcaaa tggacatgtc atcggaatgt 360
attgtatggc tcttgattaa atcctggagc aaagtggaga gtgaggaaca actgtaaaga 420
atgtgaatac ggactgtgta ttagataaca gtaccataaa tttcctggat gggataatta 480
tgttgtgact atgtaagaga atattttgcc cttagaagat atatgatgaa gcatttagaa 540
gtaaagtatc atgacatctt gcaaataact ttcaagtgat tcagccagat atataaaaaat 600
tatatataac acattatata atttatattt atataattat aatacattat ataatttata 660
cattataatt atat 674
```

<210> 459

<211> 682

<212> DNA

<213> Homo sapiens

<400> 459

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ttttttttaa tccatggctt gttaattgtc atoccagtta tttacatgtg actatagaga 60
ctgcattctc ccagctgcca ggccgccagg gctttgccac tgggtataatt tataacacga 120
ctaattaaaa tgaatttgct tgcaataagg ttctgtgtgc tatttgtggg agaggagtta 180
```

```
ttaaaatttt cagtacagta atagtaaact tgaatgcaaa gtaataataa tcatacattt 240
ttaattacat gtttaataacc catttggcta atgtagaact attctgaaaa ttacttggga 300
tcagcacaat gtctttttgt gcttagtagt atccaaagac atccttctga atgggcttag 360
caatatgcac tgtcatcaag atacagctgt ttgatgacag acacacagtg tggtcctatg 420
atactttgca caagatcagc tatgacaaat acaagttcat tttgcttatt gcaggcaaat 480
aatgtccttt gcaggaaactt ggatggagcc agaggccatt attctaagtg aaataacctca 540
ggagtggaaa accaaatacc atatgttctc acttacaagt gggaactaag ctatgggtac 600
acaaacgcat atagagtaat ggactctggc gactcatact acatattgag tacaatgtac 660
actacttggg tgatgggtgc ac 682
```

<210> 460

<211> 663

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(663)

<223> n = A,T,C or G

<400> 460

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gaattcgaac cccttcgcgg ggcgcgcgag cggcgccagc tcggggcgag ggaaccacaga 60
gaagctgagg gggcggtagc ggcgcgagcg gcgacgacga cgactccgcg gcgtgtgccc 120
agcctcttcc cgccgcagcc gcccttttcc tccctccctt acgtcccgga gtgcggcagt 180
accgcctoct tcccagccgc ggggcttcct ccagacctct cggcgcgggg gagccctatt 240
cccagaggca ggtggtgctg accctgtaac ccaaaggagg aaacagctgg ctaagctcat 300
cattgttact ggtgggcacc atgtccttga agcttcaggc aagcaatgta accaacaaga 360
atgaccccaa gtccatcaac tctcgagtct tcattggaaa cctcaacaca gctctggtga 420
agaaatcaga tgtggagacc atcttctcta agtatggccg tgtggccggc tgttctgtgc 480
acaagggcta tgcctttggt cagtactcca atgagcgcca tgcccgggca gctgtgctgg 540
gagagaatgg gcggtgctg gccgggcaga ccctggacat caacatggct ggagagccta 600
agcctgacag acccaagggg cttaaaganaa gcagcatctg gcatatacag gctcttcgac 660
tac 663
```

<210> 461

<211> 612

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(612)

<223> n = A,T,C or G

<400> 461

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ttttttggga tccaatctnt ttattgtcag ggtcccctcc ctgnngccccc ccgccaaacc 60
tatagaaaaa acccaagcct gggagtgtcc tggggagggg aggtagtatg gggaaacccc 120
tgtgtcttac cctntggcct gggcagtgc aacagggagg gctcatgggg aaggagtagg 180
ccagtaactc cacctgcana ggacatggca ctggctggga tgcgttgggg gaggagggcg 240
ctgtgcccag ctttccnttg gtaccgctg ggggggtggc tccaggggtg ggtgcccggc 300
ttgaggcctg gggcagcgat gcccttcacc tgctggnngc cattgtcct gtcaggctgc 360
ttactgcaag gccccatcat ccggtctgt gtccctggctg tgttccagct cttcctcgct 420
gngtgcagg agcccttcct catcgccgct gtctcggtgc cgtgcttccc cctggggcag 480
gcctgctca naagttgtgt tctcttgggg ggctggtggc cggttgttgc caccgcaccg 540
caccaccact ggcaccggca ccgntgcacc accaccgccc ccgcccgggn tggngccacc 600
ttcatcacc tt 612
```

<210> 462

<211> 672
<212> DNA
<213> Homo sapiens

<400> 462
gaattcgaac cccttcggat ggaagggggc ggggcagcgt cggggaaagg aagggccgga 60
ggcgcggcgg cgggcggccg agagggggcg cggcggcggc ggccggcggg ttcccgcgcc 120
gcggagcccg gcccgagagc cgcgtccacg ttccctgcctc ctgctcccgc cgccctgggg 180
cgccgccatg acgcccgatc tgctcaactt cagccccaga tgtcaccaag ctctcggact 240
ctaacaagga gaacgcgctg cacagctaca gcaccagaa gggccccctg aaggcagggg 300
agcagcgggc gggctctgag gtcctcagcc ggggtggccc tcggaaggcg gacgggcagc 360
gtcaggcctt ggactacgtg gagctctcgc cgctgaccca ggcttccccg cagcgggccc 420
gcaccccgag ccgcactcct gaccgccctg gccaaagcagg aggagctgga gcgggacctg 480
gccacgcgct ccgaggagcg ggcgaagtgg tttgaggcca cagacagcag gacccagag 540
gtgcctgctg gtgagggggc ggcgcggggc ctgggtgccc cctgactgag gaccagcaaa 600
accggcttag tgaggagatc gagaagaagt ggcaggagct ggagaagctt gcccttgccg 660
gagaataacc gg 672

<210> 463
<211> 562
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(562)
<223> n = A,T,C or G

<400> 463
ttttttaaag tataaagtgt tttggaaaaa aaggaaaaan ntctatataa aaatctcttc 60
acatatataa tcctgaagaa ggtgcaaggt gagaccaggt gcgagggggc tgctcagata 120
tgcaagtgtgt gtgtgtgtgt gtgtgtgtgt gtatccgtgt gtacatgtgt gcacgtgtgt 180
gcgtatgtgt ctgtgtgtct gtgtgtgtgt gtgtgtgtgt gtgtgtgtgt ggtgggtgca 240
agtgcacgtg tggeccacag aggggtggga gaaagcttgg ctttttactt ccatccagga 300
gggaaggagg gcggctggtc ctccagcctg gagggctctgc agctggggcg gacctctact 360
cagccaggct gttgcgcatc gactccttct cctggagggc ggccatggca agacgcaggt 420
gtccttctag ctgctcgatc tcccgcctcag accgtgtctt gatgtggctc aactccacat 480
agacgtcctg gtactttccc naggtgaagc gcttgtcctt ctgcacatc tggagctcgt 540
cccggaggca ctgcaccttc ct 562

<210> 464
<211> 553
<212> DNA
<213> Homo sapiens

<400> 464
gaattcgaac cccttcggga ccaggaaccc aggagagcat ggccacgctg cgccggcttc 60
gggaggcgcc gcggcactta ctggtttgcg agaaatccaa cttcggcaac cacaagtgcg 120
gccaccggca tcttgtgcag acgcactact ataactacag ggtttcattt ctcatctctg 180
aatgtgggat actatcgga gaactgaaaa acctggtcat gaacactgga ccctattact 240
ttgtgaagaa tttacctctt catgaattaa ttacacctga attcatcagt acctttataa 300
agaaagggtc ttgctatgca ctaacatata atacacatat tgatgaagat aatactgttg 360
ccctgctacc aaatgggaaa ttaattttgt cactggataa agacacttat gaagaaactg 420
gacttcaggg tcatccatct cagttttctg gcagaaaaat tatgaaattt agttcagaag 480
aatcgacaat gatgtcatat ttttccaagt accaaattca ggagcatcag ccaaaagtag 540
cactgagccc gtt 553

<210> 465

<211> 383
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(383)
<223> n = A,T,C or G

<400> 465
tttttggaag aaaacacgat ttttaatttt ttttttttat gggggacagn gatcatttgc 60
cccaacagcc atntgaagcc aatagtcctg attattaaaa atcacaaagt tatataaatg 120
ntctcctcct tttcgaaaac catgttcatt tttttcccaa naaacagggc tgtctgcaaa 180
gccttgaacg gacagngtaa cccatggagc taacttcggt tcatcaaagt agngacagan 240
atgttccaat agganacaga tcttntntgg aagtatgaag ccagngattg tacacaaata 300
agcttttgcc accactgtgc ttggctcagg acagcaatag gttgatatga aattattagg 360
ctcattattt agnncgacat tac 383

<210> 466
<211> 673
<212> DNA
<213> Homo sapiens

<400> 466
gaattcgaac cccttcgctc cctcctgcac gcaatggtgg cctatgatcc cgaatgagaga 60
atcgccgccc accaggccct gcagcaccac tacttccaag aacagaggaa aacagagaag 120
cggtgctctgg gcagccacag aaaagctggc tttccggagc accctgtggc accggaacca 180
ctcagtaaca gctgccagat ttccaaggag ggcagaaagc agaaacagtc cctaaagcaa 240
gaggaggacc gtcccaagag acgaggaccg gcctatgtca tggaaactgcc caaactaaag 300
ctttcgggag tggtcagact gtcgtcttac tccagcccca cgctgcagtc cgtgcttga 360
tctggaacaa atggaagagt gccggtgctg agacccttga agtgcattcc tgcgagcaag 420
aaggtagcgc ggaaccagct tctctgacgg cgctgctctt cgaccagcc caggccgcca 480
ctgaattttg tgtctgtaat ttttcttga cagacagatc cgcagaagga ccttaagcct 540
gccccgcagc agtgtcgctt gccaccata gtgcggaaag gcggaagata actgagcagc 600
accgtcgtct cgacttcgga ggcaacacca agcccgaccg ggccaggcct ggggtgatctg 660
ctgctgagac gcc 673

<210> 467
<211> 373
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(373)
<223> n = A,T,C or G

<400> 467
tttttactgg aacgacagct tatnttttaa taaaagtcag gggngtcagc agngtcactg 60
gtaanacatg atggcgctcc acgactgacc agcagcgctg ggaagggaca cgcanaaccc 120
acctccaac cagcccaaac acatnacana aatgcctgct cgtttgtttt gattcatata 180
caaagttaca aagtatttcc tgccccaat tnttaacgaa aatgaaagaa aaccctanaa 240
tgcgggggtt ttacaagtat attagccan aacatcctag gcagctgcnc gggccgcggg 300
tgcggcaggg cgcagggcaa cacccaaagc cccggccagc gcgaaacgga cgcaggcgca 360
tccccagccc tcc 373

<210> 468
<211> 573

<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(573)
<223> n = A,T,C or G

<400> 468
gaattcgaac cccttcgctg ctgtcctact tgatgcttgt cactgtcatg atgtggcccc 60
tnngctgtgta ccaccgactg tgggatcgag catatgtgcg gctgaagcca gctctgcagc 120
ggctagactt cagtgtccgt ggctacatga tgtccaagca gagagagaga caattacgcc 180
gcagagctct ccaccagaa cgagccatgg acaaccacag tgacagcgaa gaggagcttg 240
ctgccttctg tcctcagctg gacgattcta ctgttgccag ggaattggcc atcacagact 300
ctgagcactc agacgctgaa gtctcctgta cagacaatgg cacattcaat ctttcaaggg 360
gccaaacacc tctaacggaa ggctctgaag acctagatgg tcacagtgat ccagaggaat 420
cctttgccag agaccttcca gacttccctt ccattaatat ggatcctgct ggctggatg 480
atgangacga cactagcatt ggcatgccca gcttgatgta ccgttctcgc ccagggggct 540
gaggagcccc aaggcccccac ctgccagccc ggg 573

<210> 469
<211> 635
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(635)
<223> n = A,T,C or G

<400> 469
tcncgatcta gaactagggt ggacaggctt gctcaagttt caccagagtt antactggcc 60
tctgttcgca gagtttttag ttinnacactg cagaattggc agactacacg gtttatggaa 120
gttgaagtag caataagatt gctgtatatg ttggcagaag ctcttccagt atctcatgg 180
gctcacttct caggtgatgt ttcaaaaagct agtgctttgc aggatatgat gcgaactgta 240
agtatactgg agataatttt gaccataaat ttctgttttc agtataagct aatgggagtt 300
ccttaattgt tagagcttag tatatgttaa taccggggca ttttgatgtt gcaataaata 360
agaagagggt tcctaacttt ttctctgatct agctggtaac atcaggagtc agttcctatc 420
agcatacatc tgtgacattg gagttcttcg aaactgttgt tagatatgaa aagtttttca 480
cagttgaacc tcagcacatt ccatgtgtac taatggcttt ctagatcac agaggtctgc 540
ggcattccag ngcaaaaagtt cggagcagga cggttacct gttttctaga tttgtcaaat 600
ctctcaataa gcaaatgaat cctttccttg aggat 635

<210> 470
<211> 593
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(593)
<223> n = A,T,C or G

<400> 470
gaattcgaac ccttcggtat taacaaatat ntacatttct atttttataa tccataagga 60
tatgcctgtt ttaaataaca tacatattaa caatatctat caggaaaacc ctcaagacag 120
cttctagtta aaaccttngn tgctgtcttc tcaaactata tttataaaaa tttgctaggg 180
ccaaatccat acttgcagaa taattcatca aattttattt ttaagngaaa agtaaccttt 240

```

caggcatttc agcagcatatc attgacaatc tagggatatat atgtatgtat gtttcttatt 300
gtatgtctat atatgtatgt ggggaggaca ggagtgaatg ttcacacact tttcttgctg 360
actcaactaa attggagaat gtttctgaag aaaattggat gaaattagct gctgagattg 420
agtttctgcc ttaaaatctg aaacaaaaaa agggacaaat tgctggtang atctactgac 480
tgtngccatc accagaacac ttagtttctt cccagacatg aatttcctga caggctctga 540
gccagaaaca cactgtgggc gtgcatntgg gtcacccctg atatgcctcc act 593

```

```

<210> 471
<211> 581
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(581)
<223> n = A,T,C or G

```

```

<400> 471
tttttttaat cangggacat ttattaacat gtttcaaaag tgaccaaagt gtccagccag 60
cacaatagcc gaggcaatca acgttctctt agtgtgtgat ctggtccaaa acaccaaata 120
aatagggttta ggaataacct caaataaatt gtaatttaac ttgcgccaaa attatacatc 180
ctctactgct ctccctgct cctgtaaaga tactagcggg aggggagaaa gctcaaatga 240
ctctgtaatt tagaattaca accagagaag aaatacttca agcacaataa agacgttcca 300
ttgaagagcg acattcattc tggaatgttt gttttgaaaa caactcttnt gggggaattc 360
aaaagggtact gaacaaagca acataaaagta agttttgggt tgttttgcaa aataaaaaata 420
tacaattgag tggaccagat ggcaaaaaca taccaattac aatctgaatg ctatatatta 480
aacccttaaa ttctgaaggc ctgaatatca acaaacctat ttatgtttat gatcctaaaa 540
agacattaaa tattattaaa cccccaactt ccaaaacata g 581

```

```

<210> 472
<211> 674
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(674)
<223> n = A,T,C or G

```

```

<400> 472
gaattcgaac cccttcggat ggcgtgatgt ntcacagaaa gttctccgct cccagacatg 60
ggtccctcgg ctctctgctt cggaagcgca gcagcaggca tcgtgggaag gtgaagagct 120
tccctaagga tgaccgtcc aagccggtcc acctcacagc ctctctggga tacaaggctg 180
gcatgactca catcgtgcgg gaagtgcaca ggccgggatc caaggtgaac aagaaggag 240
tggtggaggc tgtgaccatt gtagagacac caccatgggt ggttgtgggc atttgtggct 300
acgtggaaac cctcagaggc ctccggacct tcaagactgt ctttgctgag cacatcagtg 360
atgaatgcaa gaggcgtttc tataagaatt ggcataaatc taagaagaag gcctttacca 420
agtactgcaa gaaatggcag gatgaggatg gcaagaagca gctggagaag gacttcagca 480
gcatgaagaa gtactgcaa gtcacccgtg tcattgccca caccagatg cgcctgcttc 540
ctctgcgcca gaagaagccc acctgatgga gatccagggt aacggaggca ctgtggccga 600
gaagctggac tgggccccgc gagangcttg agcacaggta cctgtgaacc aagtgtttgg 660
gcaggatgaa aatg. 674

```

```

<210> 473
<211> 646
<212> DNA
<213> Homo sapiens

```

<220>
<221> misc_feature
<222> (1)... (646)
<223> n = A,T,C or G

<400> 473
ttttttcagn ggaaaataac ttttattgan accccacca ctgcaaaatc tgttcctggc 60
attaagctcc ttnttccttt gcaattcggg ctttcttcag nggtcccatg aatgctttct 120
tctcctccat ggtctggaag cggccatggc caaacttga ggnggtgtca atgaacttaa 180
ggtcaatctt ctccanagcc cgccgnttcg tctgcaccag caaggacttg cggagggtga 240
gcacccgctt cttggttccc accacacagc ctttcagcat gacaaagtca ttggtcactt 300
caccatagng gacaaagcca cccanagggt tgatgctctt gtcanatagg tcatagtcag 360
tggaggcatt gttcttgatc agcttgccgt ccttgataag gtagccctgg ccaatcttat 420
aaatcttctt gttgatctca gtgcggtgat ggtagccttt ctgcccagcg cgtgccacag 480
agaaggctac acgagcagga tgccatgccc caatacaggc caccttgccg aggcctcggg 540
gggtcttgcg gggcagcttc ttggtgtgcc aacgactggg gaccctttg tagcctttgc 600
ccttggtcac cccgatgacg tcgatcatct catcctgccc aaacac 646

<210> 474
<211> 544
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)... (544)
<223> n = A,T,C or G

<400> 474
gaattcgaac cccttcggca gcacactccc antcggccgc agcctgacac gccgcgcggc 60
ccccagctct ccgcgggctg ctccccagc catggcacag ggcctcgcc cactatggca 120
gcagcacggc acagcacgct cgacttcatg ctccggcgcca aagctgatgg tgagaccatt 180
ctaaaaggcc tccagtccat tttccaggag caggggatgg cggagtcggg gcacacctgg 240
caggaccatg gctatttagc aacctacaca aacaagaacg gcagctttgc caatttgaga 300
atttaccac atggattggg gttgctggac cttcagagtt atgatgggta tgcgcaaggc 360
aaagaagaga tcgacagtat tttgaacaaa gtagaggaaa gaatgaaaga attgagtcag 420
gacaagtact gggcgggtga aacgattacc accatagtg cgaggaggag ccatcgacag 480
atactggccc accgncgacg ggcgccttgg ttgaatatga catagaatga agtggtatat 540
gacg 544

<210> 475
<211> 578
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)... (578)
<223> n = A,T,C or G

<400> 475
gaattcgaac cccttcggga gaaccccatg ngggaacttc gcatccgcaa actctgtctc 60
aacatctgtg ttggggagag tggagacaga ctgacgcgag cagccaagggt gttggagcag 120
ctcacagggc agaccctgt gttttccaaa gctagatata ctgtcagatc ctttggcatc 180
cggagaaatg aaaagattgc tgtccactgc acagttcgag gggccaaggc agaagaaatc 240
ttggagaagg gtctaagggt gcgggagtat gagttaagaa aaaacaactt ctgagatact 300
ggaactttg gttttgggat ccaggaacac atcgatctgg gtatcaaata tgacccaagc 360
attggtatct acggcctgga cttctatgtg gtgctgggta ggccagggtt cagcatcgca 420

gacaagaagc gcaggacagg ctgcattggg gccaaacaca gaatcagcaa agaggaggcc 480
atgcgctggt tccagcagaa gtatgatggg atcatccttc ctggcaaata aattcccgtt 540
tctatccaaa agagcaataa aaagttttca gtgaaaaa 578

<210> 476

<211> 619

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(619)

<223> n = A,T,C or G

<400> 476

ggaattcgaa ccccttcgct cctgcctgtc cgccatgttt tcaggncggg nctggcttgg 60
tcttcccccg taaggaaatg gccggggagc tccaggggac ccaggcgccg tcgcttcggc 120
ggagcctggg ctgaccagcc aggacagcgg ggtaaaccgg aacaattctg cgcgaggtag 180
ggaggccatg gcgtccggca gtaactggct ctccgggggtg aatgtcgtgc tggtagatggc 240
ctacggggagc ctgggtgtttg tactgctatt tatttttgtg aagaggcaaa tcatgcgctt 300
tgcaatgaaa tctcgaaggg gacctcatgt ccctgtggga cacaatgcc ccaaggactt 360
gaaagaggag attgatattc gactctccag ggttcaggat atcaagtatg agccccagct 420
ccttgacgat gatgatgcta gactactaca actggaaacc cagggaaatc aaagttgcta 480
caactatctg tataggatga aagctctgga tgccattcgt acctctgaga tcccatttca 540
ttctgaaggc cggcatcccc gttccttaat gggaagaat tttccgcttc taccttgctg 600
gatcttgcca aacactagt 619

<210> 477

<211> 674

<212> DNA

<213> Homo sapiens

<400> 477

gaattcgaac cccctcgggg tgttcgactg ctagagccga gcgaagcgat gcctaaatca 60
aaggaaactg tttcttcaag ctcttctggc agtgattctg acagtgaggt tgacaaaaag 120
ttaaagagga aaaagcaagt tgctccagaa aaacctgtaa agaaacaaaa gacaggtag 180
acttcgagag cctgtcatc ttctaaacag agcagcagca gcagagatga taacatgttt 240
cagattggga aaatgaggta cgtagtggtt cgcgatttta aaggcaaagt gctaattgat 300
attagagaat attggatgga tcctgaaggg gaaatgaaac cagggaagaaa aggtatttct 360
ttaaaccag aacaatggag ccagctgaag gaacagattt ctgacattga tgatgcagta 420
agaaaactgt aaaattcgag ccataataat aaaacctgta ctgttctagt tgttttaata 480
tgtcttttta cattggcttt tgttttctaa atgttctcca agctattgta tgtttggatt 540
gcagaagaat ttgtaagatg aatacttttt tttaatgtgc attattaaaa atattgagtg 600
aagctaattg tcaactttat taaggattac tttgtctgcc caccctagt gtaaaataaa 660
atcaagtaat acat 674

<210> 478

<211> 663

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(663)

<223> n = A,T,C or G

<400> 478

tttttttaag ctttcacaat ttttattaaa tcctagtcta nttgaacaat atctgatgtt 60

```

acagacatca tcccatggtg aacatgttta ataagtgaag gcaagtcaga catctcatct 120
aagtcattat ttctgcaga ctaagcaata actacacaga acactatggg taaacaaaca 180
cctgctcagt ttccacacaa gccatgttgt ttatcaaatt agatctgcta atattgaata 240
cagtagattc ggtgattgta gttctcatat aagtatctta ttgagataac attttgacag 300
tttactgac ttccaaata agcataccat aatcaaagaa aagaataaag agtgaagtaa 360
aaactgaaca tgaagagatt aagttattaa aggaaaatga agtaaataaa aagagtgaag 420
aaccattggg ggtggaagtc aaacaagcct agacatttga ttggaagaga aaagatcaaa 480
tatgaagttc acaaaacaaa agtttataaa ctcaatgcaa tacaatcct ttttattgta 540
aaagctgagt tgaaactaaa agatctataa aaactgttac ttttgccctt aaacagtacc 600
aactcttatg atcaaaaaag gccacacagt taagattgna ttacttgatt ttattttaca 660
cta 663

```

<210> 479

<211> 673

<212> DNA

<213> Homo sapiens

<400> 479

```

gaattcgaac cccttcgaat gaagaactct ccagggatct agtgaataaa ctaaaaccct 60
acatgagctt cctgactcag tgccgtcccc tgtcagcgag catgcacaac gccatcaagt 120
tccttaacaa ggaaatcacc agtgtgggca gttccaagcg ggaagaggag gccaagtcag 180
aacttcgagc agccattgat cggatgtgac aagagaagat tgtgctagca gctcaggcaa 240
tttcacgctt tgcttaccag aagatcagta atggagatgt gatcctggta tatggatgct 300
catctctggt atcacgaatt cttcaggagg cttggacaga gggccggcgg tttcgggtgg 360
tagtggtgga cagccggcca tggctggaag gaaggcacac actacgttct ctagtccatg 420
ctggtgtccc agcctcctac ctgctgattc ctgcagcctc ctatgtgctc ccagagggtt 480
ccaaggtgct attgggagct catgcaactc tggccaacgg gtctgtgatg tcacgggtag 540
ggacagcaca gtttagcctg gtggctcgag ccataatgt accagtgtg gtttgctgtg 600
aaacatacaa gttctgtgag cgtgtgcaga ctgatgcctt ttgtctctaa tgagctagat 660
gacctgatg atc 673

```

<210> 480

<211> 203

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(203)

<223> n = A,T,C or G

<400> 480

```

gaattcgaac cccttcgggg ggaggaagag gaggtggagg aggaggggtga tgttgatagt 60
gatgaagaag aggangaaga tgangananc tcctcgagg gcttgaggc tgaggactgg 120
gccagggag tagtgaggc cgntggcagc ttcggggctt atggtgccca ggaggaagcc 180
cantgccta ctctgcattt cct 203

```

<210> 481

<211> 482

<212> DNA

<213> Homo sapiens

<400> 481

```

ccagacgctg cccatggagg cgtccagcga gccgccgctg gatgctaagt ccgatgtcac 60
caaccagctt gtagattttc agtggaact gggataggct gtgagctcag acacttgacg 120
atctcttaag tacccttacg ttgcagtgat gctaaaagt gcagatcatt caggccaagt 180
aaagaccaag tgctttgaaa tgacgattcc acagtttcag aatttctaca gacagttcaa 240
ggaaattgct gcagttattg aaacggtgtg aagacggatt ctttggttga taaattgcta 300

```

tcattctaaa gtcattggact tcacttttcgg caacaaaact aaataaggat ggaacattta 360
ttgaatgaaa aatgcacttt tgtttttcca tttttttaaa taataaaaaat cagacaaaca 420
gaaaaaaaaa aaaaaaaggg cggccgctcg agtctagagg gcccgtttaa acccgctgat 480
ca 482

<210> 482

<211> 505

<212> DNA

<213> Homo sapiens

<400> 482

aaaatcttta gctgccaaaga aagaagttaa gactctcagt gctgagagag actgaatcca 60
cctaggtagt aaggtagact gaccagtaa accctttgtg tgctgggggg ttttatgcct 120
tgtagaaccc agtgtgagca agatttggtg accctacata cattcagtag ccaggaaaag 180
gtgattggat tgccagactc tgcctgctgg caaaaggatg agctgtagaa gctgaagtcc 240
taggtagtag atataaagaa gacaaattag gtggcacctt ctgactgtg caatgcatgg 300
atttggaatt gaatttttcc tctaattatt ctagggaac cctgggctaa gaaaccaatg 360
taaaacctga tgaggtagtc tgtagtcaca ctgggtagag gtagaggcaa ccacaaaatt 420
attcttaaga atgcctccca ggcgcctgga agatgaaact ttctggtgaa tatgagctca 480
tggtaaaaat ttaggtcgga tgcag 505

<210> 483

<211> 501

<212> DNA

<213> Homo sapiens

<400> 483

tgcaaaaagg taacaaattc ataactggaa agcaaagaga agaacaagta tgatttggat 60
gataaagcat tgttttaatg gtgaaaactt cacagatcac taatgtttct agaggttaac 120
ttcaagtggg caagctgggg tttttaggta gtcagtggcc tagttcctaa agccacagta 180
taggatctgt taaactgaat gtctgttgaa agtttgtttt agctgcttgg aggcttcctt 240
ttaagacaaa ctgtatgtga ttaagttgtt ttgagggaaac tgaagaacct gatgtagccc 300
ctggccagat aactgcctga tttctcagat attattttctc tgggaaacat tctacatagc 360
acaggagctt aagagtggca ttatcttctc gccttaattt ccagagatta tttctgtact 420
gagaatcctg gaactactat gctaggaaat ttaaagctgc atggtctgtc ttgttttcat 480
ttaattattg tgaataoccta g 501

<210> 484

<211> 501

<212> DNA

<213> Homo sapiens

<400> 484

gcactaagac caccttctat gaggagcagg gtgactacta cagccagtag atccgggcct 60
gcttggaaca cctggccccc gactccaaga gttctgggaa ggggaagaag cagccttctc 120
ttcattacac tgctgctcag ctccctggaaa aggggtgtctt ggtggaaatt gaagatcttc 180
ccgcctctca ctccagaaac gtcatctttg acatcacgcc gggagatgag gcaggaaaag 240
ttgaagtaaa tgccaagtgc ctgggtgtgg acatggagcg atttcagctt cactatcagg 300
atctcctgca gctccagtat gaggtgtggt ctgtcatgaa actcttcaac aaggccaaag 360
tcaatgtcaa cttctctatc ttctctctca acaagaagtt tttgcggaag tgacagaggc 420
aaagggtgct acccaagccc ctcttacctc tctggatgct ttctttaaca ctaactcacc 480
actgtgcttc cctgcagaca c 501

<210> 485

<211> 504

<212> DNA

<213> Homo sapiens

<400> 485

```
cgcactcttg gaacattctt tctttcaaca acccaaggca tgcttctatc tccttttgag 60
gtttccctct aagtgttacc tctaagatag gcttttcctg gacactctat gatggaacct 120
ctaggatttt ctctattggt ttatgcttat ttgatattt gattcctaga attttaaata 180
cattatatat catataaaat aaacctttaa atattgaaat gaaaagataa aaatacatat 240
actaagtga taggtcaaaa gtgtgagatc atcttgaaca ttatcttgaa gagaagatac 300
caatttacct tctgctcaga tcatgggtga cgatatcaca acctgcctag aataactctc 360
cttttctgaa ccattttattc actacttttg tcttccaatt aaatatttagc ctgacttcaa 420
atatcatata ttagtttcct ttgtttatgt aattgaatta tataacatat attcattaga 480
gcctattttt tttaaaattt ttgt                                     504
```

<210> 486

<211> 501

<212> DNA

<213> Homo sapiens

<400> 486

```
gagaggtcac tatggcgctt ttctgcagga cgagtgggac ctgctccaaa gaatgatttt 60
gctggcccac gagaaactct ctgttcctgt cacgtgcaaa atccgtgtct tcccggagat 120
tgacaagacc gtgaggtacg cccagatgct ggagaaggcc ggctgccagt tgctgacggg 180
gcacggacgc accaaggagc agaagggggc cctgtcgggt gcagcgtcct gggagcatat 240
caaggctgtg cggaaggctg tggccatccc tgtgtttgct aacgggaaca tccagtgcct 300
gcaggacgtg gagcgtgcc tccgggacac ggtgtgacag ggcgtcatga gcgcagaggg 360
caacctgcac aaccccgccc tgttcgaggg ccggagccct gccgtgtggg agctggccga 420
ggagtatctg gacatcgtgc gggagcacc cgtccccctg tcctacgtcc gggcccacct 480
cttcaagctg tggcaccaca c                                     501
```

<210> 487

<211> 501

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(501)

<223> n = A,T,C or G

<400> 487

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accattattt agcagcaaaa aggaaagttt gaagacatta acaggaactg gtttaattgta 60
gtccttatct gaaaaggaca gattgaatgc agccaaatta tggcaaagaa atcagtagga 120
caacccctat aaagggtagt tcttttaaaa aaaatttctt tattggcaac aacataaaaag 180
atatgaaaga atcactcata atttatcagc ataacatagc tattctcatt ttgcaattg 240
actttttagt tcttgaccaa atgtaatttt tattagtgtt gattaactga ttttgtgctt 300
tttttaaaaa aaaaaaaaaa ctagaataag acatttgttt tgtaattat tataaatgac 360
tgtattcatt ctgtttatgt accataattt tggatgttcc tacgatgtta aacttttagg 420
ttgtttttaa ttgtttgttc ttatagacaa ctctgtaagg gnttttaact gcttttatca 480
ggagaatgtc aaagaagtcc t                                     501
```

<210> 488

<211> 148

<212> DNA

<213> Homo sapiens

<400> 488

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attctaagga tgaaatggct acagagcaaa ctgcagctga gagaaaactg cttggagttt 60
ggacagaggt ggaattgagt gtccacaggc cagctgagga ggtggtaccc agcactctat 120
gaacccttcg ctcaagtcag cctggagt                                     148
```

<210> 489
<211> 501
<212> DNA
<213> Homo sapiens

<400> 489
gctgtggatt cccctccaag tggaggagga tgggcaggct ggggatcctg gggcaaactct 60
ctgctgtcgt cagcatctgc cacagtaggt catggattga cggcagtcaa ggaaaaagca 120
ggagccactc tacggattca tgggtgtaaat tctggatctt ctgaaggagc ccaaccaaact 180
actgaaaacg gagtccctga aataacagat gcagccacag atcagggccc tgcagaaagc 240
ccaccactt ccccttcacg agcctctcgg ggtatgctgt ctgccatcac caatgtggtt 300
caaaacacag gtaaaagtgt cttaactgga ggccttgatg cgttggaatt catcggaag 360
aaaaccatga atgtccttgc agaaagtgc cggggcttta agcggacca gacgctcatg 420
gagagaactg tttccttgc tcagatgta aggaagcta aggagaagga gaagcagaga 480
ctggcacagc agctcacgat g 501

<210> 490
<211> 482
<212> DNA
<213> Homo sapiens

<400> 490
attgcaaact gaaagtggac aaagacttaa ggtaaactg ctctcatgg tggaatgctt 60
ccaaatgctg gaaggaggac tttagggcag agttcactaa ggaggcttgt gcttatagat 120
cagtgggcct gaaagaagtt tctctaggtt ctgggtgtgt gctgtacgag gtgtaggtag 180
taataatact cttgtcagcc acagtgaagc cccaagctag cgggtagag ggactgacct 240
tgtacaggca gcatggagaa actaagacag agtgtcctgc ccaagtgtg gcaactggga 300
gcagtcactc aggtttattt ccaccagggc ccaagaaaaa aagaaatgag gcaacctaaa 360
attccatcaa gatagatacc aatatccaag gtgcttggtc ttagcgggtg gggaccacg 420
ttaaggtctt tgggtggaag gtgggaggtg ttttcagcat gagatagggt tcaggctgtg 480
aa 482

<210> 491
<211> 483
<212> DNA
<213> Homo sapiens

<400> 491
cgctctccc cgtgatccct ctctcgtaa ccgtaggcgc ttttcgtgaa ggcccgggtt 60
tttacagcac ttcgttttcc taaccacgaa cagtgtcgt tcgttcgcag ggccagcaag 120
gagagccccg cccccgcccg ccgccgccg ccgccgccg gccgccttg gatcccgcg 180
actccgcccg gcccgccctc ccagggcatg gcgccgtgc gcttctccgc caatctgtcc 240
tggctattcc ccgagctccc cggcctcccc gcgcgggtgc gggcgcggg cagctcgggc 300
ttcgaggccg tcgaggtggc ctggccgtac gcggagacgc ctgaggcgt ggcgcgcgcc 360
gcgcgagaag cggggctgcg gcttgtactg atcaacacgc ccccgggaga ccaagagaag 420
ggggaaatgg ggctgggggc cgtccccggg agacaggcgg ccttccgaga gggactggag 480
cag 483

<210> 492
<211> 266
<212> DNA
<213> Homo sapiens

<400> 492
acctcatctg ctttgctttg gcatgtgagc cttgcctaag ggggcatatc tgggtcccta 60
gaaggcccta gatgtggggc ttctagatta cccctcctc ctgccatacc cgcacatgac 120
aatggaccaa atgtgccaca cgctcgctct tttttacacc cagtgcctct gactctgtcc 180
ccatgggctg gtctccaaag ctctttccat tgcccaggga ggaaggttc tgagcaataa 240

agttttcttag atcaatcaaa aaaaaa

266

<210> 493

<211> 483

<212> DNA

<213> Homo sapiens

<400> 493

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gccgctcgcg ctaggagagc gggcttcggg cacttgacat ggcggcagtg gcggcgactg 60
cagcagcgaa ggggaatggg ggcgggcggtg gcagggcgcg ggccggggac gccagcgcca 120
cgcggaagaa gaagggcccg gggcccctgg ccacggcgta cctggtcac tacaatgtgg 180
tgatgacagc cgggtggctg gttatagcgg ttggtctggt ccgagcatac ctggctaagg 240
gtagctacca tagcctttat tattcaattg aaaagccttt gaaattcttt caaactggag 300
ccttattgga gattttacat tgtgctatag gaattgttcc atcttctgtt gtcctgactt 360
ctttccaggt gatgtcaaga gtttttctaa tatgggcagt aacacatagc gtcaaagagg 420
tacagagtga agacagtgtc ctctgtttg ttattgcatg gacgatcacg gaaatcatcc 480
gtt 483
```

<210> 494

<211> 301

<212> DNA

<213> Homo sapiens

<400> 494

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gtggctattt tcatggaata tttttatca gcctttcagt ttttaatttat ttgtgtcttt 60
ggatctaaag tcagtttggt ttggacaatg tgtagtttga tcatgatttt aaaaaatcta 120
ttctgaagct ggggtggttca cacctgtaat ccagcactt tgggaggatc tcttgagccc 180
aggagtggga gactagcctg gtctacaaag tgagactctg ttctacaaa aaaataaaat 240
aaatagttgg gtgtggtggt atgcgcttgt ggttcagct acttgggagg atgagggagg 300
a 301
```

<210> 495

<211> 496

<212> DNA

<213> Homo sapiens

<400> 495

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cgaagtgaag gctagggggc cgtacgcgcc cgcctgactg tgcgcagcag ctctcggcg 60
gccccaccgc agccgccgct ccctgaggcg cgggaggccc gcgccccgcg gctcgtgtg 120
cgtgggaggg cgcgagcgaa cgcgggcgag gagcggccga gccgctgaag aggagctggg 180
cgccggccgc ccggccgcgc tcggcccgcg gatcgctcc gcccggtctt cgccggcccc 240
ggcccctggc gagatgccgt gtggggagga ttggctcagc caccgctgg gaatcgtgca 300
gggattcttc gcccaaatg gagttaatcc tgactgggag aagaaagtaa ttgagtattt 360
taaggaaaag ctgaaggaaa ataatgctcc taagtgggta ccatcactga acgaagtccc 420
ccttcattat ttgaaaccta atagttttgt gaaatttcgt tgcattgattc aggatatgtt 480
tgaccctgag ttttac 496
```

<210> 496

<211> 494

<212> DNA

<213> Homo sapiens

<400> 496

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aaactatata aaaagtgatt tgtacagaac tttatttttag ctctttttta aaaatgattt 60
gcatggttag aaaacggcga ggacagccag gggagggaag ggcctctagg gaactttgca 120
ctttctatac ctttgacta tgcactgcc tattgattct acaccaata atgatattac 180
ttgaacccat ctgtaagaaa ctgcttcgga aattcatttg tgtgtatgta aataacacaa 240
catagaaaca ggaagggaaa aaagtctgca gtaatgcacg ttttttttt ctttcctgtt 300
```

tatcttcgggt tttgcttttaa gtcctttttat ttttaattcc ctttttggtt ttctttttgg 360
gttttggttc cttttgggtt tatgggtgcc ctgatactcc agcagagatc agaaggctac 420
agatccattc tatccatccg ttatgtggct ttgccatccc agcttgaggt gtctttacaa 480
agataataac agtt 494

<210> 497

<211> 184

<212> DNA

<213> Homo sapiens

<400> 497

gcgcgcgcgc gctggcaggg tgtgcgtgag tttgggtggcg gccggctgtg cagagacgcc 60
atgtaccggc tcctgtcagc agtgactgcc cgggctgccg ccccgggggg cttggcctca 120
agctgcggac gacgcggggg ccatcagcgc gccgggctgc cgctctcgg ccacggctgg 180
gtcg 184

<210> 498

<211> 471

<212> DNA

<213> Homo sapiens

<400> 498

tcttactaca aatggagatg gctattatga aacagcatga gcatgagcct tttatctttt 60
atacttagtg atatactttg cttgaaaatc actcagcaaa gtagttcaca tgatgtgat 120
catatttgaa gtgtggtttt tctcaaaatc attgacttta aggagctcat ttctgaacaa 180
aaagggtttgc tctgtggaaa aatcaatcac tgccaggatt ctttcatttc tgtactattt 240
tgtataattg aatttgttca cttctctcac accagcaagt gttttacagg tgccttggat 300
taaaacaaaa ttgattttta aatttttatg taagtattg tgtctatgat gccactttta 360
aaaggaaaat gcaattgcgt aatggcttat atccttattt aatgtaccta tttgtgttct 420
aataattggt tgaatgtttt attcagctta aaactttacc atgaagtcac a 471

<210> 499

<211> 478

<212> DNA

<213> Homo sapiens

<400> 499

agggtgggaaa agcggaggag gacgcccagg aggaggcggc ggcgggcgcc gggaaagtga 60
aggctctgca aagttcagcg gcggtctgcg gcgcgcagcc ccgggctagc ggagacgag 120
ccgcagggc cgtccgcgg ggcagcgcag ccaggccggc tatggtcccg gggtcccgc 180
cgccccccag gtgcccggga ccgcgccaggc cgggtgcgcga gggtcaccac acctccccgc 240
gcggtcccgc cccttggtc ccagctgccg gcgaccgctg accgagcccg gcgccccagg 300
aggaggaaga aaccaggggc ccgttcctc ccgaggacgg cggcgcttca tcccgcagcc 360
cagagggtctc ggtccctcc ggcacccgcc cggcccggt gctcccggt cctcccgcc 420
atggggagct gcgcgcggct gctgctgctc tggggctgca cgggtggtggc cgcaagga 478

<210> 500

<211> 495

<212> DNA

<213> Homo sapiens

<400> 500

gggggcttct ggcttggtgt ggaccaggag ggggcagaag gcacctgtc gtggctgggc 60
accgtcttcg gcgtgtggc tagcctctgt gtctcgctca acgcatcta caccacgaag 120
gtgctcccgg cgggtggacg cagcatctgg cgctgactt tctacaacaa cgtcaacgcc 180
tgcgtcctct tcctgccct gctcctgctg ctccgggagc ttcaggccct gcgtgacttt 240
gccagctgg gcagtgccca cttctggggg atgatgacgc tgggcggcct gtttggttt 300
gccatcggct acgtgacagg actgcagatc aagttcacca gtccgctgac ccacaatgtg 360

```

tcgggcacgg ccaaggcctg tgcccagaca gtgctggcgg tgctctacta cgaggagacc 420
aagagcttcc tctggtggac gagcaacatg atggtgctgg gcggctcctc cgcctacacc 480
tgggtcaggg gctgg                                     495

```

```

<210> 501
<211> 494
<212> DNA
<213> Homo sapiens

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<400> 501
ctgcggtgtg gttggtggtg agatgacgac cttagtgtctg gataatggag cttacaacgc 60
caaaatcggt acagccatga aaatgtgtcg gttattccta attgtcagtt ccggtcaaaa 120
acagcacgtc ttaaaacttt tactgccaac cagatagatg aaataaaaga cccttctgga 180
ctcttttaca tcctcccttt tcaaaagggc tacttggtga attgggatgt tcagagacaa 240
gtttgggatt acctttttgg aaaagaaatg tatcagggtt attttttaga tactaatatt 300
attatcaactg aaccataactt taacttcact tcaattcaag aatcaatgaa tgaaattcta 360
tttgaagaat accagtttca agcagtatta agagtaaag ctggggctct cagtgcacat 420
aggtatttcc gagataatcc ttccgaatta tgctgtatca ttgttgatag tggatattcc 480
tttacacata tagt                                     494

```

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<210> 502
<211> 479
<212> DNA
<213> Homo sapiens

```

```

<400> 502
ttgtataatg ctgaatgtgt ccagaggggac aagtttgcag aacctcatat tggatatatta 60
aagaaataat aaaataaaaa agcacttttag gttattttat ctttaacccg attgctgcaa 120
tttcttttgt gtgtatatat acatatatat actttccaca aagttttatt ttttgctcag 180
aataaaaagt taaattgagg tgtgaaaaga aaagcactta ccttggtgca atatgtgtag 240
cttgatggtc gttgtcccat gtggccctgg cctggcagcg tttttccgct caatcagccc 300
tgtgctgtga gattgtccat agggaaacac tattatgcat tctcagcaac cgctcaatct 360
atgcaagcct tccctgtgtg ccccagggcg cccctcagg ctctctgaag aactgctgtg 420
ggtcctgttt tctgctgact gttgaggccc tttttcatca cttcttggtc tctcgccat 479

```

```

<210> 503
<211> 451
<212> DNA
<213> Homo sapiens

```

```

<400> 503
ttgtgggccc ggtgggtttc ctaatctggt ttcgtctgcc tggttcatct gtgtgcatg 60
gctccggact cggatccctt ccctgaaggg ccgctcttaa agctgctacc cttagacgct 120
agagaccggg gcaccacgag ctgccgctg gggccggccg ccctccacgc cctgggcgag 180
cgcttgggct cggcagtgaa gatctcgcta cccgacggcg gctcctgcct ctgcaactgcc 240
tggcctcggc gggacggagc ggacggcttt gtgcagctgg acccgctgtg cgcgagcccc 300
ggggcgggcg tcggggcgtc gagatcccgg aggagtctca gcctgaatcg cctcctccta 360
gtgccctgtc cggccctgag gcgcgtcgcc gtgtggccgg tgttgcgaga gcgggcaggc 420
gcgcccgggt cccggaatac agccgcggtg c                                     451

```

```

<210> 504
<211> 462
<212> DNA
<213> Homo sapiens

```

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<400> 504
cagtggggaa ggggagagat gccgaggtgg tcagtatcct gactttcaga ggcctttttt 60
tgtttggttt aatttttgct agattgatat taaaaactca tgtggaggaa ctcaaggaat 120

```



```
gtttagaaga ccaaaagtcc ccaatgacag gaacaaaagc aaccaatttt taactttctc 180
ttctcattcc tgttttcatt gatttcccac atgtagtcct ttgctcagg aagtctttgg 240
ggaaattaag gatctttgaa gctctgaaat aggtgatcag gttagtggg tctgtcagct 300
gtctaagagg ttggaaaatg aactactcaa gatagtcacg aaaatactga aagtttgatt 360
tttctttcca tatttgaatt aattttttct gtttgactgg aaggggtttt tgtataacta 420
aaacctcagc gcataaagga gatttaaaag gagcacatga tt 462
```

<210> 505

<211> 136

<212> DNA

<213> Homo sapiens

<400> 505

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tcgattatat cacacatttc agttgggagg ttgtctcaac ctgtgaccac catctgagtt 60
agctggcaga cttctaggag gtcctgtctg aggtagaatc agaaatggct tccctccttc 120
tcccataaaa aaaaaa 136
```

<210> 506

<211> 466

<212> DNA

<213> Homo sapiens

<400> 506

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gggggtacaga gacagcagcc tgcgagagcgt tctaggcagg acagggcagc aaacctgaca 60
tgcgagagctg ggggcagggg taatggggcc agggggtaat ggcagggtgag gccatggcct 120
agaggggtgc catgcttggg gcaggggagg agaggcccag gtgtggctgc agtggcagca 180
ggagtcagtg tggtctgtcc cagtgggatg ttgtcagaga atggacctgg ctgctgggaa 240
aggtgattgt gtttgtctga gccacactgg actcttctct gaccagcaag cacattcttg 300
agatgcgggg cagagacgag gcctccgtga gaacctttga ggtgtgaggg ccttgatctg 360
gggtgcagcc tccagcttct tgcttacaga gcaggacctg caggagctcg ctgactgcct 420
gcacagtggg aggaagacct gtttctttta ctttccttga ggagaa 466
```

<210> 507

<211> 101

<212> DNA

<213> Homo sapiens

<400> 507

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atgatttaaat tttttaaaact gtagcaattg gatagataat tttatttgaa attttacaca 60
ctgaaagctc taaataaaca gatacattca cattcaaaaa a 101
```

<210> 508

<211> 242

<212> DNA

<213> Homo sapiens

<400> 508

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gacaatgcaa gtaacctcaa atgagagtgt ggaaaggcgg gaaagcagcc agagcttcat 60
tgttatgaaa aaagagtga atgtgctctg ttgaagagtt gaagaatgaa caaaggatat 120
ttagtttgaa tggaagctca gtaatgagaa atgagaatgg ttgagttctt aaaagaagca 180
agtaaagaag aggatttgtg ggctactatt ctcatcagtg gaatctcatw ccacccttgc 240
ct 242
```

<210> 509

<211> 101

<212> DNA

<213> Homo sapiens

<400> 509

cctttgctcc ctttttccaa tttcttattg catatctttc tgtattacaa caaaatgata 60
tgcaataaga aattggaaaa agggagcaaa ggcgaagggg y 101

<210> 510

<211> 461

<212> DNA

<213> Homo sapiens

<400> 510

gcaggttcgg gaccatgagt tggattcctt ttaagattgg gcagcccaag aaacagattg 60
tgcccaaaac agtggagaga gactttgaaa gggagtatgg aaaacttcag caccatgtca 120
aaatctgccg tgaagatata cttggactta ctctccaatc ccctctgtga gcaagaccag 180
gaccttctga acatggtgac ggccctggac acggccatga agcggatgga tgccttcaat 240
caggaaaagg tgaaccagat ccagaagact gtgatcgagc ccttaaaaaa gttcggcagt 300
gtcttcccga gcctcaacat ggctgtgaag aggcgggaac aggccttgca ggactacagg 360
aggctgcagg ccaagggtga gaagtatgag gaaaaggaga agacggggcc agtgctggcc 420
aagctccacc aggcacgaga ggagctgcgg cctgtgcggg a 461

<210> 511

<211> 461

<212> DNA

<213> Homo sapiens

<400> 511

ggctttctga tatttctaaa attgacctgg aatcaaccat tgacatgtcc tgtgctaaat 60
atgaattcac tgatgccctg ctgtgccatg atgatgagct ggaagggcgc cggattgcct 120
tcatacctgta cctggttcct ccctgggaca ggagcatggg tggtagccctg gacctgtaca 180
gcattgatga acactttcag ccgaagcaga ttgtcaagtc tcttatccct tcgtggaaca 240
aactggtttt ctttgaagta tctcctgtgt cctttcacca ggtgtctgaa gtgctgtctg 300
aagaaaagtc acgtttgtct ataagtggct ggtttcatgg tccatcattg actcggcctc 360
ccaactactt tgaacccccc atacctcgga gccctcacat cccacaagat catgagattt 420
tgtatgattg gatcaaccct acttatctgg acatggatta c 461

<210> 512

<211> 686

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(686)

<223> n = A,T,C or G

<400> 512

actgacctga aggagacctt agagtccttt ccctttttga gtttgaatca tagccttgat 60
gtggtctctt gttttatgtc cttgttccta atgtaaaaat gcttaactgc ttcttggttg 120
tattgggtag cattgggata agattttaac tgggtattct tgaattgctt ttacaataaa 180
ccaattttat aatcttttaa tttatcaact ttttacattt gtgttatttt cagtcagggc 240
ttcttagatc tacttatggt tgatggagca cattgatttg gagtttcaga tcttccaaag 300
cactattttg tgaataaact tttctaaatg tagtgccttt aaaggaaaaa tgaacacagg 360
gaagtgactt tgctacaaat aatgttgctg tgtaagtat tcatattaaa tacatgcctt 420
ctatatggaa catggcagaa agactgaaaa ataacagtaa ttaattgtgt aattcagaat 480
tcataccaat cagtgttgaa actcaaacat tgcaaaaagt ggtggcaata ttcagtgcct 540
aacacttttc tagcgttggt acctcgccgc gaccacgctg gaattccgga agggcctgtc 600

ctangatcca gtgtggtgga attctgcaga tatccagcac agtggcggn cgtcgagtct 660
 aaanggcccg ttttaaccgc tgatca 686

<210> 513
 <211> 429
 <212> DNA
 <213> Homo sapiens

<400> 513
 catgaacgac accgtaacta tccgcactag aaagttcatg accaaccgac tacttcagag 60
 gaaacaaatg gtcattgatg tccttcaccc cggaaggcg acagtgccta agacagaaat 120
 tcgggaaaaa ctaggcaaaa tgtacaagac cacaccgat gtcattcttg ttttggatt 180
 cagaactcat tttggtggtg gcaagacaac tggctttggc atgatttatg attccctgga 240
 ttatgcaaag aaaaatgaac ccaaaccatg acttgcaaga catggcctgt atgagaagaa 300
 aaagacctca agaaagcaac gaaaggacg caagaacaga atgaagaaag tcagggggac 360
 tgcaaaaggcc aatgttggtg ctggcaaaaa gccgaaggag taaagggtgt gcaatgatgt 420
 tagctgtgg 429

<210> 514
 <211> 346
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(346)
 <223> n = A,T,C or G

<400> 514
 aaaactttct ctacttattt agttttntcc tctgagttca accgctgctg gattcgtttg 60
 gcataacttt gtgccatgga gttaatgata gataggatga agtaacacac catgacaacg 120
 accaactttt caaacatcca ggacaaccag ttttctccct gtggtgtgcc catttcgctt 180
 ttgtggtgaa gcttctgccg ttgagcctcc aggtactcct gaaatggctt ctgcagagat 240
 ggacctatgc cggggacagc actggaagca ggggtacagta gcccaaagaa aaagacacat 300
 ttgggaagaa aagcaggaaa aacgttaaaag aaaatgtact taccac 346

<210> 515
 <211> 549
 <212> DNA
 <213> Homo sapiens

<400> 515
 ctgaccagga ctgtgaagat gcggttccgc tgcgaagatg gggagacatt ttccaggaac 60
 gtcagtatga tccagtcttg caaatgcaac tacaactgcc cgcattgcaa tgaagcagcg 120
 tttcccttct acaggctggt caatgacatt cacaaattta gggactaaat gctacctggg 180
 tttccagggc acacctagac aaacaaggga gaagagtgtc agaatcagaa tcatggagaa 240
 aatgggcggg ggtggtgtgg gtgatggaac tcattgtaga aaggaagcct tgctcattct 300
 tgaggagcat taaggatatt cgaaactgcc aagggtgctg gtgcggatgg aactaatgc 360
 agccacgatt ggagaatact ttgcttcata gtattggagc acatgttact gcttcatttt 420
 ggagcttggt gagttgatga ctttctgttt tctgtttgta aattatttgc taagcatatt 480
 ttctctagc ttttttcctt ttgggttctt acagtcgtaa aagagataat aagattagtt 540
 ggacagttt 549

<210> 516
 <211> 382
 <212> DNA
 <213> Homo sapiens

<400> 516
ccgctcgtca gactccagca gccaaagatgg tgaagcagat cgagagcaag actgcttttc 60
aggaagcctt ggacgctgca ggtgataaac ttgtagtagt tgacttctca gccacgtggt 120
gtgggccttg caaaatgac aagcctttct ttcattccct ctctgaaaag tattccaacg 180
tgatactcct tgaagtagat gtggatgact gtcaggatgt tgcctcagag tgtgaagtca 240
aatgcatgcc aacattccag ttttttaaga agggacaaaa ggtgggtgaa ttttctggag 300
ccaataagga aaagcttgaa gccaccatta atgaattagt ctaatcatgt tttctgaaaa 360
tataaccagc cattggctat tt 382

<210> 517
<211> 323
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(323)
<223> n = A,T,C or G

<400> 517
acgagcgtag gacgatgctt ctcttntgtc agcctgcaac tgagtcagga ttgaatactt 60
ggacccaggg tctggagatt gggatactgt aatgcttctt tgttattata acataaaagc 120
accactgttc tgttcatttc ctactgtgtc taattaagaa aactattaag atgagcaacc 180
acatttagaa atgtttattg acaggtcttt tcaaataatg cttttctaata taatagccaa 240
agatttcata tctaactttg taaccagaat tatacagtaa gttgacacca cttagattta 300
aaggcagaca gttttgcttt agt 323

<210> 518
<211> 605
<212> DNA
<213> Homo sapiens

<400> 518
ctggataccg aggctggggc cccacactgt ggaacaaacc cacagcttgc tcaggatcca 60
tcccagaatc agcagacatc aaatccaacg cacagttcag aagatgtgaa gccaaaaacc 120
ctcccgtctg ataaaagcat taaccatcag atcgagtctc ccagtgaag gcggaagtct 180
ataagtggaa agaagctgtg ctcttcctgt gggcttctt tgggtaaagg agctgcaatg 240
atcatcgaga ccctcaatct ctattttcac atccagtgtt tcagggtgtg aatttgtaaa 300
ggccagcttg gagatgcagt gagtgggacg gatgttagga ttcgaaatgg tctcctgaac 360
tgtaatgatt gctacatgcg atccagaagt gccgggcagc ctacaacatt gtgacacggc 420
tttcaagctt ccggtact caccatttct ttactgagag tgtcccctgg caactgctta 480
acaaaatccc aagctcaggg gcttctcagc atttacctaa tttctgaaag gctcttctga 540
aagggtggtat ctgttctttc gtagcacagt gtttatgttt ttctgttta ttgggttggg 600
ttttt 605

<210> 519
<211> 462
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(462)
<223> n = A,T,C or G

<400> 519
ctgctgggtca tgnccctggc agtcttttgt gcaaaataag gcatattnga gctccacatt 60
aaccttgccg caggcgncta cttgctctgc atgctgtanc agngcacgct ctccttcccc 120

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ttggtggtgt agcctgngan aggetgceca tacttatcca cacaccagca naagccccgc 180
ttcctgcctt tggaagggcg acactgcttt ttcttataaa atcccttctt gtcacagttg 240
ggaatgtgna cccccctggg actcagcaca ttgaggaact tcaagtgatt cagtgtgnct 300
tccatttctc tacggcangn accatattct gtctcccgtc tggactcgga ggagaagttc 360
tgggtatctg tgctctgaga ctgtagtca actttgtagc gctggctgnc tttagcatgc 420
cctttcttga tgatgantat ctttgaatgg agggggtgga ac 462

```

<210> 520

<211> 565

<212> DNA

<213> Homo sapiens

<400> 520

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actcgtaata aatatgcatc cggaaacaag ataaaaggct acacctcgtc aggcatccta 60
caaaaatgtc tcaagtttta tatactctgc agcatttctg tgcgggggca gaaggggctg 120
ttgtgtatct tctgaagtgc tgtgacaaaa ggctctttca catttctttg gagcattttt 180
gaaattgctt aactataatt aaacaactta agaaaagtaa caccaagctt taaagccatt 240
tttgctttgc tgtcatttgt ctttatccaa tacagatcaa catatcatcc agcacagcca 300
agcaccactt gaggccaagc agccttgtgg gacatgggcc ctgtcagagc aggccttact 360
ttcagttaaa tactttggag agtccaggat tctgtctctc tccctcaaca agattaatgc 420
cataagggaa gttgcaagcg tgttagaaac atttttaacc tgaaagtaaa gtgaacagaa 480
atattttttt ttccgagacc tctgctatgc accataatat taccatatca gggtttttag 540
cttcaaagtt gaaaaacaga ttggt 565

```

<210> 521

<211> 127

<212> DNA

<213> Homo sapiens

<400> 521

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acatggctga cgtcaccgtc cagtgcacaaa tcaaaaaaga aagaaagaaa aaccccaaaag 60
aaagaggatt ttctcagtga gaacatggtg ggctgattag gcttctatta gattacattc 120
atttcac 127

```

<210> 522

<211> 642

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(642)

<223> n = A,T,C or G

<400> 522

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actatgtttc gtaaattaaa taggtntggc ccagaagacc cactcaattg cctttgagat 60
taaaaaaaaa aaaaaaaaaa aaagaaaaat gcaagtttct ttcaaaataa agagacattt 120
ttcctagtct caggaatccc ccaaatcact tcctcattgg cttagttaa agccaggaga 180
ctgataaaaag ggctcagggt ttgttcttta attcatatc taaacattct gctttttatta 240
cagttaaatg gttcaagatg taacaactag ttttaaagggt atttgctcat tgggtctggct 300
tagagacagg aagacatatg agcaataaaa aaaagattct ttgcattha ccaatttagc 360
aaaaatttat taaaactgaa taaagtgtct ttcttaagt cttgaaagac gtaaaccaaa 420
gtgcacttta tctcatttat cttatgngg aaacacagga acaaattctc taagagactg 480
tgtttcttta gttgagaaga aacttcattg agtagctgtg atatgttcga tactaaggaa 540
aaactaaaca gatcaccttt gacatgcgtt gtagagtggg aataagagag ggctttttat 600
tttttcgttc atacgagtat tgatgaagat gatactaaat gc 642

```

<210> 523

<211> 244
<212> DNA
<213> Homo sapiens

<400> 523
ctgaaggagc tgatccagaa ggagctcacc attggctcga agctgcagga tgctgaaatt 60
gcaaggctga tggagacctt ggaccggaac aaggaccagg aggtgaactt ccaggagtat 120
gtcaccttcc tgggggcctt ggctttgatc tacaatgaag ccctcaaggg ctgaaaataa 180
ataggggaaga tggggacacc ctctgggggt cctctctgag tcaaaccag tggtgggtaa 240
ttgt 244

<210> 524
<211> 407
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(407)
<223> n = A,T,C or G

<400> 524
acgttagtg tgatgtcacc caccctnnng ctggggccga ggatgctctc attgtgcact 60
gcgtagatga ctctggccac tggggcagag gtggtttatt tacagctctg gaaaagcgat 120
ccgctgagcc aagaaaaata tatgagctgg ctgggaaaat gaaagacctg agtttgggag 180
gtgtcctttt atttctgtt gatgataaag aatcaagaaa caaagggcaa gatttgttgg 240
ccttgattgt ggctcagcat cgtgatcgtt ccaatgtcct gtctggcatt aagatggcag 300
ccctagaaga gggcctgaag aagatatttt tagcagcaaa aaagaagaaa gcaagtgttc 360
atcttcacg tattggacat gccacgaaag gttttaactg gtatggt 407

<210> 525
<211> 276
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(276)
<223> n = A,T,C or G

<400> 525
acacaggagg caacgtgttt cacatnatag acttcacttc caactccttg gaatgttcat 60
ttcttttgct tacaggagag actagacagg aaggccaggc aatgcttagg caactaaaat 120
gaggttgggg gtaatgctaa cgtcaccttc acagggatgg ccacggggac tgttattcgc 180
aagctggttt tctagacctg ttagctggaa gcatgggtgag caccatttct ggacgctcag 240
gccgtgtcgg gcttcagtca tctccaccac acaggt 276

<210> 526
<211> 288
<212> DNA
<213> Homo sapiens

<400> 526
acaattaccc accactggat ttgactcaga gaggaccccc agagggtgtc tccatcttcc 60
ctatttattt tcagcccttg agggcttcat tgtagatcaa agccaaggcc cccagggaag 120
tgacatactc ctggaagtcc acctcctggg ccttgttccg gtccaagtct tccatcagcc 180
ttgcaatttc agcatcctgc agcttcgagc caatgggtgag ctcttcttgg atcagctcct 240
tcagctcctt cttgctcagg gtgtgcttgt caccctccct gccggagt 288

<210> 527
<211> 412
<212> DNA
<213> Homo sapiens

<400> 527
actttgagct tattgttttt attctgtatt aaatatattc agggttttta acactaatca 60
caaaactgaat gacttgactt caaaagcaac aaccttaaaag gccgtcattt cattagtatt 120
cctcattctg catcctggct tgaaaaacag ctctgttgaa tcacagtatc agtattttca 180
cacgtaagca cattcggacc atttccgtgg tttctcatga gctgtgttca cagacctcag 240
cagggcatcg catggaccgc aggagggcag attcggacca ctaggcctga aatgacattt 300
cactaaaagt ctccaaaaca tttctaagac tactaaggcc ttttatgtaa tttctttaaa 360
tgtgtatttc ttaagaattc aaatttgtaa taaaactatt tgtgtaaaaa aa 412

<210> 528
<211> 489
<212> DNA
<213> Homo sapiens

<400> 528
aaatgcaaaa agtcaaagta ggtaacaggt tggtaatata agtgtcagga agactggaag 60
aggcaaaaat caagcagagt tccaataagt gtatgaaaaa aaaaatcata actgaagggt 120
taagaaaagt ccccaaaggc agaatacaca tatgagcagg aggaataaaa agcttttgga 180
tataccaggc agctttctgt acgactcagg ttacagggtg aaattcctca gtttgagttc 240
agaagaattt gaacttattc cagcaaaaata cttcaatctt tttattactg cctcctcccc 300
catcttcttt ctgggcaaaag ggatgcttgg attaggtcca aagctcctgg cagggggagg 360
ggccatgtgt cacagcataa cagacgggtg caagtgcttt actgagcagg ggtcagggtt 420
gcagcaactc tgataggctc acacaatggc ctccatttta cagcccctcc ttggaggccc 480
actgatcag 489

<210> 529
<211> 631
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(631)
<223> n = A,T,C or G

<400> 529
acttgcctaa agtttttata tctgnntctt ctgctgtaaa tcttcccttc ataaatgaaa 60
attttaataa aatcaactat gtggaaatat ataattaaag gaattcacta actgtgattt 120
tcataattta gggacattct ctctagtaga gcatgggtgca ttatttacta gagatataat 180
atgcattaaa acaaaaaatg ttttctatca tcatagaaaa gtttgaggtc cagggataat 240
catctctgga tacattattt cctaccgtcg tggtagacac tgaacacatt tgaggcttat 300
gactggttct tttacttaca aatattgttt agacacattt tcaaattgtc caccaatcaa 360
taataataag gaatggattt tatctatatt gacagttctt tcaaccttaa gagtgaactg 420
ctacaggtaa gattcaatca cttttttcag gagaaagcta ttgagaccaa tatgcttttg 480
ttatctaata ggggtggaat gacttataat gctatttact ccaggcaaaag agaaaataca 540
acagacatag gatcttgatt tcaacgtagt tctcctccat gtgcatttct ctgtccggtt 600
aggcaatgcc aactggtcca ccagtgaaca t 631

<210> 530
<211> 316
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(316)
<223> n = A,T,C or G

<400> 530
acacatttaa atgactcacg agantnaagt ttttttcaaa tatattaaga tcacaccacc 60
ttgttgttta tcgaaagata ttcaaggaga aagatctgac tctccaaact gcatctgaga 120
ttgccacttt aaacagacct catttcaaac atgcaacaac gccactggta ataaagcttt 180
ggaatgggtg ctcattctat tatttcacta caaacagcat agaaagcaag agaagttggg 240
aatttattct aaaatagaat ggaggttgtc atctacagca gcactcctca ctcctctgtt 300
gccattttta gcaagt 316

<210> 531
<211> 296
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(296)
<223> n = A,T,C or G

<400> 531
aaagtatcat ttatttgaaa aacatacatt atcattntgt ttttgatatt tgataatgaa 60
aaaaatcttt gnttgtttat ttctgaaaaa gaactgtatt tagngattat tttagatagt 120
gatattatan cattcatctg tgtgtaaatt atttcatata gggaagagtt ctgatctgta 180
cctatgggtc ttattgaaaa caacattgga tgtgcatttc tgtgatgta tgaatacatt 240
tctactttat ttgaaacat ttgccaaact aaatactgta acactgtata acattt 296

<210> 532
<211> 266
<212> DNA
<213> Homo sapiens

<400> 532
acatatgcac caaattccat tttagaagtt tccatatcat tttcatagaa aacaaagttt 60
gaaaaaaggt aacatttaaa cacagcacgg tattctacca caactgaaac ttttttcttc 120
ttcttcttta caggactcaa caaatcttaa aaatgaacta tgctgtagat ttacctcatg 180
caaagatctt tatgttatct ctgaaaatga aaaggatggc cttttaagca cattttactg 240
ttttatacta ttatggcaac ttgtgt 266

<210> 533
<211> 289
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(289)
<223> n = A,T,C or G

<400> 533
actcagaagt cacttttaat atcancgaca gaaatatttc actaattcaa ctgaggcaaa 60
tttcctttct agacaaagga cctagaaatt gagcatgcaa aacatccatc cattcattca 120
ttcaaataat tagccaattt taccgtcatt taattccacc agaagcaaatt actagaatat 180
ctagaagtag tttgggttaa gaaacattta cattttaata ttgtgtaatg tcataaattt 240

ggggctaaaa taacaccagg tcaaatttga tccctttgta tgtgagggt 289

<210> 534
<211> 293
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(293)
<223> n = A,T,C or G

<400> 534
aaaataaaag gttctttaca agatgatacc ttaattacac tcccgcaaca cagccattat 60
tttattgtct anctccagtt atctgtattt tatgtaattg aattgacagg atggctgctg 120
cagaatgctg gttgacacag ggattattat actgctattt tccctgaat ttttttcctt 180
tgaattccaa ctgtggacct tttatatgtg ccttcacttt agctgtttgc cttaattctt 240
acagccttgc tctccggggn ggtaataaaa atgcaacact tggcattttt atg 293

<210> 535
<211> 408
<212> DNA
<213> Homo sapiens

<400> 535
actgaacac ttaaagagaa aaactctaaa taaagtcata gaggggatgg tagagatgac 60
cacagaaaat gaccacggag agtattatga agattgcaag attagacatt gatgatgtaa 120
attactccct ttctagataa aataatccat agatgtttat gaatcatatt tgtatgatta 180
ttgctgttac tattattttg acacattatt tattattatt gttgtcacta ttattaccat 240
taagatagca ggcgtaaaac tgtactgggt ccttcagtag tgagtatttc tcatagtgca 300
gctttattta tctccaggat gtttttgtgg ctgtatttga ttgatatgtg cttcttctga 360
ttcttgctaa tttccaacca tattgaataa atgtgatcaa gacaaaaa 408

<210> 536
<211> 184
<212> DNA
<213> Homo sapiens

<400> 536
acctctcatc aaggctctgc ctacaggcac attgtgatgt atctctgcac tgatcaccta 60
ggcatgtaa cttttttcta ggctctacct acgatggcat tgtgacataa ctctgcacta 120
atcatccacg tgatgtaact cttgtctagg atgtgcctaa attaactttt tgacgtaacc 180
ctgt 184

<210> 537
<211> 311
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(311)
<223> n = A,T,C or G

<400> 537
ccacagttgt atcatatagc atctntaaca tttcatctag gattatctag tatagatctt 60
actatatttg gggctatggt gtatacaatg ttaacaagaa catatcttct ctgcatatat 120
gtgtgaatta taaagaaaag catgagaatg actctaagtt caacaaacat ggggtgaatct 180

ctatgtgctc ccagtgtcct ggatgggctc cccagcaagc cattcctcct tcctgttctg 240
atattactat tcttttttac attgtgctaa ggaggacaaa aggtgagaga tgaaaaataa 300
gccttgccct t 311

<210> 538

<211> 302

<212> DNA

<213> Homo sapiens

<400> 538

aaaataaaaa agcaaaaact cttgtggtac ctagtcagat ggtagacgag ctgtctgctg 60
ccgcaggagc acctctatac aggacttaga agtagtatgt tattcctggt taagcaggca 120
ttgctttgcc ctggagcagc tattttaagc catctcagat tctgtctaaa ggggtttttt 180
gggaagacgt tttctttatc gccctgagaa gatctacccc agggagaatc tgagacatct 240
tgcctacttt tctttattag ctttctcctc attcatttct tttatacctt tccttttttg 300
gg 302

<210> 539

<211> 396

<212> DNA

<213> Homo sapiens

<400> 539

actgtttatt tgetccttct cttcatgcct gtggctggat gtcccacaac actataagaa 60
atataagtca agccctttgt gttaagcaag aactacagac tccatctttt caccctaaac 120
atgaatgacc aataaaaagc aagttattcc agaggaagaa gcagcccttg aaatgttaag 180
gcttaggctt gaaagggtgaa gagcaggaat tctctctttc aaatcctaga gcataaaccc 240
atgtgtggcc aagttagatc agccctcaag ggcacatgcc aagggcagag cagcccatgt 300
agacagcttc ggagggcatg ggggtgtagg gagttcgggg tagctcctca ttaactattt 360
gttggtgtgag taaaggggtg aggctcagtg gcaggt 396

<210> 540

<211> 634

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(634)

<223> n = A,T,C or G

<400> 540

ccaaaaacaa gatgaccaga tttgnttttna gcctgatgac cctacaggtc gtgctatgat 60
atggagtccat catgggtaaa gcaggaagag agtgggaaag agaaccaccc cactctgtct 120
tcatatttgc atttcattgt taacctccgg ctggaaatag aaagcattcc cttagagatg 180
aggataaaaag aaagtttcag attcaacagg gggaagaaaa tggagattta atcctaaaac 240
tgtgacttgg ggaggtcagt catttacagt tagtctgtg tctttcgact tctgtgatta 300
ttaacccccc tcaactaccct gtttcagatg catttggaat accaaagatt aaatccttga 360
cataagatct catttgcaga aagcagatta aagaccatca gaaggaaatt atttaggttg 420
taatgcacag gcaactgtga gaaactgttg tgccaaaaat agaattcctt ctagtttttc 480
ttgtttctcat ttgaaaggag aaaattccac tttgttttagc atttcaagct tttatgtatc 540
catcccatct aaaaactcct caaactccac ttgttcagtc tgaaatgcag ctccctgtcc 600
aagtgccttg gagaactcac agcagcacgc ctta 634

<210> 541

<211> 221

<212> DNA

<213> Homo sapiens

<400> 541
cacacaagca gcagagacca tgggaaccct ctcagcccct ccctgcacac agcgcatcaa 60
atggaagggg ctcctgctca cagcatcact tttaaacttc tggaacctgc ccaccactgc 120
ccaagtacag attgaagccg agccaaccaa agtttccgag gggaaggatg ttcttctact 180
tgtccacaat ttgccccaga atcttaccgg ctacatctgg t 221

<210> 542
<211> 287
<212> DNA
<213> Homo sapiens

<400> 542
cctcttctac tatggcagga gatgtggcgt gctgttgcaa agttttcacg tcatcgtttc 60
ctggctagtt catttcatta agtggctaca tcctaacata tgcatttggt caagggttgca 120
gaagaggact gaagattgac tgccaagcta gtttgggtga agttcactcc agcaagtctc 180
aggccacaat ggggtgggtt gggttggtt ccttttaact ttcttttgt tatttgcttt 240
tctcctccac ctgtgtggta tattttttaa gcagaatttt atttttt 287

<210> 543
<211> 274
<212> DNA
<213> Homo sapiens

<400> 543
acttgtgaaa cacagctggt cttctgttct gcagacacgc cttccctca gccacacca 60
ggcacttaag cacaagcaga gtgcacagct gtccactggg ccattgtggt gtgagcttca 120
gatgtgaag catttcccc agtgtatgtc ttgtatccga tatctaacgc tttaaattggc 180
tactttggtt tctgtctgta agttaagacc ttggatgtgg tttaattggt tgtcctcaaa 240
aggaataaaa cttttctgct gataagataa aaaa 274

<210> 544
<211> 307
<212> DNA
<213> Homo sapiens

<400> 544
ccagggtggt gtcttattgc accatactcc ttgcttcctg atgctgggca atgaggcaga 60
tagcactggg tgtgagaatg atcaaggatc tggaccccaa agaatagact ggatggaaag 120
acaaactgca caggcagatg tttgctcat aatagtcgta agtggagtcc tggaatttgg 180
acaagtgtctg ttgggatata gtcaacttat tctttgagta atgtgactaa aggaaaaaac 240
tttgactttg cccaggcatg aaattcttcc taatgtcaga acagagtgc acccagtcac 300
actgtgg 307

<210> 545
<211> 570
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(570)
<223> n = A,T,C or G

<400> 545
accttagaaa tttgcaacca cctccctgaa agtcttctcc cactttatta agtgcaatgt 60
ttatggtaaa tgtagaagca tcatgatgag gacgaagaga acgctgtcgt tcaggggagt 120
attttactac aaaattcagt agtgcaaadc ccttcgtata atagcctgca aagaccttca 180

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gtgtaactgg ngcaatgaac tcccgataa aatgaagcca tacattctcc agatcaactt 240
gcttcatgtg gatatcatca gttgggacat tttcataacc accagatata cggctatcat 300
gatgttttcc cccagacccat ttgccgtaat gttccatttc ttctaccaat tcatcacagg 360
ctttttcaga aaatatgggg aacaaaaaga catctggaca gggctgttca actatatttt 420
cagtgaaaat ctttgaataa tcacgggttta tatacttttc cttccagtcc acaggatttt 480
caaaaatctg ccagagggtca ttgttataat ggggaagtatt gtaattagca gtggataata 540
gccttccaaa ttcattgtcta ttagaaatgt 570

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<210> 546

<211> 589

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(589)

<223> n = A,T,C or G

<400> 546

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aaaaataactt tttaccaaag gtgctatttc tctgtaaaac actttttttt ggcaagttga 60
ctttattctt caattattat cattatatta ttgtttttta atattttatt ttcttgacta 120
ggtattaagc ttttgaatt atttttcagt agtcccacca cttcataggt ggaaggagtt 180
tggggttctt cctggtgcag gggctgaaat aaccagatg cccccaccct gccacatact 240
agatgcagcc catagttggc cccctagct tccagcagtc cactatctgc cagaggagca 300
agggtgcctt agaccgaagc caggggaaga agcatcttca taaaaaactt tcaagatcca 360
aacattaatt tgtttttatt tattctgaga agttgaggca aatcagtatt cccaaggatg 420
gcgacaaggg cagccaagca gggcttagga tatcccagcc taccaatatg ctcatcgac 480
taactaggag ggtgagttgg ccctgtctct tcttttttct ggacctcagt ttccttcagt 540
ggagcttggt aaaaatgcac tacnntttga tttgataagg tataaatct 589

```

<210> 547

<211> 293

<212> DNA

<213> Homo sapiens

<400> 547

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actcctatta ttgactgtag tcaatcaaac ataaaaaggt gaaagtaaaa ttttaattttt 60
tacccttatt ttactgacca atatggaagt tcttggtatc ttttaaggctg accttcctgg 120
tattgtgtaa tgattgaatg tatctaaact gtaataattt gaaactgaca aacataacct 180
tctcagactt acaaaactat gttctttcta aagatacaga tttttattat tttattttga 240
ctaggaagga tttataaata aatgtaatga aaaatctttg atcttaataa agt 293

```

<210> 548

<211> 98

<212> DNA

<213> Homo sapiens

<400> 548

```

aaacaaaggt tgagatgtaa aaggatttaa attgatgttg ctggactgtc atagaaatta 60
cacccaaaga ggtattttatc ttactttttt tttgtaca 98

```

<210> 549

<211> 121

<212> DNA

<213> Homo sapiens

<400> 549

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acatgcatat ttcaaagacc tgttaatggc gtccactttg gattcttaca tgaaacgatt 60

```

cagtgcacat tgtaagccta aggaccacgc aaaagggttt cccacatatt aagtattcag 120
t 121

<210> 550

<211> 509

<212> DNA

<213> Homo sapiens

<400> 550

acaatagtat acattttata atgatgaact tataatgatt aagggacatt tctataaaaa 60
tactacaata gttttatgca caacttccca ttaaaaatga gatttcttat ttgtttgtct 120
gtttttactc tgggagtaat actttttaaa ttacctttac atatatagtc actggcatac 180
tgagaatata caatgatcct ggaaattgca gtaacaaaag cacacaacga ttatagtaac 240
tataagatac aataaaaaca ataaatgtga aagtagattc atgaaaatgt attcctttaa 300
aatattgttt tcctacaggc ctattttaaca agatgtttca ttttactgta tattttgtag 360
ttaatatata tgttgctcta atcagattgc ttaaaagcat ttttattata tttatgttgt 420
tgaactaata tatgaaataa gtaaattgtag ctcccacaag gtaaaacttca ttggtaagat 480
tgcactgttc tgattatgta agcatttgt 509

<210> 551

<211> 427

<212> DNA

<213> Homo sapiens

<400> 551

accatggtta tatgattaat cttgggacaa agaattttat agaaattttt aaacatctgg 60
aaaagaagct taagttttat catccttttt tttctcgtga attcttaaag gattatgctt 120
taatgctgtt atctatctta ttgttcttga aaatacctgc attttttggt atcatgttca 180
accaacatca ttatgaaatt aattagattc ccatggccat aaaatggctt taaagaatat 240
atatatatatt ttaaagtagc ttgagaagca aattggcagg taatatttca tacctaaatt 300
aagactctga cttggattgt gaattataat gatatgcccc ttttcttata aaaacaaaaa 360
aaaaaataat gaaacacagt gaattttag agtgggggta ttgacatat ttacaggggt 420
ggagtgc 427

<210> 552

<211> 340

<212> DNA

<213> Homo sapiens

<400> 552

cctcaaggcg gtccaattat ccacttgacg attctacaga aagagtgttt caaaactgct 60
ctgtcaagag aaatggtcca ccgtgtgtgt ggaatgcagc catcacacat tagtttctga 120
gattgcttct gtcttggttt tatggggaga tatttccatt tctagcatag gcttcaaggc 180
gctctaaata tccgcttgga aatactacaa aaacagtgtt tcaaaaactgc tgtatccaaa 240
ggaagggtgcc actcgtgtag ttgaatgcac acatcacaaag gaagtttctg agaattcttc 300
tgtctagatt catacgaaga aatcccgttt ccaacgaagg 340

<210> 553

<211> 549

<212> DNA

<213> Homo sapiens

<400> 553

acttgagctg tgaggtcac ggaatcccga cacctgtcct catctggaac aaggtaaaaa 60
ggggtcacta tggagttcaa aggacagaac tcctgcctgg tgaccgggac aacctggcca 120
ttcagacccg ggggtgcccc gaaaagcatg aagtaactgg ctgggtgctg gtatctcctc 180
taagtaagga agatgctgga gaatatgagt gccatgcac caattcccaa ggacaggctt 240
cagcatcagc aaaaattaca gtggttgatg ccttacatga aataccagtg aaaaagggtg 300

aagggtgccga gctataaaacc tccagaatat tattagtctg catgggttaaa agtagtcatg 360
gataactaca ttacctgttc ttgcctaata agtttctttt aatccaatcc actaacactt 420
tagttatatt cactggtttt acacagagaa atacaaaata aagatcacac atcaagacta 480
tctacaaaaa tttattatat atttacagaa gaaaagcatg catatcatta aacaaataaa 540
atacttttt 549

<210> 554

<211> 321

<212> DNA

<213> Homo sapiens

<400> 554

acctaataat atgttaacat aaacataaca acacacatat ttttttcta ccccttggca 60
actgaaaatg aagttaccat tcctaggcca aattttttaga caaagctttc taaaaccatc 120
tttataaagt aaattcagat atgcttaca taaaaagaca taaaagattc atcctgagat 180
gaattctgag tcaataacta aaaaccattt ctaccagtgc atcactacca tgtaatccat 240
tctacgcaag ctctacaaat attgagtcaa atcctgtctg tcagaaaatg aagacccaat 300
aagtttgccg aagtattcag t 321

<210> 555

<211> 322

<212> DNA

<213> Homo sapiens

<400> 555

ctggatcccg agaatactgg aacaatagag ctcgacctta tctcttggct ctgtttctca 60
gtactttgaa gttataacta atctgcctga agacttctca tgatggaaaa tcagccaagg 120
actaagcttc catagaaata cactttgtat ctggacctca aaattatggg aacatttact 180
taaacggatg atcatagctg aaaataatga tactgtcaat ttgagatagc agaagtttca 240
cacatcaaag taaaagattt gcatatcatt atactaaatg caaatgagtc gcttaaccct 300
tgacaaggtc aaagaaaact tt 322

<210> 556

<211> 286

<212> DNA

<213> Homo sapiens

<400> 556

aaaaaatatg tatctaagaa tgttctaggg cactctggga acctataaag gcaggatattt 60
cgggccctcc tcttcaggaa tcttctgaa gacatggccc agtcgaaggc ccaggatggc 120
ttttgctgcy gccccgtggg gtaggaggga cagagagaca gggagagtca gcctccacat 180
tcagaggcat cacaagtaat ggcacaattc ttcggatgac tgcagaaaat agtgttttgt 240
agttcaacaa ctcaagacga agcttatttc tgaggataag ctcttt 286

<210> 557

<211> 459

<212> DNA

<213> Homo sapiens

<400> 557

acagaagatg aataataatg aaaaactgtg attttttgac tatcacatac attgtgttaa 60
aaaacaggta aatataatga ctattactgt taagaaagac aaggaggaaa actgtttcaa 120
tgttcagggt taaataactaa gcacaaaaat ataacaaatt ctgtgtctac aataattttt 180
gaagtgtata caagtgcatt gcaaatgagc tctttaaaat ttaaagtcca tttccccttt 240
agccaagcat atgtctacat ttatgatttc tttctcttat tttaaagtct cttctggttt 300
agttttttta aaagtttcat catggctgtc atcttgggaat ctagcctcca gctcaaagct 360
gagacttcac gcatacatat tctcctttct ggggtgcatct tcacctagtt tctccaagta 420
ttcagagtta aatagcacaa cttcttttat atgttcctt 459

<210> 558
<211> 303
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(303)
<223> n = A,T,C or G

<400> 558
aaaaaataaa aaacaagaca acaatttagt agaagtaccn ctgggaggga ggggaggga 60
aaaaggata tacaggggca ggngtattct ctgtacagag gtgcananaa aatttcacat 120
anccttanag aatgccttgt ggaaaaaaaa aaataggccc caatacttgt tactgccctt 180
tatcaaaact gtgtgcatga cctgcacaaa taaaatcaca aaacagtgtt gccacattct 240
tcaaggaaac aaagcaaaat ttagggggnt tcttttcct ctccttgta aaagtcattt 300
ttt 303

<210> 559
<211> 232
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(232)
<223> n = A,T,C or G

<400> 559
aaagcattta ttaagaattt actcaggcat gatggcccat acttgtaatc ccagctattg 60
ggaaggatga gatgggagga tggcttgagg ccagagggtt gagaccgacc agccaggga 120
acacagttag accccttctc aaaaaaaaaa aaaaaaaaag agagagtgtg tgattagaag 180
ctaaatagga aagttttgag cttcaagtca gngaggagta aaaaagattt tt 232

<210> 560
<211> 336
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(336)
<223> n = A,T,C or G

<400> 560
ctctgcaaaa ataannataa aaaaataaat aaaattttta aaataataaa attcactata 60
tacacatata aagaaataaa aagaagtctc agttgcagct atttgtcaaa attaatatcc 120
atttcttttt atatacgggtg aatattgcgc aattatagat ctggattttg aaccacttaa 180
tgaagcgga acaccagggtg ttttgagggtg ttggcattct tcgctgattt ggctgttccc 240
aatgtttaca ttatttaatc ttgcaaaaat ggttctgtgc acttggatgn gaaatgctgn 300
ccagntttat tttttttatg ttgntatcct tggatg 336

<210> 561
<211> 636
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(636)
<223> n = A,T,C or G

<400> 561
acattatggg ttttattgct ttcttttatg gtagacctgt taatggggaa aaaatacatc 60
aaatcaaata gaatcttata tctgtatgtt aaaatagagc acttacctga agtcagtggc 120
ctggatcata gccctggatc atttccagc ctgtcctgtg ctgtgtgacc ttggacaagg 180
cgcttcacat ctctgggcct ctatttctcc atttgtaaaa caagtggctg cagtagatga 240
tggctgagag cccttcctgt tcccagatgc cttgggtcaa agacccacc cctctgctgg 300
tcctgccaac gtgttggtgc tataagctgc ttcagatata aaattgggtt atctataatg 360
tttgttcatt taatagcttc taaaaggcct ttttggtata cagtgccttt tttctagttt 420
tatggacttg gttactgtaa taatgtcttg tttttagcca tgtaactaca aacagatatt 480
ctcttgatgt cttagtaaat ttgcatttga tatatcattg atgagatttt gttgttatgt 540
aatattcitt ggctacgcat ctgtccagca tcttattaac cataatactg ngatcattat 600
ttggaaatat gtcctatgga aagaataaaa gcatgt 636

<210> 562
<211> 708
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(708)
<223> n = A,T,C or G

<400> 562
acagtcacc ttttgatata tgccatgcct ttgatcaaag aacaggacat aaaaacaaag 60
tcacaatgac attccatagt aaatttgga tcagaactcc aaatgcaact tcgggctcgc 120
tggagaacaa ctaaggggca ccaaaccctc tgagggtttta cttaagggt cgctgtatgt 180
ttgccttga caaaaaggct acctaccacg tgctatccag taatatactt aaataagcca 240
atacttagat ctactgtaag gcagatgcta attataaggc attaagtaag caaatagtgc 300
cctcagctac tgcagaagaa aagtcocact gaggaaga aagtcttggt atttttaaag 360
gcaagtttcc aagtgtcttc atagtcttat cctctaattc cattaaatcc atactaggag 420
cgctcagtga ggttttcata gcttttgga atactttggt ctctgaactg taattagcaa 480
gaagtataaa cagaaacgct aaacgtcaa tgtttgctt gttacctgga ggactaaatg 540
tagatgtctt tagtatactt tgtatgttct taatattgga agataatttt gtgaatctgt 600
agattttatt ttttcagtct taccttaca atttcttttc tatgaataat agaggactta 660
cngcactctg ccatttggtta atgaaaggaa ggcngangat ttagaaag 708

<210> 563
<211> 290
<212> DNA
<213> Homo sapiens

<400> 563
ccagatgctc atccactttc agactttcat ctcttctgcc atctgccaaa gtcaacagag 60
ctttccggaa gtcaccagat gtttcggaac taatgtcatc tccaagactc ttcttgata 120
ctgtataata ggcttgagag atatccttca tttgcctgct tgcctggta gtttaagattt 180
caatcaaggc atcttcgttt gttcccgcc ccttcatgga tttcttttag tgctttgcac 240
caaagactgc tgggtggagtc actagggcc ccatgagatg ctcaaagtgg 290

<210> 564
<211> 530
<212> DNA
<213> Homo sapiens


```

<400> 564
accaccagat acttaaagct tcaaaaagac tgcccctacc accacaggag gaccagccta 60
accatacgct ccaaaaagatg gctgtgatag atcttgtgaa gcaattactg agcagatcaa 120
gatcttttggg aaggaacact aaagatggtt tgaatgaatt atagtccact ggcatttttag 180
tgtattttttt tttctttttta gaaacacaca tttctaaaaa tgtcatgtta cattcctgca 240
tgtccctttt gatagcatta gtggatccat tggatttctt ttttctttt gtgagacagc 300
ttttagtctt acctgaattt atgtgtgttt ttccgacagt ggtaataat tatattggtg 360
atgtagcagc aattgtgttg gcagggtttt catatattat tagtaattaa cactaactgt 420
tggaactgact tgtgtcgata gcgctcacgc aagcatgggt aacgtcccta aaacccgcg 480
gactttctgt aagaagtgtg gcaagcacca accccataaa gtgacacagt 530

```

```

<210> 565
<211> 450
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(450)
<223> n = A,T,C or G

```

```

<400> 565
ctgcttacgg aagcgctgnn tgactaggat gtgatttatt aacgaccaac ttctgttatt 60
gtgtgttaag tttttcatct gtgcatcaaa tcacaaaaag aataaataga gctttttcct 120
ttatcagtcct cttgggcaca gcaggtcctg aacaccctgc tctacaatgt tgcatcaaga 180
gttcaaacaa caaaataaaa aatattaaga ggaaatcccc atcctgtgac ttgagtccct 240
taagtctaca ggggctggtg acctcttttt gctaatagga aaatcacatt actacaaaat 300
ggggagaaaa ctgtttgcct gtggtagaca cctgcacgca taggattgaa gacagtacag 360
gctgctgtac agagaagcgc ctctcacatc tgaactgcat actgagcggg caagtcgggt 420
gtaagttcag taaaaccctc tgatgatgcc 450

```

```

<210> 566
<211> 563
<212> DNA
<213> Homo sapiens

```

```

<400> 566
acttgagctg tgaggtcacg ggaatcccga cacctgtcct catctggaac aaggtaaaaa 60
ggggtcacta tggagttcaa aggacagaac tcctgcctgg tgaccgggac aacctggcca 120
ttcagaccgg ggggtggcca gaaaagcatg aagtaactgg ctgggtgctg gtatctcctc 180
taagtaagga agatgctgga gaatatgagt gccatgcatc caattcccaa ggacaggctt 240
cagcatcagc aaaaattaca gtggttgatg ccttacatga aataccagtg aaaaaagggtg 300
aagggtgccg gctataaacc tccagaatat tattagtctg catgggttaa agtagtcatg 360
gataactaca ttacctgttc ttgcctaata agtttctttt aatccaatcc actaacactt 420
tagttatatt cactggtttt acacagagaa atacaaaata aagatcacac atcaagacta 480
tctacaaaaa ttattatat atttacagaa gaaaagcatg catatcatta aacaaataaa 540
atacttttta tcacaaaaaa aaa 563

```

```

<210> 567
<211> 424
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(424)
<223> n = A,T,C or G

```

<400> 567

```
ccagtgagca aattgaaaac caactgaaag caaatccaaa tgaggaagat ttttaataaag 60
gaataccctt ctccatagca ggtgcaatgc tgactgctca aggcgtgcgt gcgcgcgcac 120
acacacacac acacacacac atacatactc tcacacacnc atctttccaa ttaaaactgca 180
ggtagaatga gatttttgtgt tattcaaaaa atttgtaagt gatcaaaaanc actgctatgg 240
aatgcctgtt tatctgcctt tgnctctggt aaaaatctcat aaaaatacat tcaacaggaa 300
aacatanatt gtatgtgtat aaatatatat gtatatatat atattatata cacatgcaca 360
caaatacttt tgttttttga agcataagat agttacataa atactcctat aattgctaaa 420
gttt 424
```

<210> 568

<211> 392

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(392)

<223> n = A,T,C or G

<400> 568

```
actggctcac tcagagagga cgtccttcaa ctatgccatg aaggaggctg ctgcagcggc 60
tttgaagaag aaaggatggg aggtgggtga gtcggaacctc tatgccatga acttcaatcc 120
catcatttcc agaaaggaca tcacaggtaa actgaaggac cctgcgaact ttcagtatcc 180
tgccgagtct gttctggctt ataaagaagg ccatctgagc ccagatattg tgggttganc 240
aaaagaaaagc ttggaagccn caagaacctt gtgatattcc agttccccct gcantgggtt 300
tggaagtcc ctgcencttt gaaagctggt ttgaagcgaa tgttcatagg aaagtttgct 360
taccacttac cctgcccctg gtangacaaa ag 392
```

<210> 569

<211> 559

<212> DNA

<213> Homo sapiens

<400> 569

```
aaagagattt attaaatcat cttatcacaa agatggaaac atatacaaac tagaaacatg 60
caaccatcat cttccacagt caagtcacaa tgtcaaatat ttttcttgcc tctgcagatg 120
aaaagttcag atcttatacc caactactta ctaccccgga atatttaagt cagtcttcc 180
gaaagtactc agggtagcaa gtaacaaaat gcaaacgatt atataaagaa agtgagttta 240
aaaaggaaac tatgtggcaa gtaccctctt tcccttccca cccccaatt aaaggcaaac 300
aatggcactt tgctcttgct taacctagat tgtcttcaaa aactattaaa atgtaaaaga 360
cttaacaaaa aaacaaaaag acgtttaaca gatgtcaaaa agctccttag tgtttgaaaa 420
taaagtctta aacaaaagac aacatatttt atatcaaaca agtttgaaga gccctgaatt 480
gcagcattct gtaacataaa caaacaaaaa gctggtatag gatttattgg caaaggcaga 540
atttcttcaa gcagggtaa 559
```

<210> 570

<211> 368

<212> DNA

<213> Homo sapiens

<400> 570

```
agccgcgcgt ggatgctaag tccgatgtca ccaaccagct tgtagatttt cagtggaaac 60
tggtatggc tgtgagctca gacacttgca gatctcttaa gtatccttac gttgcagtga 120
tgctaaaagt ggcagatcat tcaggccaag taaagaccaa gtgctttgaa atgacgattc 180
cacagtttca gaatttctac agacagttca aggaaattgc tgcagttatt gaaacgggtg 240
gaagacggat tctttggttg ataaattgct atcattctaa agtcatggac ttcactttcg 300
```

gcaacaaaaac taaataagga tggaacattt attgaatgaa aaatgcactt ttgtttttcc 360
attttttt 368

<210> 571
<211> 261
<212> DNA
<213> Homo sapiens

<400> 571
acacgattgc tgcttccgct atatttgtga tataggaatt aagaggatac acacgtttgt 60
ttcttcgtgc ctgttttatg tgcacacatt aggcatgag acttcaagct tttctttttt 120
tgtccacgta tctttgggtc tttgataaag aaaagaatcc ctgttcattg taagcacttt 180
tacggggctg gtggggaggg gtgctctgct ggtcttcaat taccaagaat tctccaaaaac 240
aattttctgc aggatgattg t 261

<210> 572
<211> 488
<212> DNA
<213> Homo sapiens

<400> 572
ctctcagctc tgggcgcacg gccagcttc cttcaaaatg tctactgttc acgaaatcct 60
gtgcaagctc agcttgaggg gtgatcactc tacaccccca agtgcataat ggtctgtcaa 120
agcctatact aactttgatg ctgagcggga tgctttgaac attgaaacag ccatcaagac 180
caaagggtgt gatgaggtca ccattgtcaa cttttgacc aaccgcagca atgcacagag 240
acaggatatt gccttcgcct accagagaag gaccaaaaaag gaacttgcac cagcactgaa 300
gtcagcctta tctggccacc tggagacggt gattttgggc ctattgaaga cacctgctca 360
gtatgacgct tctgagctaa aagcttccat gaaggggctg ggaaccgacg aggactctct 420
cattgagatc atctgctcca gaaccaacca ggagctgcag gaaattaaca gagtctacaa 480
ggaaatgt 488

<210> 573
<211> 619
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(619)
<223> n = A,T,C or G

<400> 573
actttactga aagaacacta ntgttctttc ctttccgttg tgaaaaaagt tgtttctgag 60
gaattgaaac ccagagaagat aactacaaca aaaacatgtt aatttttttt taaaaatgat 120
gattcaaagg cagatttgaa gggaagtaat atttaggtgg cagaagaagg caaatgcagc 180
ctctgaaggg aactgttcta attattacct aaaaaataaa gttacacaac tatattcaag 240
gacatgagat aaagcactgc ttgaaaacca gaatgactga acagttaggt gaaaaggac 300
agctgaaata ggaaggggaa atggactgaa gaataatttg aatcgggaca gtgatccatc 360
agtctagat gcttctggta tgtaaatata ttgaatcaca ttgtttcctt tcttctgaaa 420
tctcaaagga gaattctcac agcactacat taaggttgcc attttgtag gattcaaaa 480
ttcaatccag tagccatcag gatcttgaat aaatgccagg cctttcattt taccatcatc 540
aggtttcttc acaaatttga ctccagtctt caaccttttc aagcctgac atcaggaaca 600
caattccata tgaccgatc 619

<210> 574
<211> 202
<212> DNA
<213> Homo sapiens

<400> 574

```
acatccaccc cactatttct tcacataccg aatcaggatt gaaatgtcaa aagatgcact 60
tcttgagaag gcctgtcagt tggacagtcg ctattggaga ataacaaatg ctaagggtga 120
cgtggaagaa gttcaaggac ctggagtagt tggatgaattt ccaatcatca gccaggtcg 180
ggtatatgaa tacacaagct gt 202
```

<210> 575

<211> 311

<212> DNA

<213> Homo sapiens

<400> 575

```
ccacagttgt atcatatagc atctctaaca tttcatctag gattatctag tatagatctt 60
actatatitg ggactatgtt gtatacaatg ttaacaagaa catatcttct ctgcatatat 120
gtgtgaatta taaagaaaag catgagaatg actctaagtt caacaaacat gggatgaatct 180
ctatgtgctc ccagtgtcct ggatgggctc cccagcaagc cattcctcct tcctgttctg 240
atattactat tcttttttac attgtgctaa ggaggacaaa agatgagaga tgaaaataaa 300
gctttgcctt t 311
```

<210> 576

<211> 134

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(134)

<223> n = A,T,C or G

<400> 576

```
ttttttgcat caaaaagctt tatttccatt tggnccaagg ctgttagga tagttaaaaa 60
agctgcctat tggtggagg ganaggctta ggcaaaancc ctattacttt gcaagggggc 120
cttcaaaagt cgct 134
```

<210> 577

<211> 488

<212> DNA

<213> Homo sapiens

<400> 577

```
ctgatcagtg ggcctccaag gaggggctgt aaaatggagg ccattgtgtg agcctatcag 60
agttgctgca aacctgaccc ctgctcagta aagcacttgc aaccgtctgt tatgctgtga 120
cacatggccc ctccccctgc caggagcttt ggacctaata caagcatccc ttgcccaga 180
aagaagatgg gggaggaggc agtaataaaa agattgaagt attttgctgg aataagttca 240
aattcttctg aactcaaact gaggaatttc acctgtaaac ctgagtcgta cagaaagctg 300
cctggtatat ccaaaagctt tttattcctc ctgctcatat tgtgattctg cctttgggga 360
cttttcttaa accttcagtt atgatttttt tttcatacac ttattggaac tctgcttgat 420
ttttgcctct tccagtcttc ctgacacttt aattaccaac ctgttaccta ctttgacttt 480
ttgcattt 488
```

<210> 578

<211> 476

<212> DNA

<213> Homo sapiens

<400> 578

```
accatgcatt aagagcttcc tgattgagat tcagtgcac agccgtgtct attccatcta 60
```

```
cgccacacc gtctgtgacc cactctttga agctgttggg aaaatattca gcaatgtccg 120
catcaacttg cagaaagaaa tataaatgac atttcaagga tagaagtata cctgattttt 180
ttccttttaa ttttcctggg gccaatttca agttccaagt tgctaataca gcaacaattt 240
atgaattgaa ttatcttggg tgaaaataaa aagatcactt tctcagtttt cataagtatt 300
atgtctcttc tgagctattt catctatttt tggcagctctg aattttttaa acccatttaa 360
atttttttcc ttaccttttt atttgcatgt ggatcaacca tcgctttatt ggctgagata 420
tgaacatatt gttgaaagggt aatttgagag aaatatgaag aactgaggaa aaaaaa 476
```

<210> 579

<211> 246

<212> DNA

<213> Homo sapiens

<400> 579

```
ctgggtgctca ctgagatggt aggttttctt attttcctgc tacatctgca caagctacat 60
ctagaatgaa gccaccaatt tcaatgtgac caggcaatgg cagccagcac tgccctacac 120
tggtttgatt ctgattccct aattctggcc actgcaggtg atgagtaagg gtggggatca 180
gggaggaaagt ccagaagcca gtctttgtct ccctttcctg cttatatatta agtgcctatt 240
tacatg 246
```

<210> 580

<211> 615

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(615)

<223> n = A,T,C or G

<400> 580

```
gtcttcacag taataactaa tgggtggatcc taagggtgaaa ttatttcctt caaaatagnc 60
atgaactgna ttcccaggag ggncacagtc cctacttttg canatgggaa agggaggtgc 120
ccagggtgtg tcctctagac actgggtccg attgctgccc ttgaggatgt agtgggtcatt 180
gcacataaac gtgattttgt cacttacatt cacaggccct gaagaactga actctccatt 240
caccagcaca ggatcaggac agtggcccaa gcggcactca gtagtggtgt tatccactc 300
cttagaggca ttgcaaaaaa ggggtcttctt tcctaccagg tggtagccct tgatacaaac 360
gtaagtcccc agaactctgtc cttccacctc ctttgcgaca aatatgctat tgtccactgg 420
aggaagctct ggacagtgtc catctgaagc agaaactcgc cagcaacca taagacagca 480
cgcacaccaa aaaaacatct ggtgatcaaa gtccctctccc caggctggaa ttcaccagc 540
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<210> 581

<211> 576

<212> DNA

<213> Homo sapiens

<400> 581

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gagttctggg caaagaaaga aagtttagaa gctgagacac aaagggttgg gagctgatga 180
aactcacaaa tgatggtagg aagaagctct cgacaatacc cgttggcaag gagtctgcct 240
ccatgctgca gtgttcgagt ggattgtagg tgcaagatgg aaaggattgt aggtgcaagc 300
tgtccagaga aaagagtcct tgttccagcc ctattctgcc actcctgaca gggtagacct 360
gggtatttgc aatattcctt tgggcctctg cttctctcac ctaaaaaaag agaattagat 420
tatattgggtg gttctcagca agagaaggag tatgtgtcca atgctgcctt cccatgaatc 480
tgtctccagc ttatgaatca gtgggcagga taaactgaaa actcccattt acgtgtctga 540
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atcgagtgag acaaaatttt agtccaaata acaagt

576

<210> 582

<211> 939

<212> DNA

<213> Homo sapiens

<400> 582

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cagtgtgccc aggatatgaa ccatgaatac atgtcctggt atcgacaaga cccaggcatg 180
gggctgaggg tgattcatta ctcagttggt gctgggtatca ctgaccaagg agaagtcacc 240
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gtccctccc agacatctgt gtacttctgt gccagcagtt actcagtcgg ggagggcggg 360
gattcacccc tccactttgg gaatgggacc aggtcactg tgacagagga cctgaacaag 420
gtgttccac ccgaggtgc tgtgtttgag ccatcagaag cagagatctc ccacacccaa 480
aaggceacac tgggtgtcct ggccacaggc ttcttccctg accacgtgga gctgagctgg 540
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accatcctct atgagatcct gctagggaa gcccacctgt atgctgtgct ggtcagcgcc 900
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<210> 583

<211> 828

<212> DNA

<213> Homo sapiens

<400> 583

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aactgcacgt acacagccac aggataccct tcccttttct ggtatgtcca atatcctgga 180
gaaggtctac agctctcct gaaagccacg aaggctgatg acaagggaag caacaaagg 240
tttgaagcca cataccgtaa agaaaccact tctttccact tggagaaagg ctcagttcaa 300
gtgtcagact cagcgggtga ctctgtgct ccgaaccctt ctcttcaggg cggatctgaa 360
aagctgggtct ttggaaagg aacgaaactg acagtaaacc catatatcca gaaccctgac 420
cctgccgtgt accagctgag agactctaaa tccagtgaac agtctgtctg cctattcacc 480
gattttgatt ctcaacaaa tgtgtcaca agtaaggatt ctgatgtgta tatcacagac 540
aaaactgtgc tagacatgag gtctatggac ttcaagagca acagtgtgtt ggctggagc 600
aacaatatctg actttgcatg tgcaaacgcc ttcaacaaca gcattattcc agaagacacc 660
ttcttcccc gcccagaaa ttcctgtgat gtcaagctgg tcgagaaaag ctttgaaaca 720
gatacgaacc taaactttca aaacctgtca gtgattgggt tccgaatcct cctcctgaaa 780
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<210> 584

<211> 275

<212> PRT

<213> Homo sapiens

<400> 584

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Arg Thr Arg Gly Asn Ser Val Thr Gln Met Glu Gly Pro Val Thr Leu

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20 25 30
 Ser Glu Glu Ala Phe Leu Thr Ile Asn Cys Thr Tyr Thr Ala Thr Gly
 35 40 45
 Tyr Pro Ser Leu Phe Trp Tyr Val Gln Tyr Pro Gly Glu Gly Leu Gln
 50 55 60
 Leu Leu Leu Lys Ala Thr Lys Ala Asp Asp Lys Gly Ser Asn Lys Gly
 65 70 75 80
 Phe Glu Ala Thr Tyr Arg Lys Glu Thr Thr Ser Phe His Leu Glu Lys
 85 90 95
 Gly Ser Val Gln Val Ser Asp Ser Ala Val Tyr Phe Cys Ala Pro Asn
 100 105 110
 Pro Ser Leu Gln Gly Gly Ser Glu Lys Leu Val Phe Gly Lys Gly Thr
 115 120 125
 Lys Leu Thr Val Asn Pro Tyr Ile Gln Asn Pro Asp Pro Ala Val Tyr
 130 135 140
 Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr
 145 150 155 160
 Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val
 165 170 175
 Tyr Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys
 180 185 190
 Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala
 195 200 205
 Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser
 210 215 220
 Pro Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr
 225 230 235 240
 Asp Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile
 245 250 255
 Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu
 260 265 270
 Trp Ser Ser
 275

<210> 585

<211> 312

<212> PRT

<213> Homo sapiens

<400> 585

Met Ser Ile Gly Leu Leu Cys Cys Ala Ala Leu Ser Leu Leu Trp Ala
 5 10 15
 Gly Pro Val Asn Ala Gly Val Thr Gln Thr Pro Lys Phe Gln Val Leu
 20 25 30
 Lys Thr Gly Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His
 35 40 45
 Glu Tyr Met Ser Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu
 50 55 60
 Ile His Tyr Ser Val Gly Ala Gly Ile Thr Asp Gln Gly Glu Val Pro
 65 70 75 80
 Asn Gly Tyr Asn Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg
 85 90 95
 Leu Leu Ser Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser
 100 105 110
 Ser Tyr Ser Val Gly Glu Gly Gly Asp Ser Pro Leu His Phe Gly Asn
 115 120 125
 Gly Thr Arg Leu Thr Val Thr Glu Asp Leu Asn Lys Val Phe Pro Pro

238

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      130              135              140
Glu Val Ala Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln
145              150              155              160
Lys Ala Thr Leu Val Cys Leu Ala Thr Gly Phe Phe Pro Asp His Val
      165              170              175
Glu Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser
      180              185              190
Thr Asp Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg
      195              200              205
Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn
      210              215              220
Pro Arg Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu
225              230              235              240
Asn Asp Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val
      245              250              255
Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Val Ser
      260              265              270
Tyr Gln Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu
      275              280              285
Gly Lys Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met
      290              295              300
Ala Met Val Lys Arg Lys Asp Phe
305              310

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<210> 586

<211> 97

<212> PRT

<213> Homo sapiens

<400> 586

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Glu Val Glu Val Ser Arg Asp His Ala Ser Leu Gly Asp Ser Glu Thr
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Leu Ser Gln Thr Glu Leu Arg Lys Lys Glu Arg Lys Lys Lys Arg Glu
      20              25              30
Arg Lys Phe Gln Ala Asn Cys Gly Ile Asp Phe Ile Ile Phe Trp Ile
      35              40              45
Phe Trp Ile Leu Leu Phe Ser His His Trp Ile Gln Glu Ser Leu Leu
      50              55              60
Cys Pro Pro Ser Pro Lys Glu Val Thr Cys Arg Glu Met Leu Thr Gly
      65              70              75              80
Gly Cys Leu Pro Trp Ala Thr Arg Ser His Leu Gly Arg Arg Lys Cys
      85              90              95
Ser

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<210> 587

<211> 16

<212> PRT

<213> Homo sapiens

<400> 587

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Phe Gln Ala Asn Cys Gly Ile Asp Phe Ile Ile Phe Trp Ile Phe Trp
1              5              10              15

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